Full wwPDB EM Validation Report ⓘ

Dec 31, 2024 – 11:06 PM EST

PDB ID	:	8PKH
EMDB ID	:	EMD-17739
Title	:	Borrelia bacteriophage BB1 procapsid, fivefold-symmetrized outer shell
Authors	:	Rumnieks, J.; Fuzik, T.; Tars, K.
Deposited on	:	2023-06-26
Resolution	:	3.35 Å(reported)
Based on initial model	:	.

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

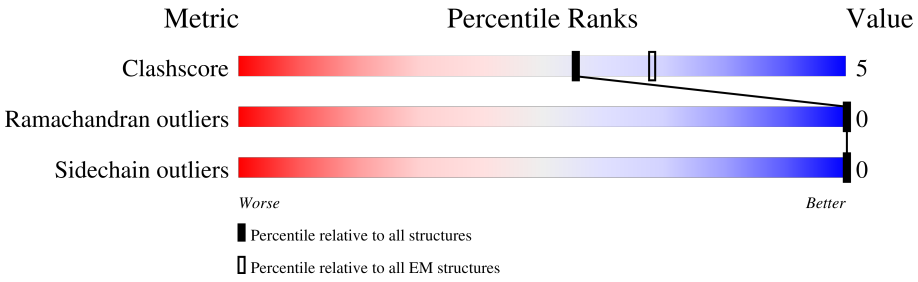
EMDB validation analysis	:	0.0.1.dev113
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.35 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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

Mol	Chain	Length	Quality of chain
1	AA	319	85% 12% •
1	AB	319	85% 13% •
1	AC	319	84% 14% •
1	AD	319	85% 12% •
1	AE	319	86% 12% •
1	AF	319	83% 15% •
1	AG	319	81% 16% •
1	AH	319	82% 16% •

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Mol	Chain	Length	Quality of chain
1	AI	319	87% 12%
1	AJ	319	82% 15%
1	AK	319	83% 15%
1	AL	319	84% 14%
1	AM	319	83% 13%
1	AN	319	83% 15%
1	AO	319	83% 15%
1	AP	319	81% 16%
1	AQ	319	86% 12%
1	AR	319	84% 14%
1	AS	319	78% 20%
1	AT	319	81% 17%
1	AU	319	81% 18%
1	AV	319	79% 19%
1	AW	319	85% 13%
1	AX	319	81% 18%
1	AY	319	81% 17%
1	AZ	319	82% 16%
1	BA	319	79% 19%
1	BB	319	85% 13%
1	BC	319	83% 11% 6%
1	BD	319	85% 12%
1	BE	319	87% 11%
1	BF	319	87% 12%
1	BG	319	84% 13%

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Mol	Chain	Length	Quality of chain
1	BH	319	85% 13%
1	BI	319	86% 12%
1	BJ	319	83% 14%
1	BK	319	83% 15%
1	BL	319	87% 11%
1	BM	319	85% 13%
1	BN	319	88% 10%
1	BO	319	85% 13%
1	BP	319	82% 15%
1	BQ	319	86% 12%
1	BR	319	84% 14%
1	BS	319	82% 16%
1	BT	319	81% 13% 7%
1	BU	319	82% 17%
1	BV	319	83% 15%
1	BW	319	87% 11%
1	BX	319	82% 11% 7%
1	BY	319	78% 20%
1	BZ	319	83% 15%
1	CA	319	81% 18%
1	CB	319	82% 16%
1	CC	319	85% 13%
1	CD	319	84% 14%
1	CE	319	84% 14%
1	CF	319	80% 18%

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Mol	Chain	Length	Quality of chain
1	CG	319	82% 16%
1	CH	319	82% 17%
1	CI	319	87% 11%
1	CJ	319	86% 12%
1	CK	319	80% 18%
1	CL	319	80% 18%
1	CM	319	82% 16%
1	CN	319	84% 14%
1	CO	319	79% 19%
1	CP	319	81% 17%
1	CQ	319	84% 14%
1	CR	319	85% 13%
1	CS	319	83% 15%
1	CT	319	83% 15%
1	CU	319	78% 20%
1	CV	319	81% 18%
1	CW	319	82% 17%
1	CX	319	86% 12%
1	CY	319	86% 12%
1	CZ	319	82% 16%
1	DA	319	81% 17%
1	DB	319	84% 14%
1	DC	319	83% 15%
1	DD	319	80% 18%
1	DE	319	82% 16%

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Mol	Chain	Length	Quality of chain
2	DF	185	78% 6% 16%
2	DG	185	75% 8% 18%
2	DH	185	75% 8% 17%
2	DI	185	77% 5% 17%
2	DJ	185	72% 11% 17%
2	DK	185	72% 11% 17%
2	DL	185	74% 9% 17%
2	DM	185	73% 10% 17%
2	DN	185	72% 11% 17%
2	DO	185	74% 9% 17%
2	DP	185	69% 14% 17%
2	DQ	185	73% 9% 18%
2	DR	185	75% 9% 17%
2	DS	185	81% 10% 9%
2	DT	185	65% 18% 17%
2	DU	185	71% 11% 17%
2	DV	185	70% 12% 17%
2	DW	185	71% 11% 17%
2	DX	185	75% 10% 15%
2	DY	185	69% 13% 18%
2	DZ	185	73% 10% 17%
2	EA	185	57% 8% 35%
2	EB	185	72% 13% 15%
2	EC	185	73% 10% 17%
2	ED	185	79% 7% 14%

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Mol	Chain	Length	Quality of chain
2	EE	185	75% 10% 15%
2	EF	185	72% 11% 17%
2	EG	185	82% 13% 5%
2	EH	185	72% 10% 17%
2	EI	185	75% 10% 15%
2	EJ	185	83% 7% 10%
2	EK	185	78% 13% 9%
2	EL	185	73% 9% 18%
2	EM	185	68% 16% 17%
2	EN	185	70% 13% 17%
2	EO	185	82% 10% 8%
2	EP	185	68% 15% 17%
2	EQ	185	77% 8% 15%
2	ER	185	68% 14% 18%
2	ES	185	74% 10% 17%
2	ET	185	69% 14% 17%
2	EU	185	74% 12% 15%
2	EV	185	69% 12% 18%
2	EW	185	73% 10% 17%
2	EX	185	72% 11% 17%
2	EY	185	76% 10% 15%
2	EZ	185	71% 10% 18%
2	FA	185	74% 10% 17%
2	FB	185	70% 12% 17%
2	FC	185	76% 10% 15%

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Mol	Chain	Length	Quality of chain
2	FD	185	68% 14% 18%
2	FE	185	72% 11% 17%
2	FF	185	72% 11% 17%
2	FG	185	73% 12% 15%
2	FH	185	69% 12% 18%
2	FI	185	74% 9% 17%
3	FJ	254	55% 9% 37%
4	FK	190	71% 9% 20%
4	FL	190	70% 10% 20%
4	FM	190	72% 9% 19%
4	FN	190	68% 12% 20%
4	FO	190	71% 12% 18%
4	FP	190	68% 12% 20%
4	FQ	190	75% 15% 10%
4	FR	190	5% 77% 13% 10%
4	FS	190	74% 16% 10%
4	FT	190	67% 8% 24%
4	FU	190	69% 11% 21%
4	FV	190	71% 10% 19%
4	FW	190	66% 15% 19%
4	FX	190	71% 9% 21%
4	FY	190	68% 11% 21%
4	FZ	190	66% 14% 20%
4	GA	190	77% 13% 10%
4	GB	190	77% 13% 10%

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Mol	Chain	Length	Quality of chain
4	GC	190	
4	GD	190	
4	GE	190	
4	GF	190	
4	GG	190	
4	GH	190	
4	GI	190	
4	GJ	190	
5	GK	230	
5	GL	230	
5	GM	230	
5	GN	230	
5	GO	230	
5	GP	230	
5	GQ	230	
5	GR	230	
5	GS	230	
5	GT	230	
5	GU	230	
5	GV	230	
5	GW	230	
5	GX	230	
5	GY	230	
5	GZ	230	
5	HA	230	

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Mol	Chain	Length	Quality of chain
5	HB	230	14% 84%
5	HC	230	13% 84%
5	HD	230	11% 87%
5	HE	230	15% 84%
5	HF	230	13% 84%
5	HG	230	16% 84%
5	HH	230	11% 87%
5	HI	230	11% 87%
5	HJ	230	10% 87%
5	HK	230	10% 87%
5	HL	230	15% 84%
5	HM	230	12% 87%
5	HN	230	15% 84%
5	HO	230	16% 84%
5	HP	230	16% 84%
5	HQ	230	15% 84%
5	HR	230	15% 84%
5	HS	230	16% 84%
5	HT	230	16% 84%
5	HU	230	16% 84%
5	HV	230	14% 84%
5	HW	230	12% 88%
5	HX	230	16% 84%
5	HY	230	15% 84%
5	HZ	230	15% 84%

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Mol	Chain	Length	Quality of chain
5	IA	230	15% 84%
5	IB	230	11% 87%
5	IC	230	14% 84%
5	ID	230	13% 87%
5	IE	230	15% 84%
5	IF	230	14% 84%
5	IG	230	16% 84%
5	IH	230	11% 87%
5	II	230	12% 87%
5	IJ	230	12% 87%
5	IK	230	12% 87%
5	IL	230	16% 83%
5	IM	230	16% 84%
5	IN	230	15% 84%
5	IO	230	17% 83%
5	IP	230	15% 84%
5	IQ	230	15% 84%
5	IR	230	16% 83%
5	IS	230	15% 84%
5	IT	230	16% 84%
5	IU	230	17% 83%
5	IV	230	15% 84%
5	IW	230	16% 84%
5	IX	230	16% 84%
5	IY	230	17% 83%

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Mol	Chain	Length	Quality of chain
5	IZ	230	14% 84%
5	JA	230	16% 83%
5	JB	230	16% 84%
5	JC	230	16% 84%
5	JD	230	17% 83%
5	JE	230	15% 84%
5	JF	230	15% 84%
5	JG	230	15% 83%
5	JH	230	15% 84%
5	JI	230	15% 84%
5	JJ	230	17% 83%
5	JK	230	14% 84%
5	JL	230	15% 84%
5	JM	230	15% 84%
5	JN	230	16% 83%
5	JO	230	14% 84%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 333778 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 Major capsid protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	309	Total	C	N	O	S	0	0
			2488	1604	400	475	9		
1	AB	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	AC	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	AD	309	Total	C	N	O	S	0	0
			2488	1604	400	475	9		
1	AE	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	AF	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	AG	309	Total	C	N	O	S	0	0
			2488	1604	400	475	9		
1	AH	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	AI	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	AJ	309	Total	C	N	O	S	0	0
			2488	1604	400	475	9		
1	AK	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	AL	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	AM	309	Total	C	N	O	S	0	0
			2488	1604	400	475	9		
1	AN	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	AO	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	AP	309	Total	C	N	O	S	0	0
			2488	1604	400	475	9		
1	AQ	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	AR	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	AS	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	AT	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	AU	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	AV	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	AW	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	AX	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	AY	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	AZ	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	BA	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	BB	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	BC	300	Total	C	N	O	S	0	0
			2405	1549	390	457	9		
1	BD	309	Total	C	N	O	S	0	0
			2488	1604	400	475	9		
1	BE	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	BF	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	BG	309	Total	C	N	O	S	0	0
			2488	1604	400	475	9		
1	BH	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	BI	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	BJ	309	Total	C	N	O	S	0	0
			2488	1604	400	475	9		
1	BK	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	BL	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	BM	311	Total	C	N	O	S	0	0
			2505	1614	402	479	10		
1	BN	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	BO	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	BP	309	Total	C	N	O	S	0	0
			2488	1604	400	475	9		
1	BQ	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	BR	311	Total	C	N	O	S	0	0
			2505	1614	402	479	10		
1	BS	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	BT	297	Total	C	N	O	S	0	0
			2383	1532	385	457	9		
1	BU	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	BV	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	BW	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	BX	297	Total	C	N	O	S	0	0
			2383	1532	385	457	9		
1	BY	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	BZ	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CA	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CB	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CC	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CD	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CE	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CF	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CG	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	CH	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CI	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CJ	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CK	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CL	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CM	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CN	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CO	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CP	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CQ	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CR	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CS	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CT	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CU	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CV	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CW	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CX	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CY	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	CZ	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	DA	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	DB	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	DC	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	DD	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		
1	DE	313	Total	C	N	O	S	0	0
			2510	1616	404	481	9		

- Molecule 2 is a protein called Decorator protein P03.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	DF	155	Total	C	N	O	S	0	0
			1178	742	197	235	4		
2	DG	152	Total	C	N	O	S	0	0
			1160	730	194	232	4		
2	DH	154	Total	C	N	O	S	0	0
			1173	739	196	234	4		
2	DI	153	Total	C	N	O	S	0	0
			1165	733	195	233	4		
2	DJ	154	Total	C	N	O	S	0	0
			1173	739	196	234	4		
2	DK	153	Total	C	N	O	S	0	0
			1165	733	195	233	4		
2	DL	154	Total	C	N	O	S	0	0
			1173	739	196	234	4		
2	DM	154	Total	C	N	O	S	0	0
			1170	736	196	234	4		
2	DN	154	Total	C	N	O	S	0	0
			1173	739	196	234	4		
2	DO	153	Total	C	N	O	S	0	0
			1165	733	195	233	4		
2	DP	153	Total	C	N	O	S	0	0
			1165	733	195	233	4		
2	DQ	152	Total	C	N	O	S	0	0
			1160	730	194	232	4		
2	DR	154	Total	C	N	O	S	0	0
			1173	739	196	234	4		
2	DS	168	Total	C	N	O	S	0	0
			1288	813	215	256	4		
2	DT	154	Total	C	N	O	S	0	0
			1173	739	196	234	4		
2	DU	153	Total	C	N	O	S	0	0
			1161	730	194	233	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	DV	153	Total	C	N	O	S	0	0
			1165	733	195	233	4		
2	DW	153	Total	C	N	O	S	0	0
			1161	730	194	233	4		
2	DX	158	Total	C	N	O	S	0	0
			1198	750	202	242	4		
2	DY	151	Total	C	N	O	S	0	0
			1148	721	192	231	4		
2	DZ	154	Total	C	N	O	S	0	0
			1173	739	196	234	4		
2	EA	120	Total	C	N	O	S	0	0
			917	584	151	180	2		
2	EB	158	Total	C	N	O	S	0	0
			1198	750	202	242	4		
2	EC	153	Total	C	N	O	S	0	0
			1164	733	194	233	4		
2	ED	160	Total	C	N	O	S	0	0
			1211	759	204	244	4		
2	EE	158	Total	C	N	O	S	0	0
			1194	747	201	242	4		
2	EF	154	Total	C	N	O	S	0	0
			1173	739	196	234	4		
2	EG	175	Total	C	N	O	S	0	0
			1337	840	225	268	4		
2	EH	153	Total	C	N	O	S	0	0
			1165	733	195	233	4		
2	EI	157	Total	C	N	O	S	0	0
			1189	744	200	241	4		
2	EJ	166	Total	C	N	O	S	0	0
			1275	804	213	254	4		
2	EK	168	Total	C	N	O	S	0	0
			1288	813	215	256	4		
2	EL	152	Total	C	N	O	S	0	0
			1160	730	194	232	4		
2	EM	154	Total	C	N	O	S	0	0
			1173	739	196	234	4		
2	EN	153	Total	C	N	O	S	0	0
			1165	733	195	233	4		
2	EO	170	Total	C	N	O	S	0	0
			1304	823	218	259	4		
2	EP	153	Total	C	N	O	S	0	0
			1161	730	194	233	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	EQ	158	Total	C	N	O	S	0	0
			1198	750	202	242	4		
2	ER	151	Total	C	N	O	S	0	0
			1148	721	192	231	4		
2	ES	154	Total	C	N	O	S	0	0
			1173	739	196	234	4		
2	ET	153	Total	C	N	O	S	0	0
			1161	730	194	233	4		
2	EU	158	Total	C	N	O	S	0	0
			1198	750	202	242	4		
2	EV	151	Total	C	N	O	S	0	0
			1148	721	192	231	4		
2	EW	154	Total	C	N	O	S	0	0
			1173	739	196	234	4		
2	EX	153	Total	C	N	O	S	0	0
			1161	730	194	233	4		
2	EY	158	Total	C	N	O	S	0	0
			1198	750	202	242	4		
2	EZ	151	Total	C	N	O	S	0	0
			1148	721	192	231	4		
2	FA	154	Total	C	N	O	S	0	0
			1173	739	196	234	4		
2	FB	153	Total	C	N	O	S	0	0
			1161	730	194	233	4		
2	FC	158	Total	C	N	O	S	0	0
			1198	750	202	242	4		
2	FD	151	Total	C	N	O	S	0	0
			1148	721	192	231	4		
2	FE	154	Total	C	N	O	S	0	0
			1173	739	196	234	4		
2	FF	153	Total	C	N	O	S	0	0
			1161	730	194	233	4		
2	FG	158	Total	C	N	O	S	0	0
			1198	750	202	242	4		
2	FH	151	Total	C	N	O	S	0	0
			1148	721	192	231	4		
2	FI	154	Total	C	N	O	S	0	0
			1173	739	196	234	4		

- Molecule 3 is a protein called Decorator protein P04.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	FJ	161	Total	C	N	O	S	0	0
			1252	801	199	245	7		

- Molecule 4 is a protein called Decorator protein P05.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	FK	152	Total	C	N	O	S	0	0
			1195	761	203	229	2		
4	FL	152	Total	C	N	O	S	0	0
			1195	761	203	229	2		
4	FM	153	Total	C	N	O	S	0	0
			1203	767	203	231	2		
4	FN	152	Total	C	N	O	S	0	0
			1197	764	202	229	2		
4	FO	156	Total	C	N	O	S	0	0
			1222	776	208	235	3		
4	FP	152	Total	C	N	O	S	0	0
			1191	758	202	229	2		
4	FQ	171	Total	C	N	O	S	0	0
			1358	865	231	260	2		
4	FR	171	Total	C	N	O	S	0	0
			1358	865	231	260	2		
4	FS	171	Total	C	N	O	S	0	0
			1358	865	231	260	2		
4	FT	144	Total	C	N	O	S	0	0
			1137	726	191	218	2		
4	FU	151	Total	C	N	O	S	0	0
			1187	755	201	229	2		
4	FV	154	Total	C	N	O	S	0	0
			1208	769	205	231	3		
4	FW	154	Total	C	N	O	S	0	0
			1208	769	205	231	3		
4	FX	151	Total	C	N	O	S	0	0
			1186	755	201	228	2		
4	FY	151	Total	C	N	O	S	0	0
			1186	755	201	228	2		
4	FZ	152	Total	C	N	O	S	0	0
			1195	761	203	229	2		
4	GA	171	Total	C	N	O	S	0	0
			1358	865	231	260	2		
4	GB	171	Total	C	N	O	S	0	0
			1358	865	231	260	2		
4	GC	171	Total	C	N	O	S	0	0
			1358	865	231	260	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	GD	171	Total	C	N	O	S	0	0
			1358	865	231	260	2		
4	GE	171	Total	C	N	O	S	0	0
			1358	865	231	260	2		
4	GF	171	Total	C	N	O	S	0	0
			1358	865	231	260	2		
4	GG	171	Total	C	N	O	S	0	0
			1358	865	231	260	2		
4	GH	171	Total	C	N	O	S	0	0
			1358	865	231	260	2		
4	GI	171	Total	C	N	O	S	0	0
			1358	865	231	260	2		
4	GJ	171	Total	C	N	O	S	0	0
			1358	865	231	260	2		

- Molecule 5 is a protein called Scaffold protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	GK	30	Total	C	N	O	0	0
			266	174	47	45		
5	GL	37	Total	C	N	O	0	0
			315	203	55	57		
5	GM	37	Total	C	N	O	0	0
			315	203	55	57		
5	GN	37	Total	C	N	O	0	0
			315	203	55	57		
5	GO	37	Total	C	N	O	0	0
			315	203	55	57		
5	GP	37	Total	C	N	O	0	0
			315	203	55	57		
5	GQ	37	Total	C	N	O	0	0
			315	203	55	57		
5	GR	37	Total	C	N	O	0	0
			315	203	55	57		
5	GS	37	Total	C	N	O	0	0
			315	203	55	57		
5	GT	37	Total	C	N	O	0	0
			315	203	55	57		
5	GU	37	Total	C	N	O	0	0
			315	203	55	57		
5	GV	37	Total	C	N	O	0	0
			315	203	55	57		

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Mol	Chain	Residues	Atoms				AltConf	Trace
5	GW	30	Total	C	N	O	0	0
			266	174	47	45		
5	GX	37	Total	C	N	O	0	0
			315	203	55	57		
5	GY	37	Total	C	N	O	0	0
			315	203	55	57		
5	GZ	37	Total	C	N	O	0	0
			315	203	55	57		
5	HA	37	Total	C	N	O	0	0
			315	203	55	57		
5	HB	37	Total	C	N	O	0	0
			315	203	55	57		
5	HC	37	Total	C	N	O	0	0
			315	203	55	57		
5	HD	30	Total	C	N	O	0	0
			266	174	47	45		
5	HE	37	Total	C	N	O	0	0
			315	203	55	57		
5	HF	37	Total	C	N	O	0	0
			315	203	55	57		
5	HG	37	Total	C	N	O	0	0
			315	203	55	57		
5	HH	30	Total	C	N	O	0	0
			266	174	47	45		
5	HI	30	Total	C	N	O	0	0
			266	174	47	45		
5	HJ	30	Total	C	N	O	0	0
			266	174	47	45		
5	HK	30	Total	C	N	O	0	0
			266	174	47	45		
5	HL	37	Total	C	N	O	0	0
			315	203	55	57		
5	HM	29	Total	C	N	O	0	0
			255	165	46	44		
5	HN	37	Total	C	N	O	0	0
			315	203	55	57		
5	HO	37	Total	C	N	O	0	0
			315	203	55	57		
5	HP	37	Total	C	N	O	0	0
			315	203	55	57		
5	HQ	37	Total	C	N	O	0	0
			315	203	55	57		

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Mol	Chain	Residues	Atoms				AltConf	Trace
5	HR	37	Total	C	N	O	0	0
			315	203	55	57		
5	HS	37	Total	C	N	O	0	0
			315	203	55	57		
5	HT	37	Total	C	N	O	0	0
			315	203	55	57		
5	HU	37	Total	C	N	O	0	0
			315	203	55	57		
5	HV	37	Total	C	N	O	0	0
			315	203	55	57		
5	HW	28	Total	C	N	O	0	0
			248	160	45	43		
5	HX	37	Total	C	N	O	0	0
			315	203	55	57		
5	HY	37	Total	C	N	O	0	0
			315	203	55	57		
5	HZ	37	Total	C	N	O	0	0
			315	203	55	57		
5	IA	37	Total	C	N	O	0	0
			315	203	55	57		
5	IB	29	Total	C	N	O	0	0
			255	165	46	44		
5	IC	37	Total	C	N	O	0	0
			315	203	55	57		
5	ID	29	Total	C	N	O	0	0
			255	165	46	44		
5	IE	37	Total	C	N	O	0	0
			315	203	55	57		
5	IF	37	Total	C	N	O	0	0
			315	203	55	57		
5	IG	37	Total	C	N	O	0	0
			315	203	55	57		
5	IH	29	Total	C	N	O	0	0
			255	165	46	44		
5	II	30	Total	C	N	O	0	0
			266	174	47	45		
5	IJ	30	Total	C	N	O	0	0
			266	174	47	45		
5	IK	30	Total	C	N	O	0	0
			266	174	47	45		
5	IL	40	Total	C	N	O	0	0
			345	221	64	60		

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Mol	Chain	Residues	Atoms				AltConf	Trace
5	IM	37	Total	C	N	O	0	0
			315	203	55	57		
5	IN	37	Total	C	N	O	0	0
			315	203	55	57		
5	IO	40	Total	C	N	O	0	0
			345	221	64	60		
5	IP	37	Total	C	N	O	0	0
			315	203	55	57		
5	IQ	37	Total	C	N	O	0	0
			315	203	55	57		
5	IR	40	Total	C	N	O	0	0
			345	221	64	60		
5	IS	37	Total	C	N	O	0	0
			315	203	55	57		
5	IT	37	Total	C	N	O	0	0
			315	203	55	57		
5	IU	40	Total	C	N	O	0	0
			345	221	64	60		
5	IV	37	Total	C	N	O	0	0
			315	203	55	57		
5	IW	37	Total	C	N	O	0	0
			315	203	55	57		
5	IX	37	Total	C	N	O	0	0
			315	203	55	57		
5	IY	40	Total	C	N	O	0	0
			345	221	64	60		
5	IZ	37	Total	C	N	O	0	0
			315	203	55	57		
5	JA	40	Total	C	N	O	0	0
			345	221	64	60		
5	JB	37	Total	C	N	O	0	0
			315	203	55	57		
5	JC	37	Total	C	N	O	0	0
			315	203	55	57		
5	JD	40	Total	C	N	O	0	0
			345	221	64	60		
5	JE	37	Total	C	N	O	0	0
			315	203	55	57		
5	JF	37	Total	C	N	O	0	0
			315	203	55	57		
5	JG	40	Total	C	N	O	0	0
			345	221	64	60		

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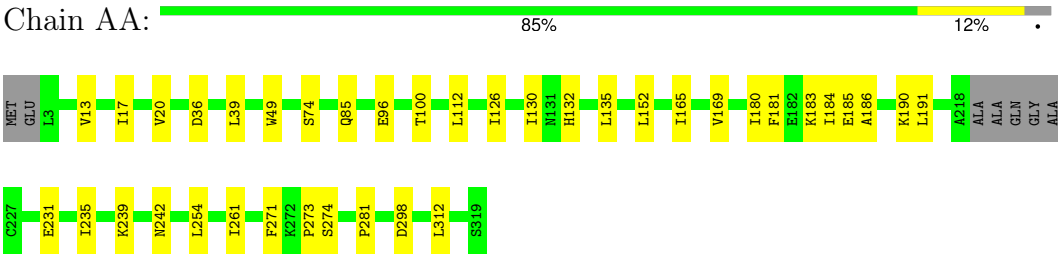
Mol	Chain	Residues	Atoms				AltConf	Trace
5	JH	37	Total	C	N	O	0	0
			315	203	55	57		
5	JI	37	Total	C	N	O	0	0
			315	203	55	57		
5	JJ	40	Total	C	N	O	0	0
			345	221	64	60		
5	JK	37	Total	C	N	O	0	0
			315	203	55	57		
5	JL	37	Total	C	N	O	0	0
			315	203	55	57		
5	JM	37	Total	C	N	O	0	0
			315	203	55	57		
5	JN	40	Total	C	N	O	0	0
			345	221	64	60		
5	JO	37	Total	C	N	O	0	0
			315	203	55	57		

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.

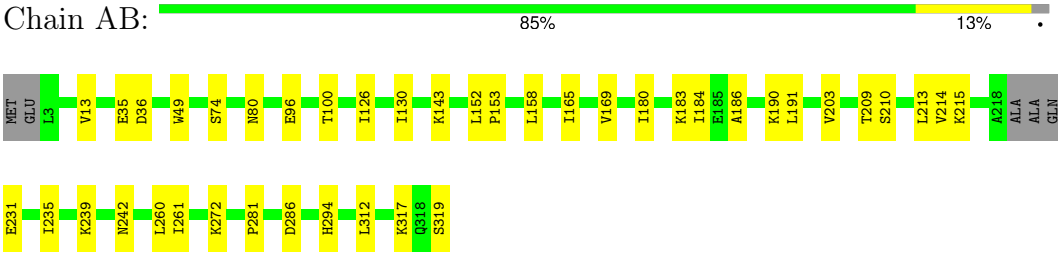
• Molecule 1: Major capsid protein

Chain AA:



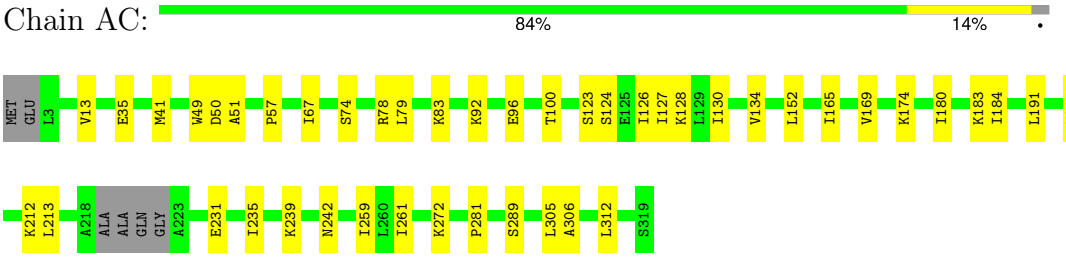
• Molecule 1: Major capsid protein

Chain AB:



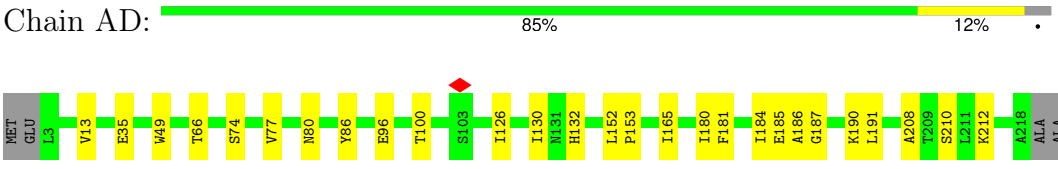
• Molecule 1: Major capsid protein

Chain AC:



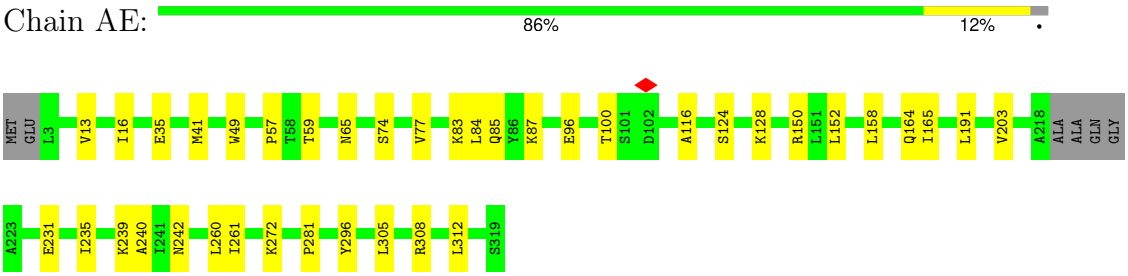
• Molecule 1: Major capsid protein

Chain AD:



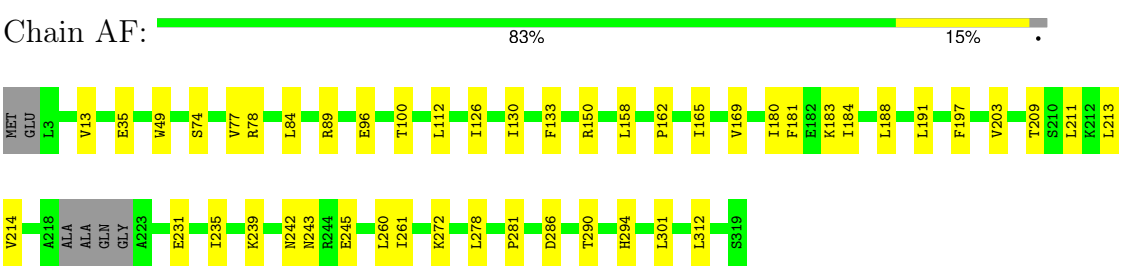
• Molecule 1: Major capsid protein

Chain AE:



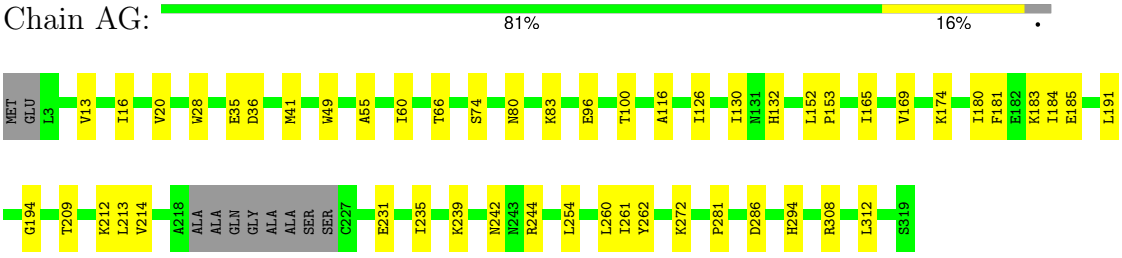
• Molecule 1: Major capsid protein

Chain AF:



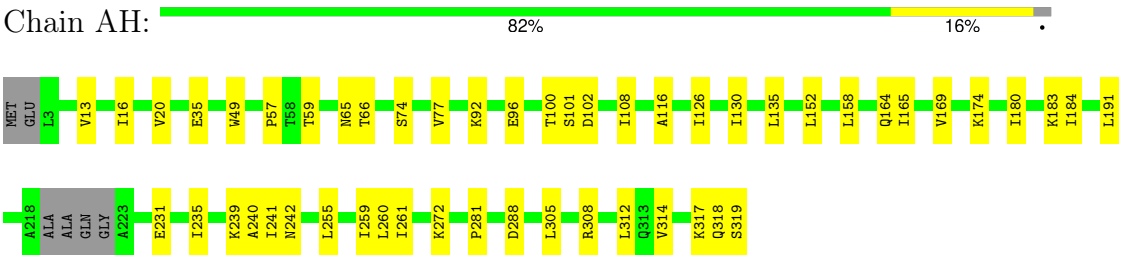
• Molecule 1: Major capsid protein

Chain AG:



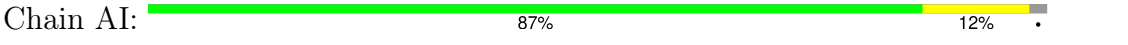
• Molecule 1: Major capsid protein

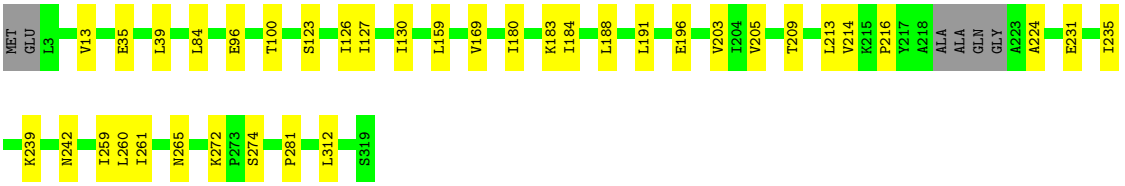
Chain AH:



• Molecule 1: Major capsid protein

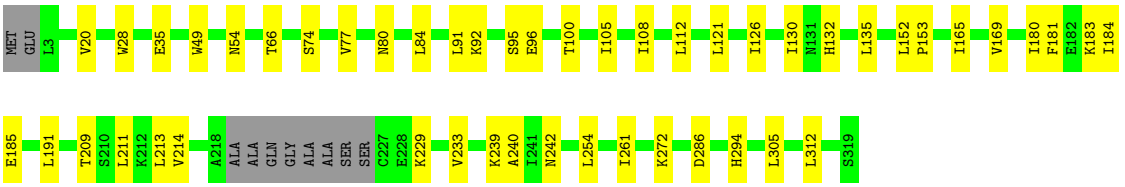
Chain AI:





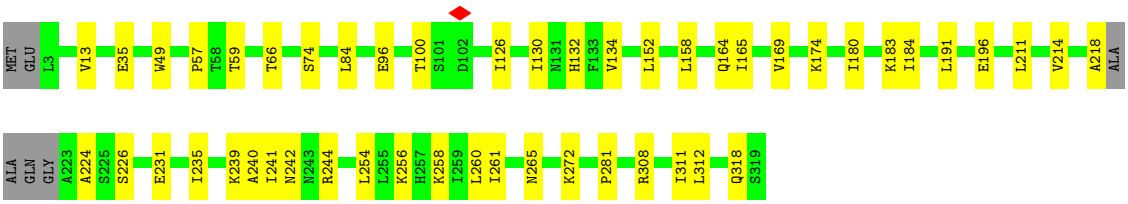
• Molecule 1: Major capsid protein

Chain AJ:



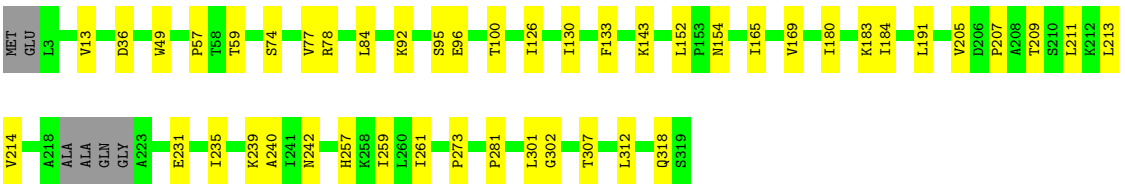
• Molecule 1: Major capsid protein

Chain AK:



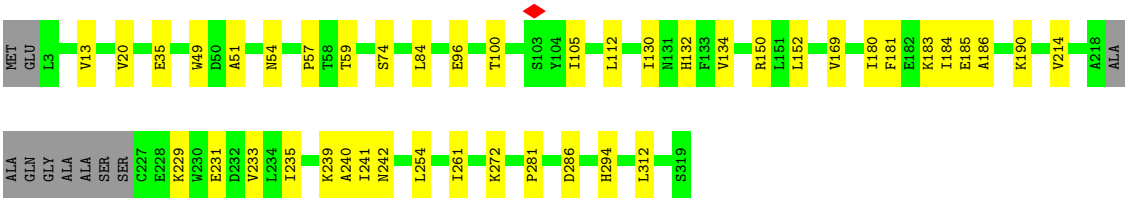
• Molecule 1: Major capsid protein

Chain AL:



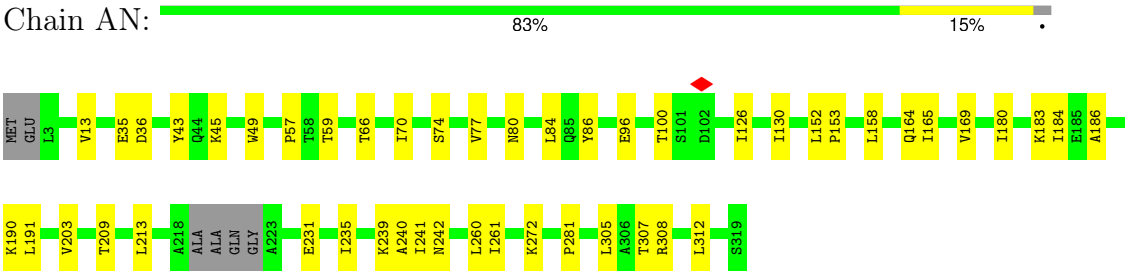
• Molecule 1: Major capsid protein

Chain AM:



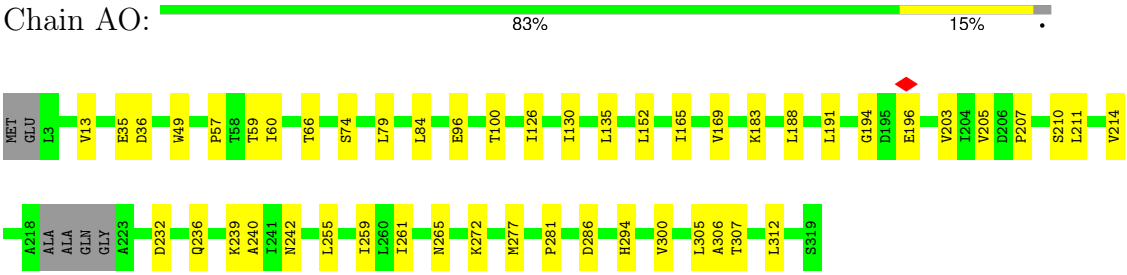
• Molecule 1: Major capsid protein

Chain AN:



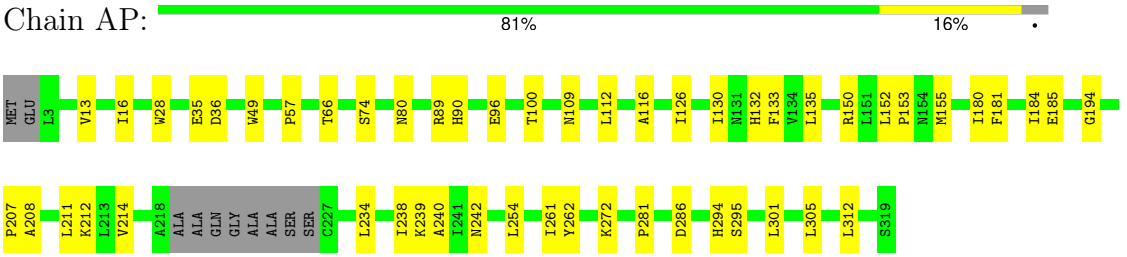
• Molecule 1: Major capsid protein

Chain AO:



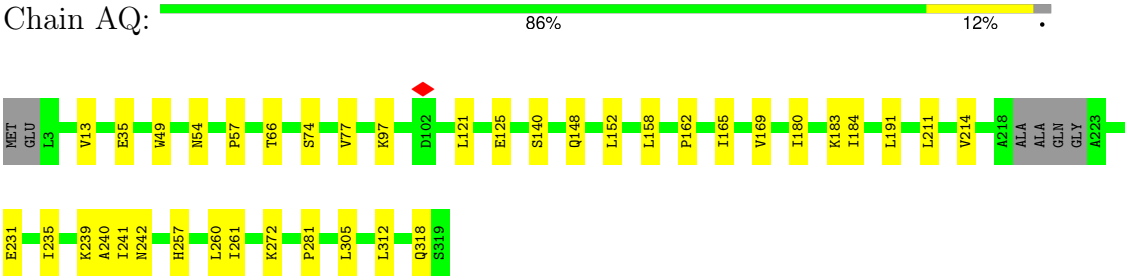
• Molecule 1: Major capsid protein

Chain AP:



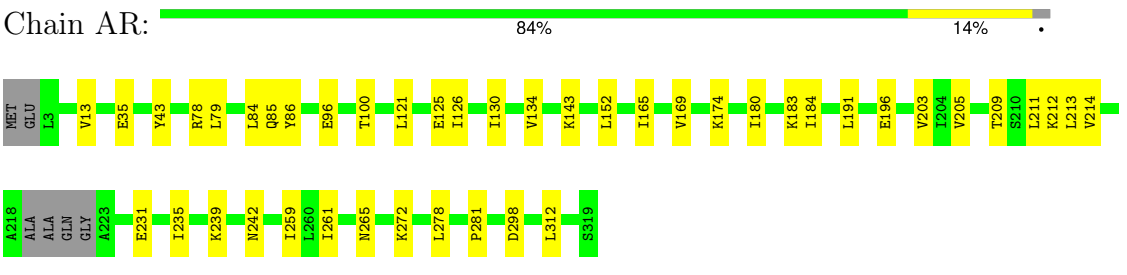
• Molecule 1: Major capsid protein

Chain AQ:



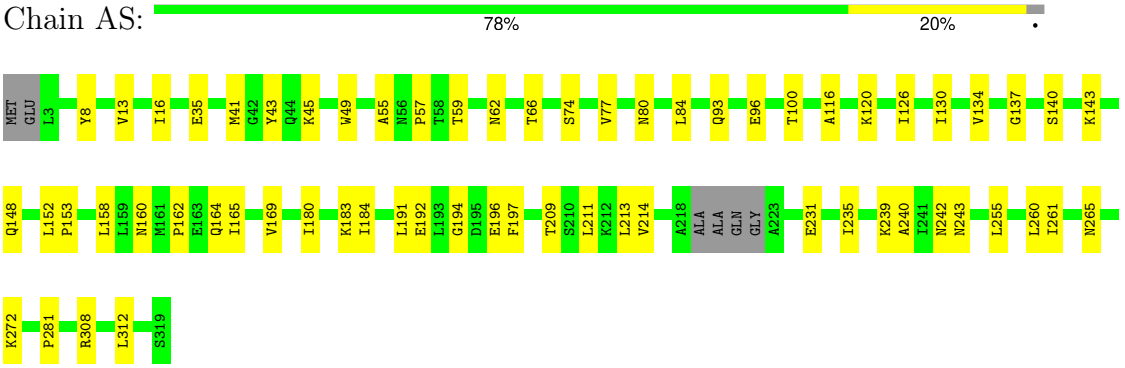
• Molecule 1: Major capsid protein

Chain AR:



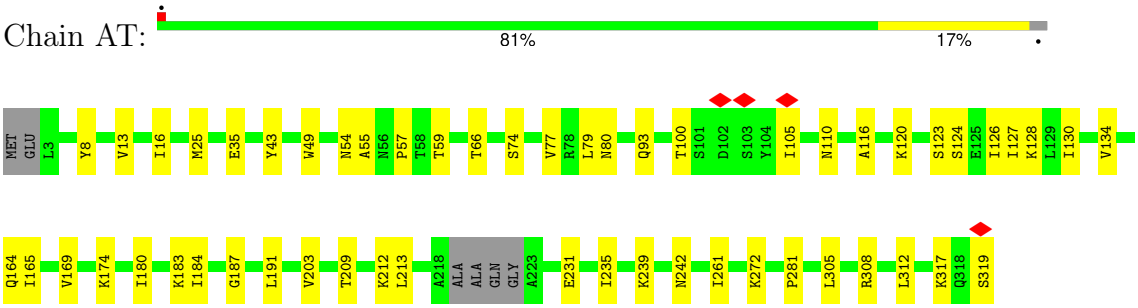
• Molecule 1: Major capsid protein

Chain AS:



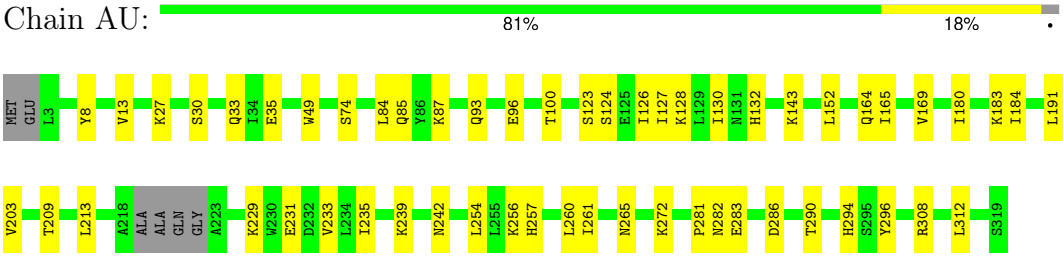
• Molecule 1: Major capsid protein

Chain AT:



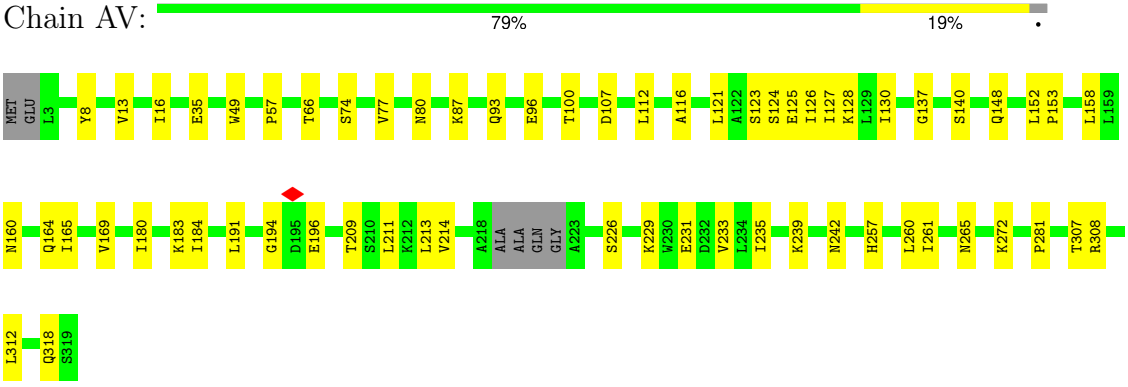
• Molecule 1: Major capsid protein

Chain AU:



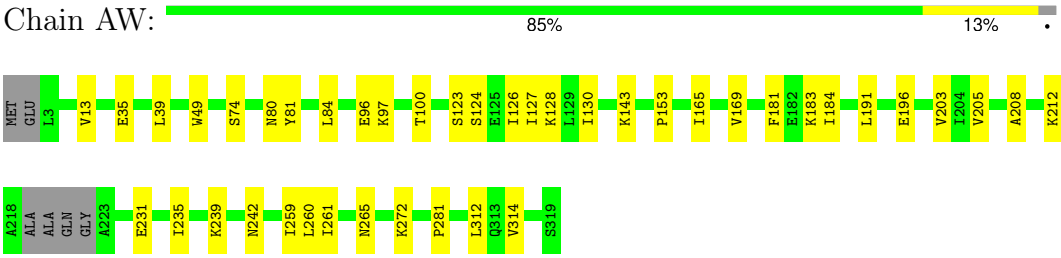
• Molecule 1: Major capsid protein

Chain AV:



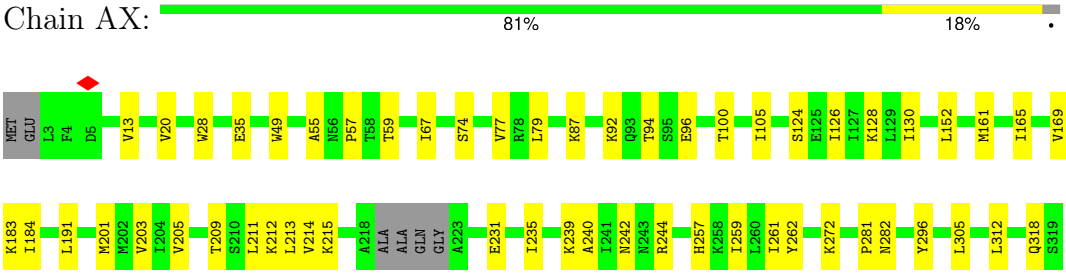
• Molecule 1: Major capsid protein

Chain AW:



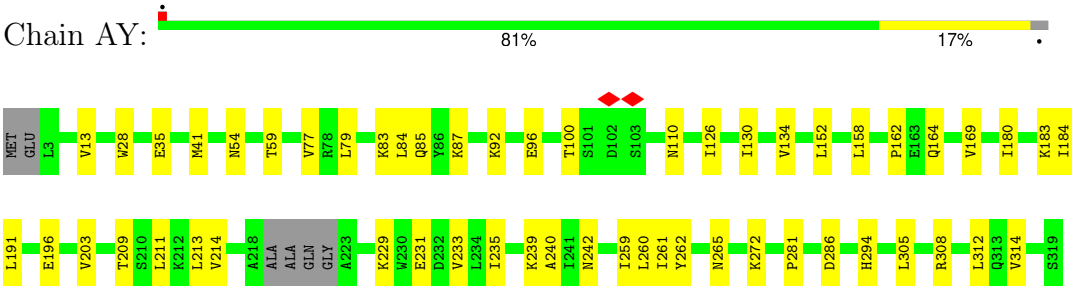
• Molecule 1: Major capsid protein

Chain AX:



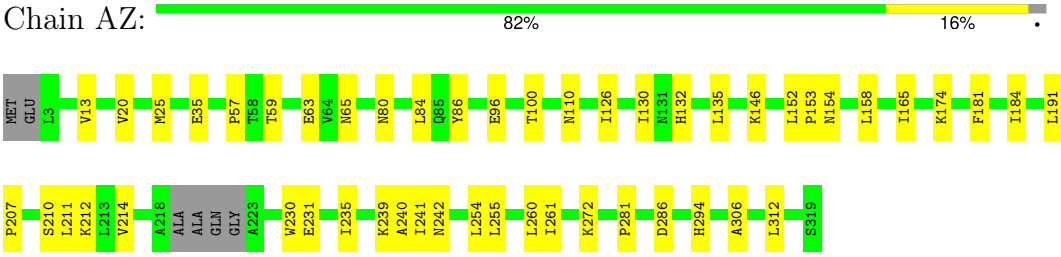
• Molecule 1: Major capsid protein

Chain AY:



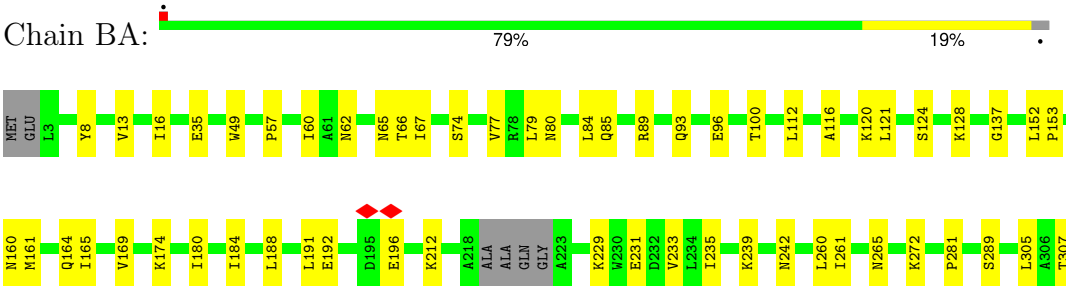
• Molecule 1: Major capsid protein

Chain AZ:



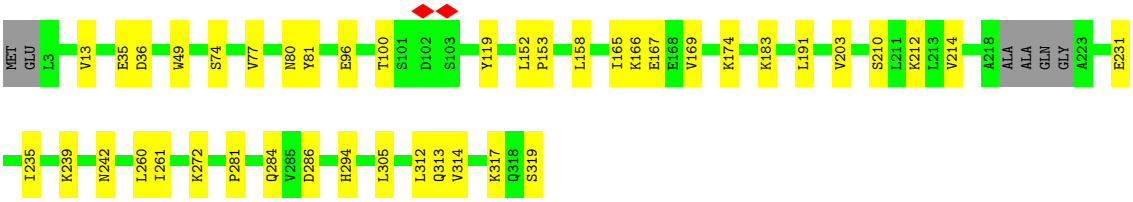
• Molecule 1: Major capsid protein

Chain BA:



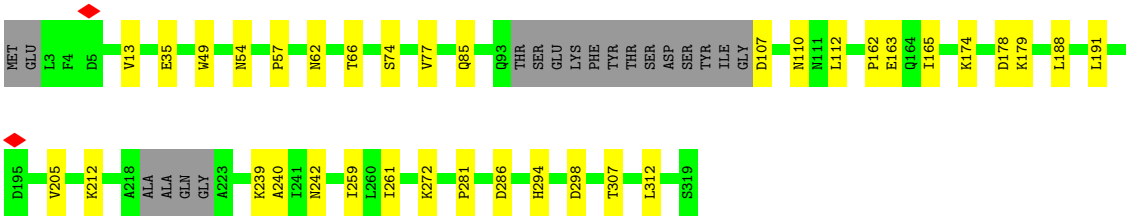
• Molecule 1: Major capsid protein

Chain BB:



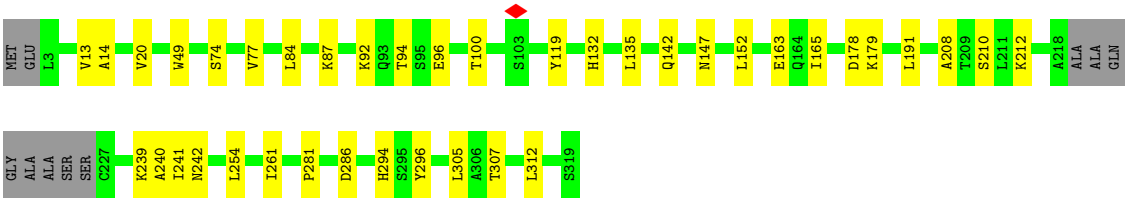
• Molecule 1: Major capsid protein

Chain BC:



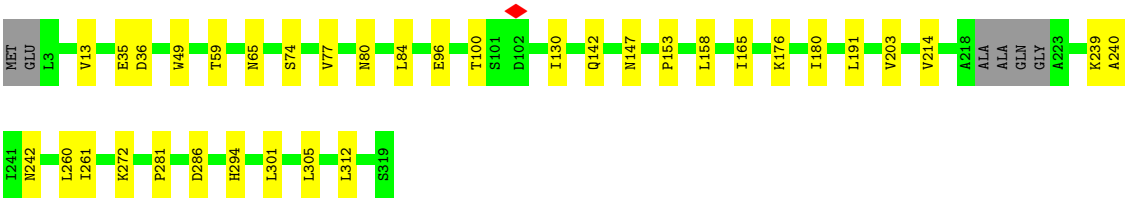
• Molecule 1: Major capsid protein

Chain BD:



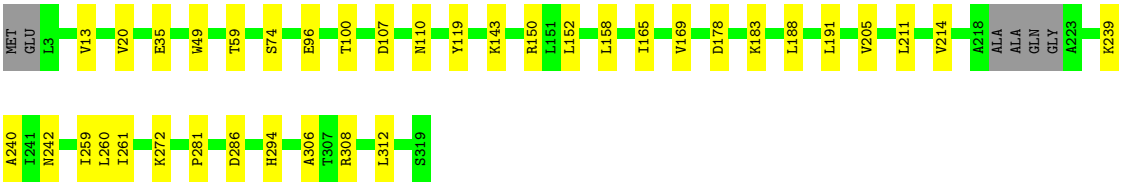
• Molecule 1: Major capsid protein

Chain BE:



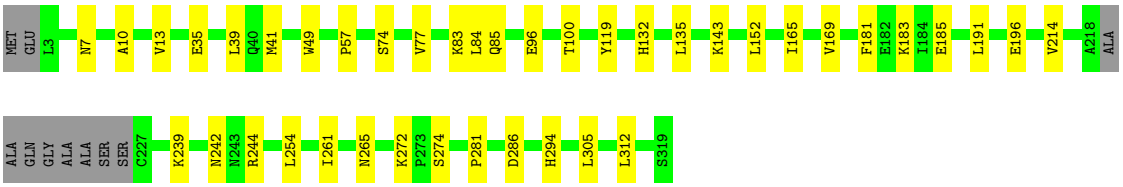
• Molecule 1: Major capsid protein

Chain BF:



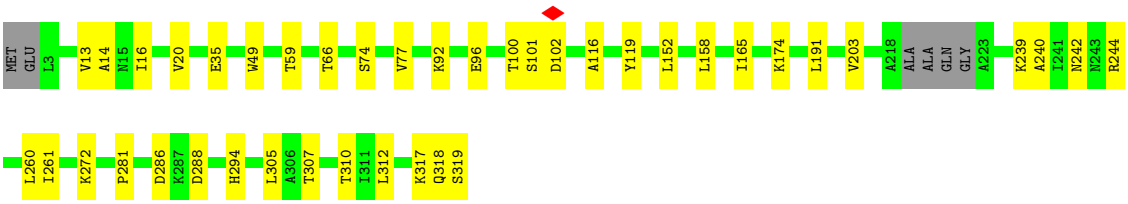
• Molecule 1: Major capsid protein

Chain BG:



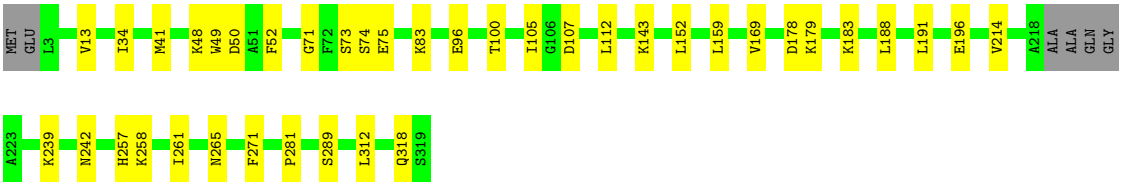
• Molecule 1: Major capsid protein

Chain BH:



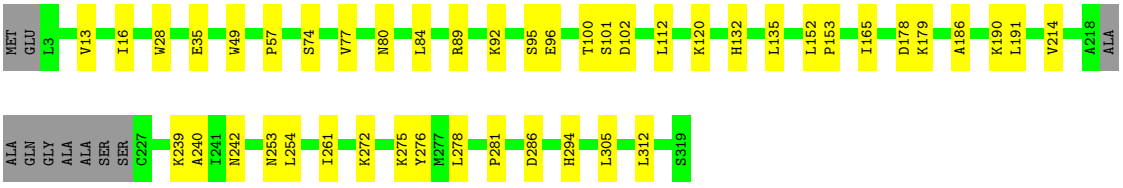
• Molecule 1: Major capsid protein

Chain BI:



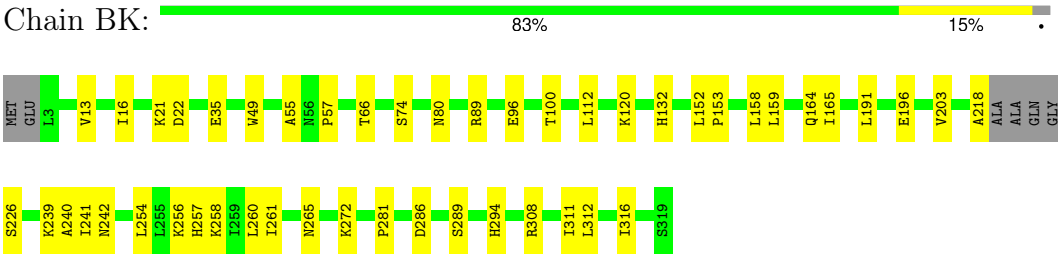
• Molecule 1: Major capsid protein

Chain BJ:



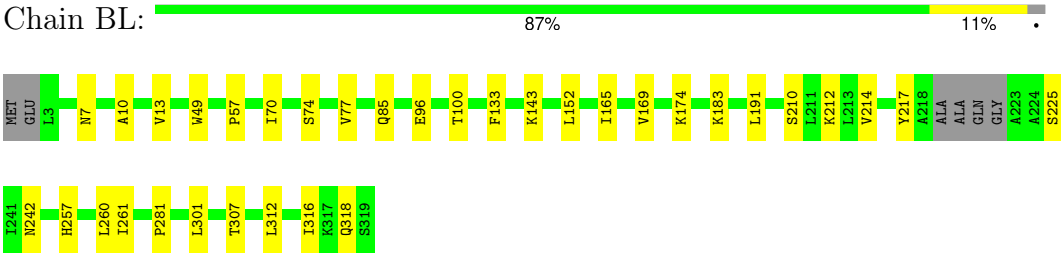
• Molecule 1: Major capsid protein

Chain BK:



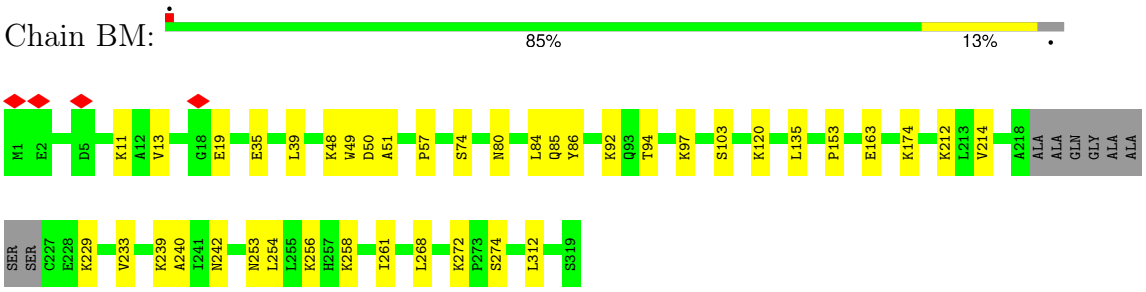
• Molecule 1: Major capsid protein

Chain BL:



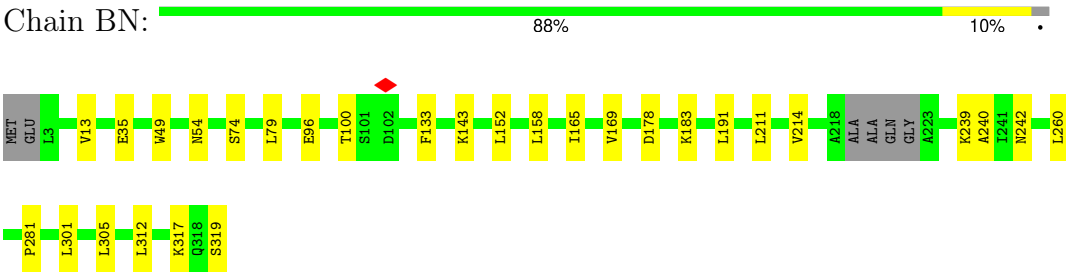
• Molecule 1: Major capsid protein

Chain BM:



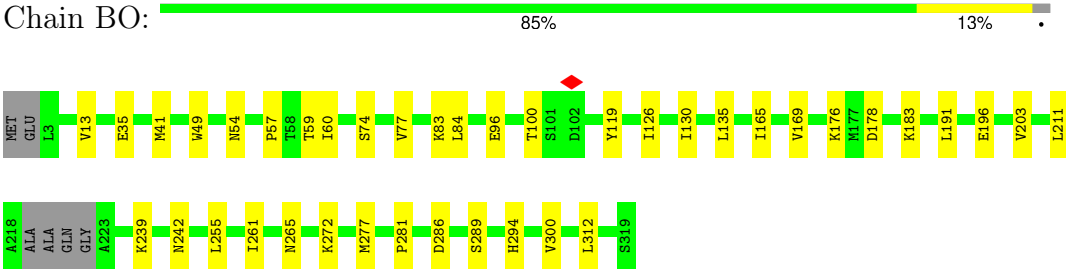
• Molecule 1: Major capsid protein

Chain BN:



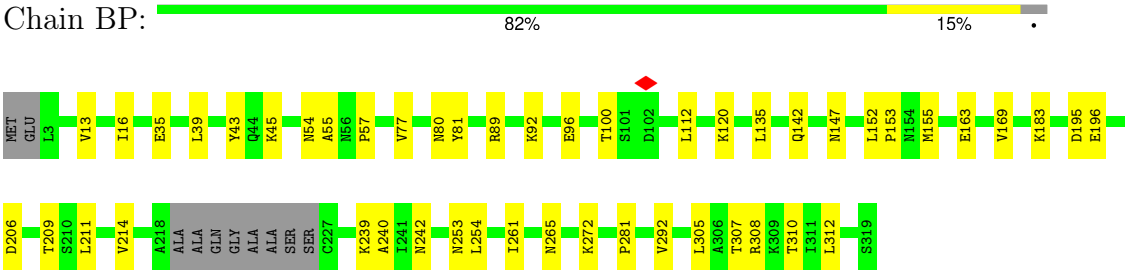
• Molecule 1: Major capsid protein

Chain BO:



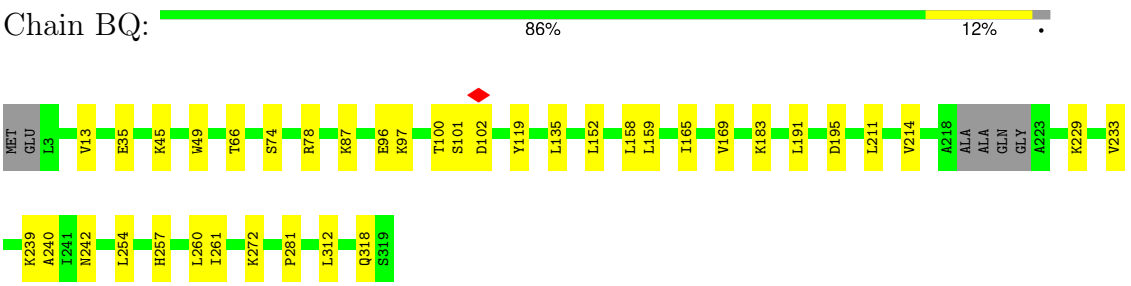
• Molecule 1: Major capsid protein

Chain BP:



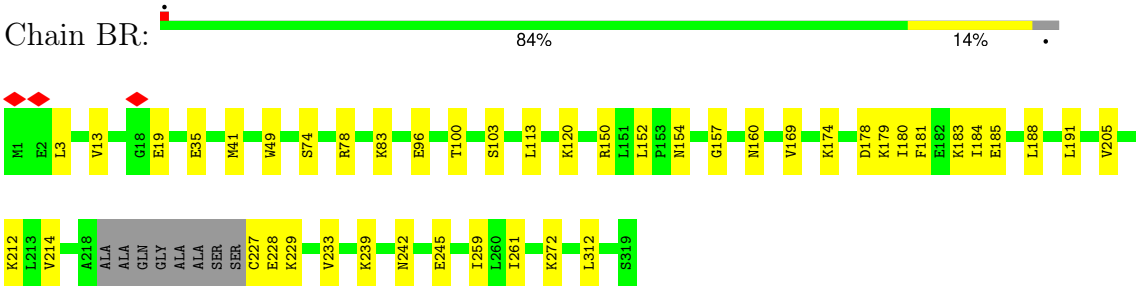
• Molecule 1: Major capsid protein

Chain BQ:



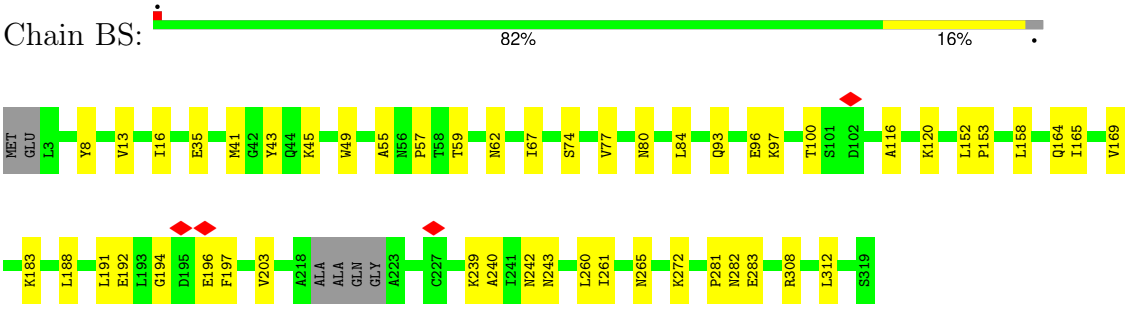
• Molecule 1: Major capsid protein

Chain BR:



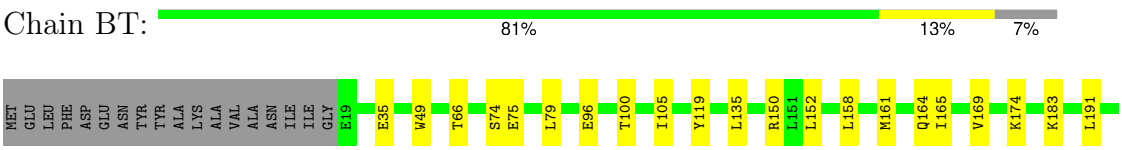
• Molecule 1: Major capsid protein

Chain BS:



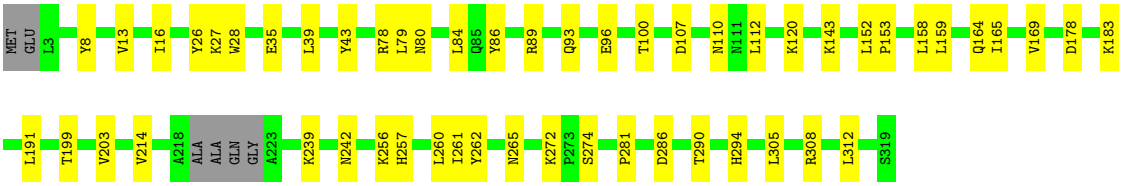
• Molecule 1: Major capsid protein

Chain BT:



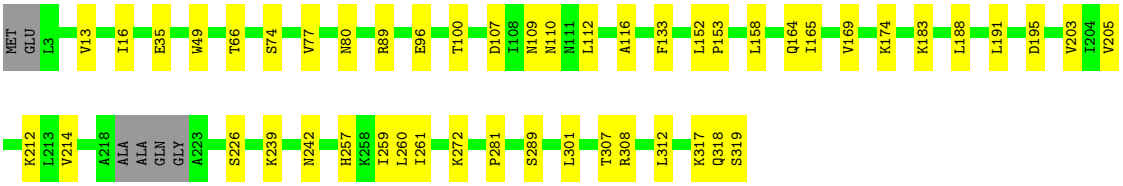
• Molecule 1: Major capsid protein

Chain BU:



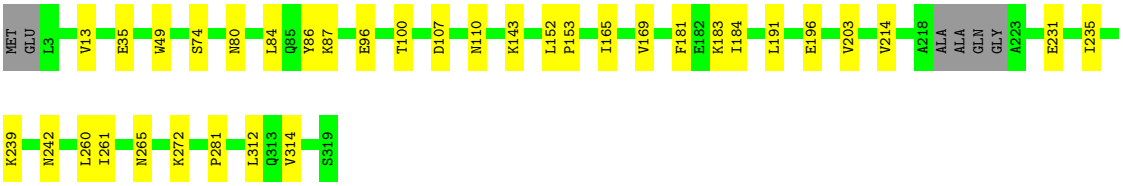
• Molecule 1: Major capsid protein

Chain BV:



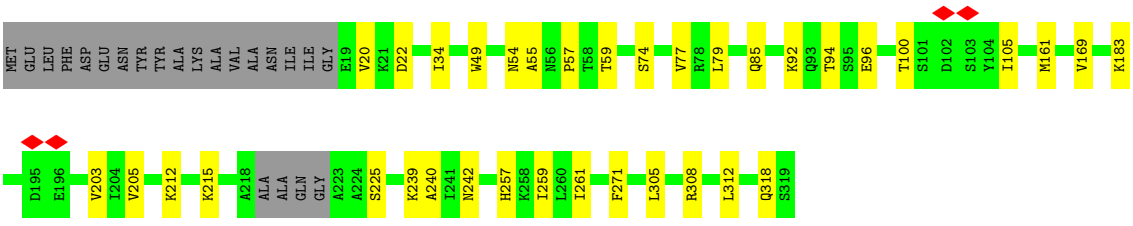
• Molecule 1: Major capsid protein

Chain BW:



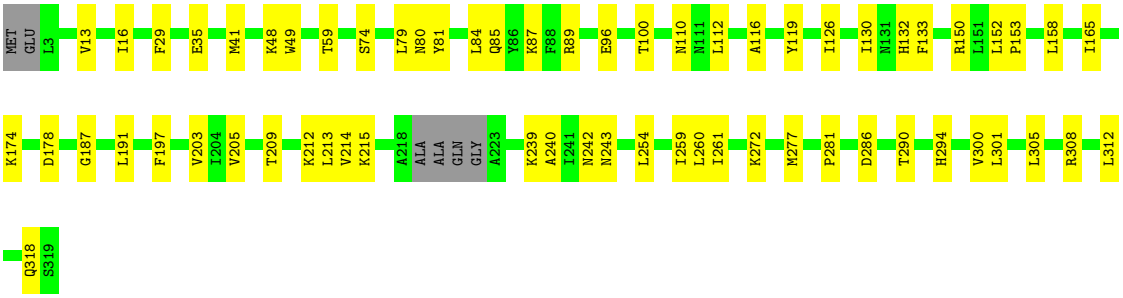
• Molecule 1: Major capsid protein

Chain BX:



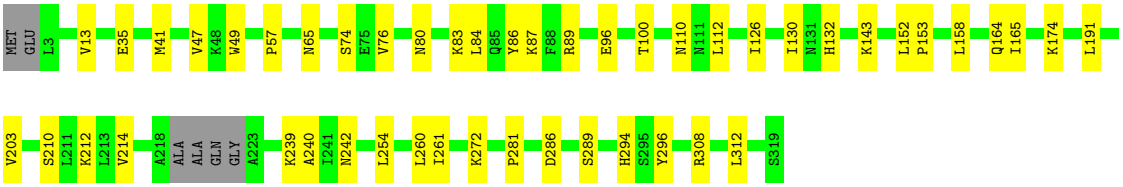
• Molecule 1: Major capsid protein

Chain BY:



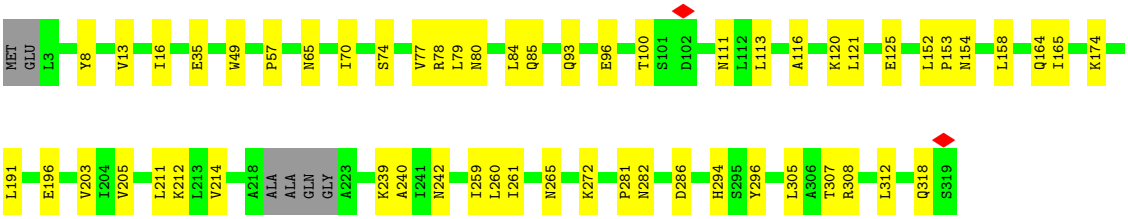
• Molecule 1: Major capsid protein

Chain BZ:



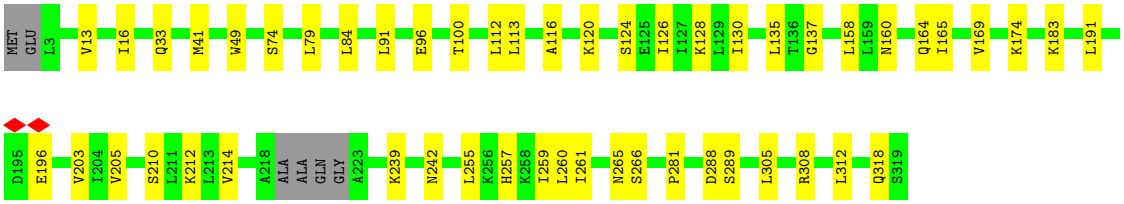
• Molecule 1: Major capsid protein

Chain CA:



• Molecule 1: Major capsid protein

Chain CB:

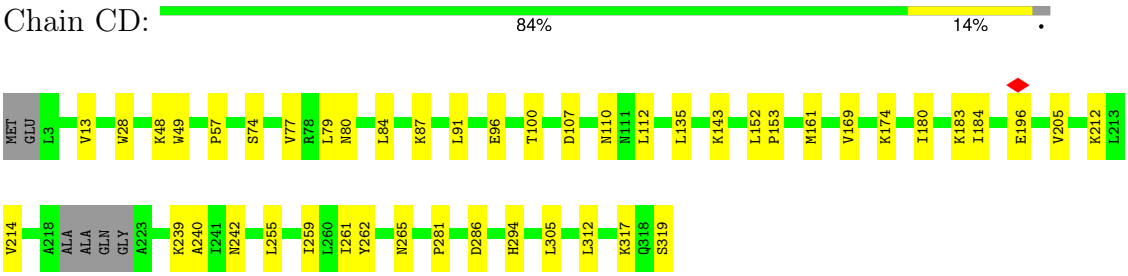


• Molecule 1: Major capsid protein

Chain CC:

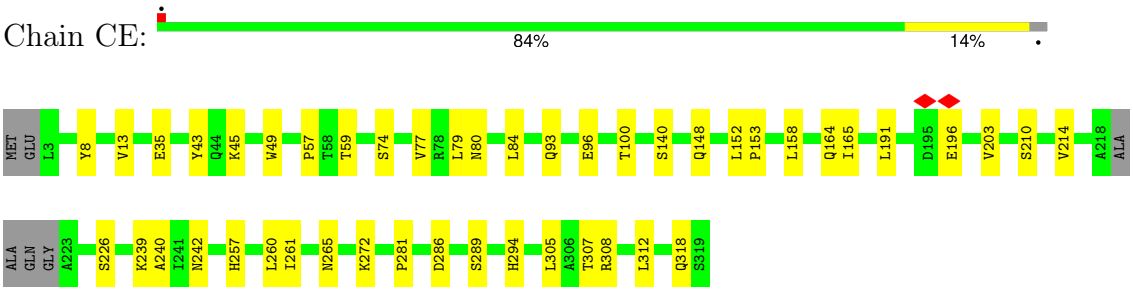
• Molecule 1: Major capsid protein

Chain CD:



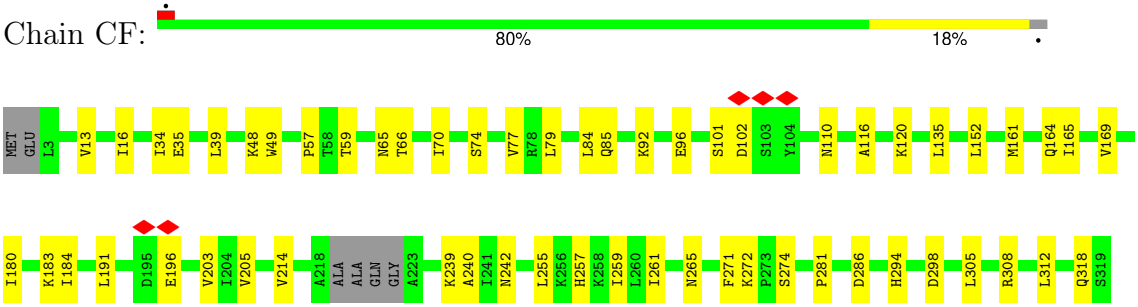
• Molecule 1: Major capsid protein

Chain CE:



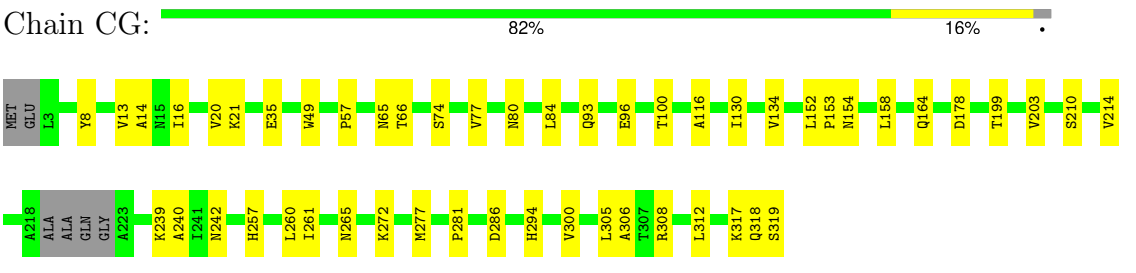
• Molecule 1: Major capsid protein

Chain CF:



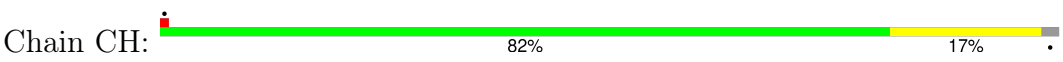
• Molecule 1: Major capsid protein

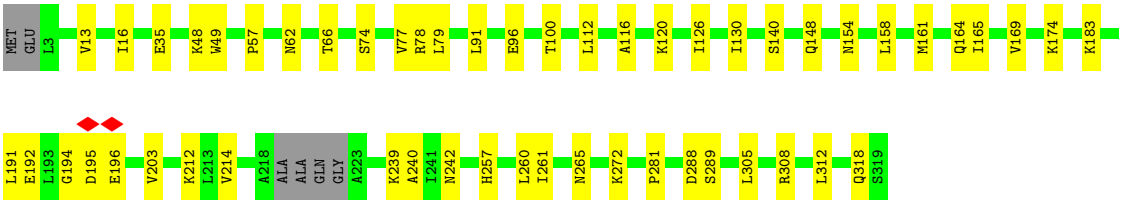
Chain CG:



• Molecule 1: Major capsid protein

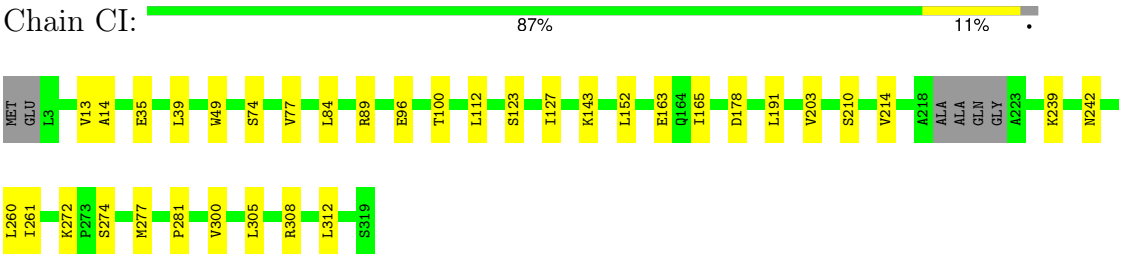
Chain CH:





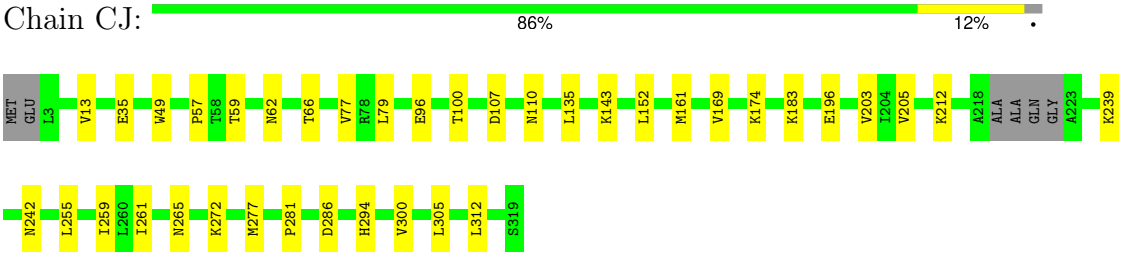
• Molecule 1: Major capsid protein

Chain CI:



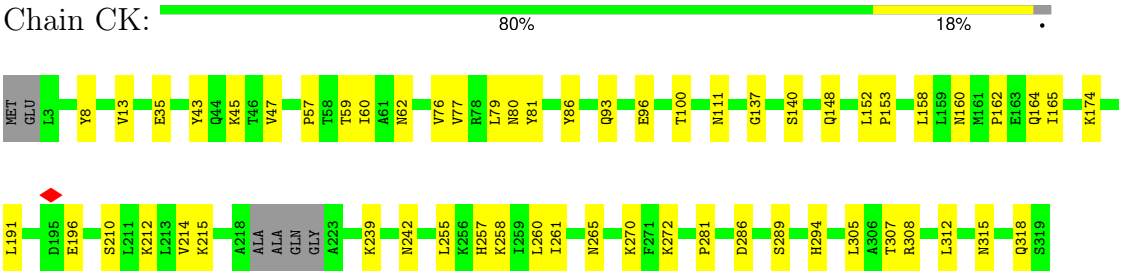
• Molecule 1: Major capsid protein

Chain CJ:



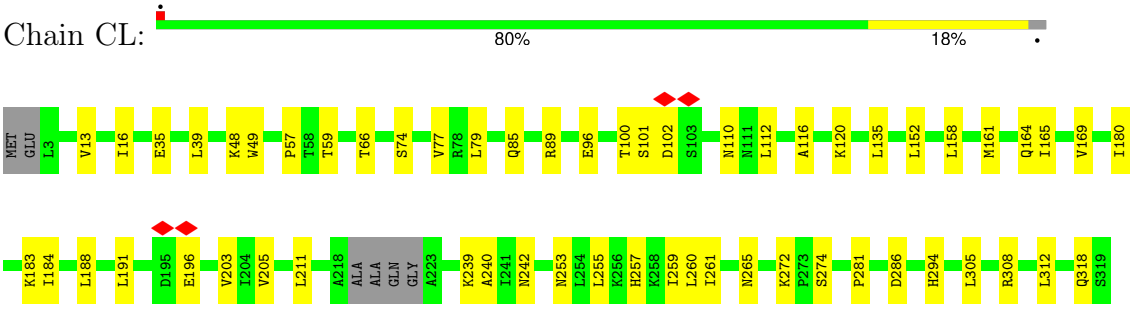
• Molecule 1: Major capsid protein

Chain CK:



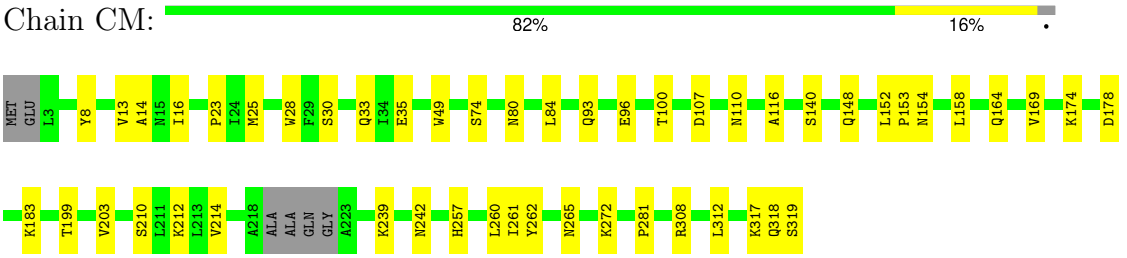
• Molecule 1: Major capsid protein

Chain CL:



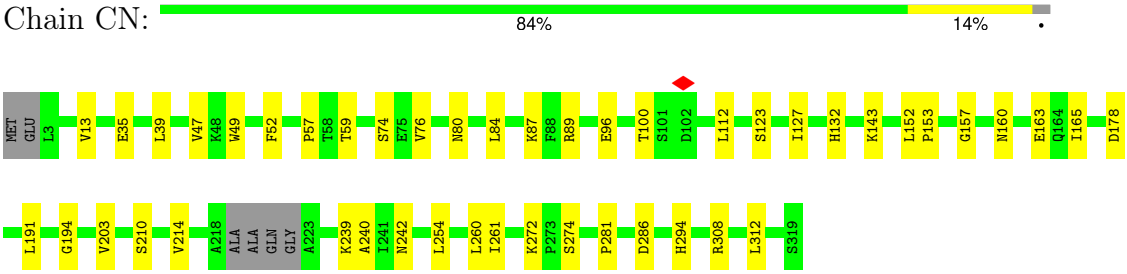
• Molecule 1: Major capsid protein

Chain CM:



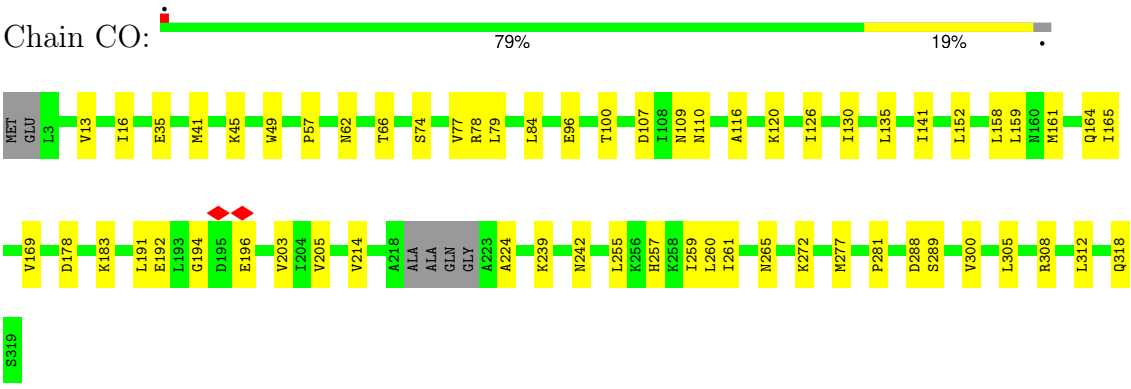
• Molecule 1: Major capsid protein

Chain CN:



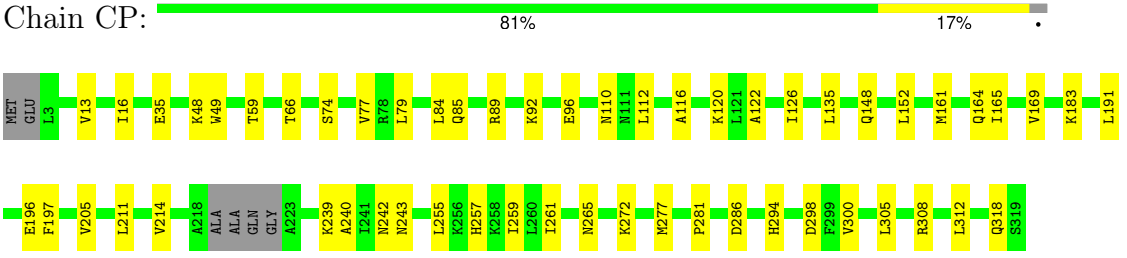
• Molecule 1: Major capsid protein

Chain CO:



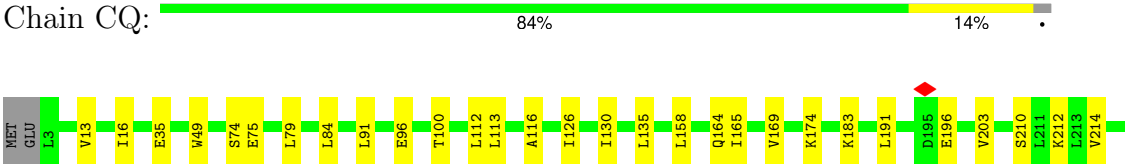
• Molecule 1: Major capsid protein

Chain CP:



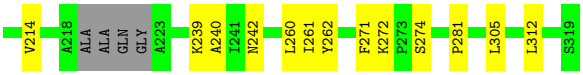
• Molecule 1: Major capsid protein

Chain CQ:



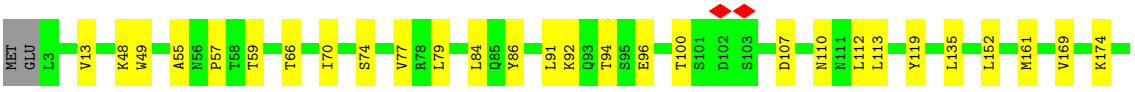
• Molecule 1: Major capsid protein

Chain CR:



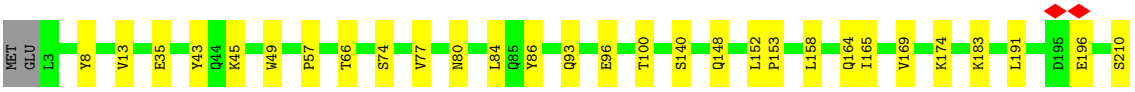
• Molecule 1: Major capsid protein

Chain CS:



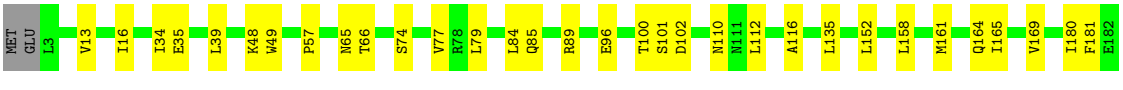
• Molecule 1: Major capsid protein

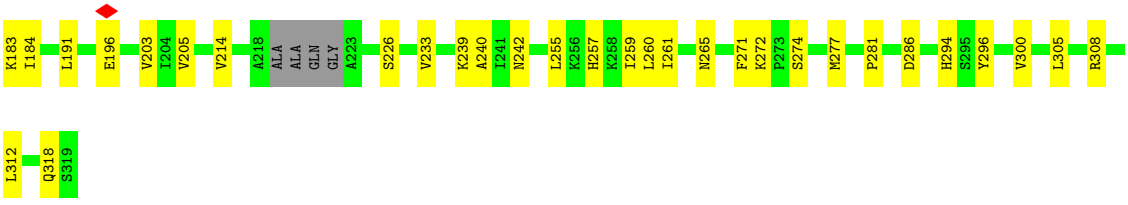
Chain CT:



• Molecule 1: Major capsid protein

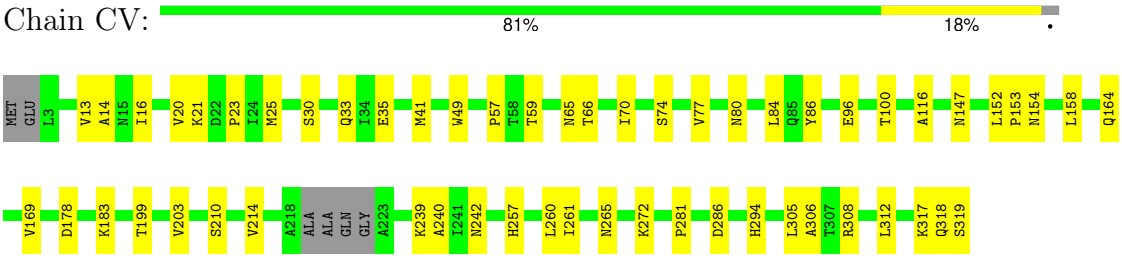
Chain CU:





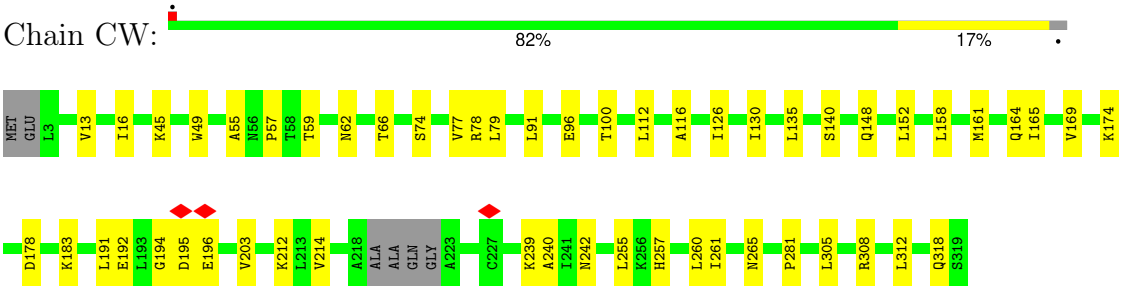
• Molecule 1: Major capsid protein

Chain CV:



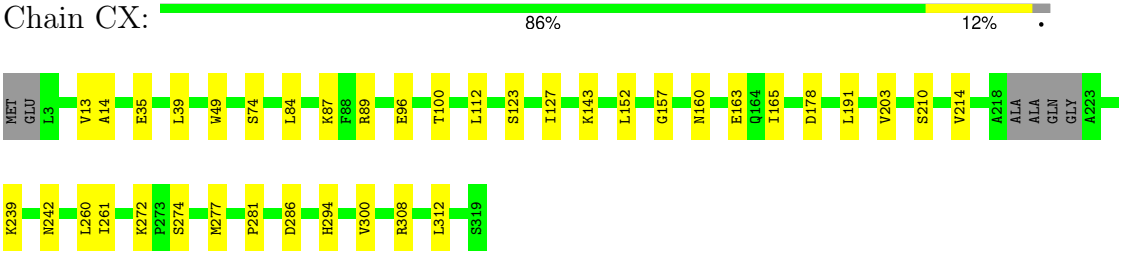
• Molecule 1: Major capsid protein

Chain CW:



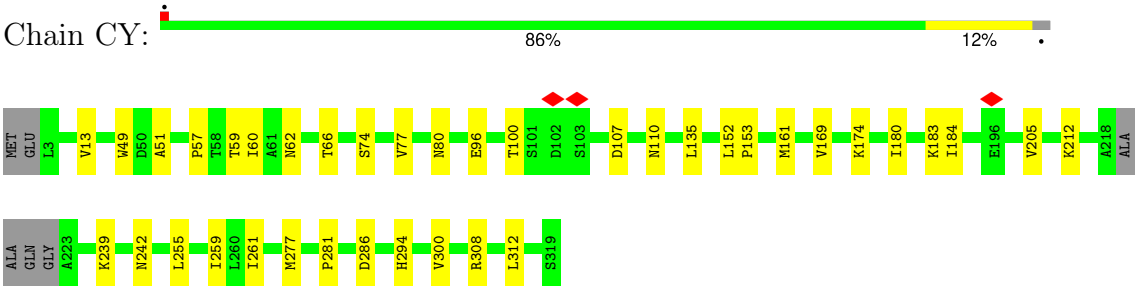
• Molecule 1: Major capsid protein

Chain CX:



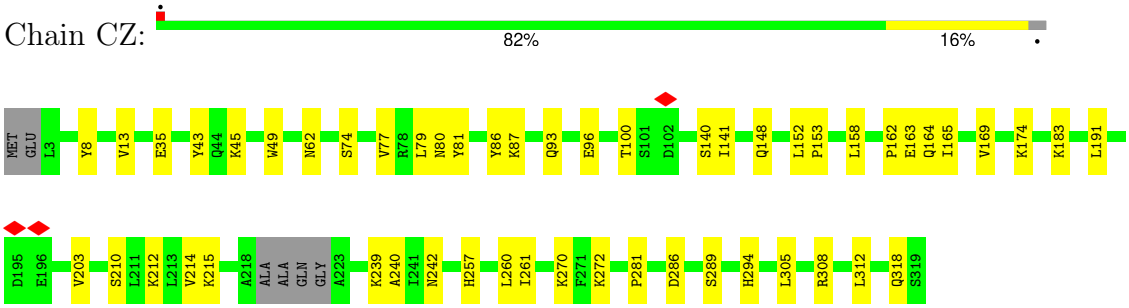
• Molecule 1: Major capsid protein

Chain CY:



• Molecule 1: Major capsid protein

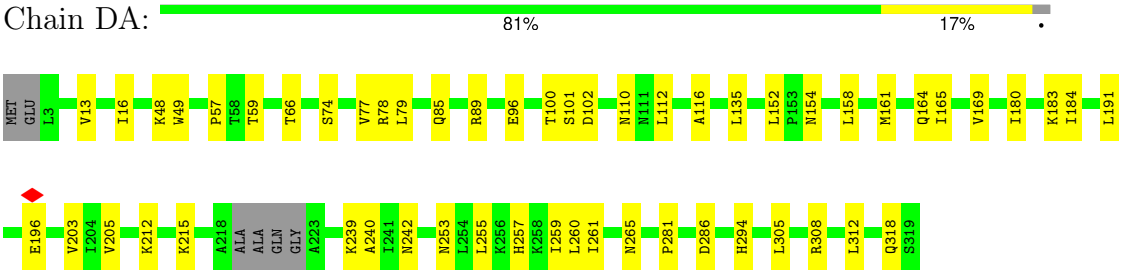
Chain CZ:



• Molecule 1: Major capsid protein

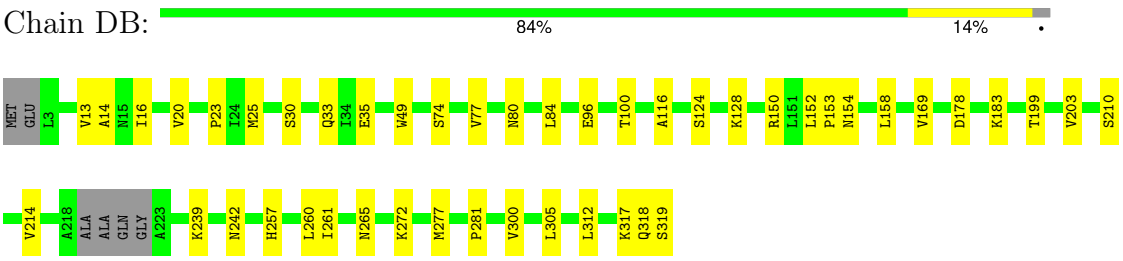
• Molecule 1: Major capsid protein

Chain DA:



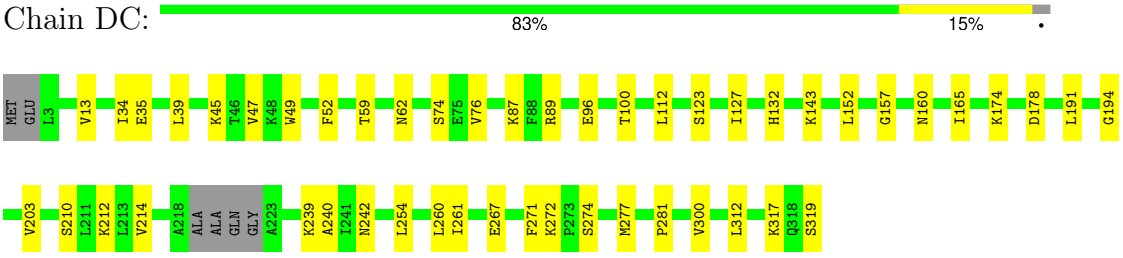
• Molecule 1: Major capsid protein

Chain DB:



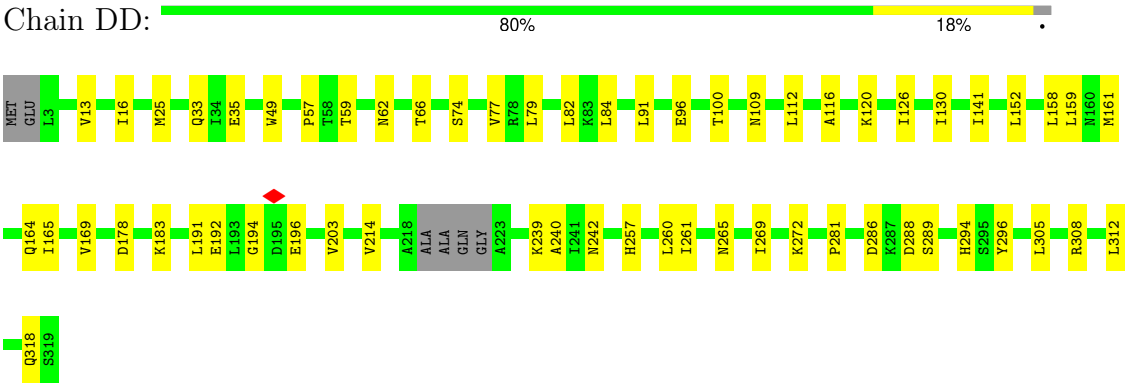
• Molecule 1: Major capsid protein

Chain DC:



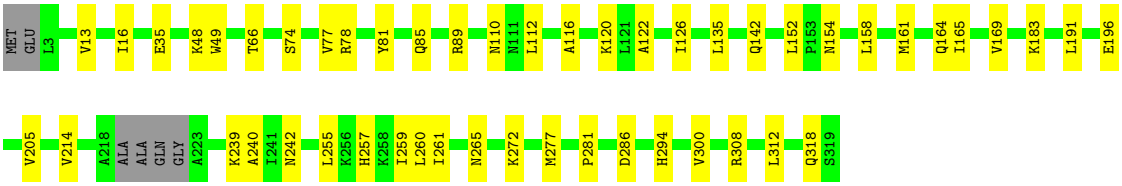
• Molecule 1: Major capsid protein

Chain DD:



• Molecule 1: Major capsid protein

Chain DE:

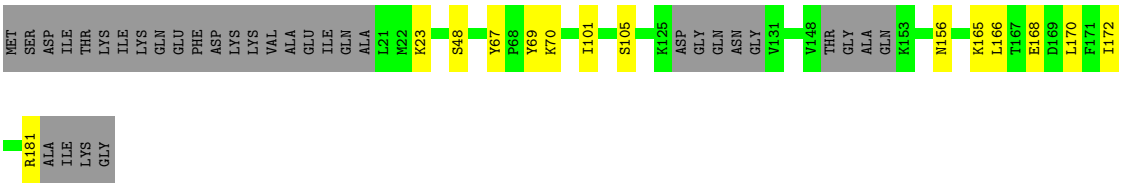


• Molecule 2: Decorator protein P03

Chain DF:

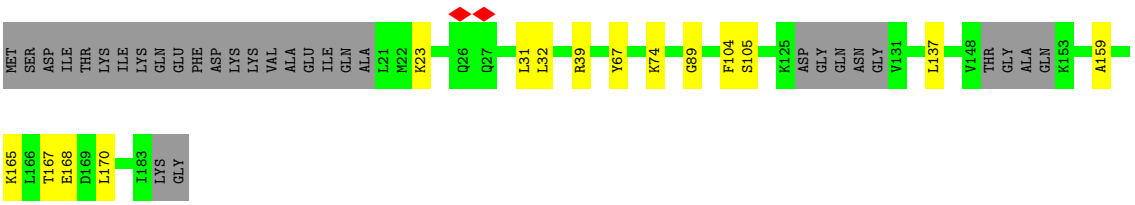
• Molecule 2: Decorator protein P03

Chain DG:



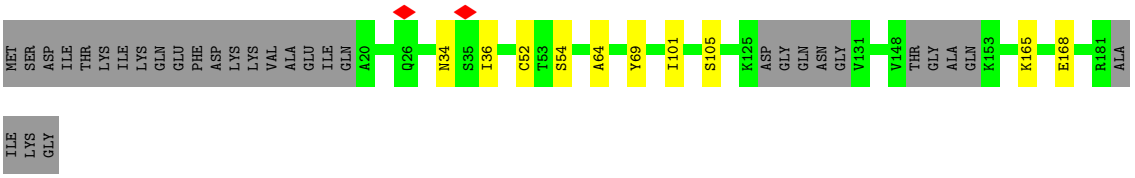
• Molecule 2: Decorator protein P03

Chain DH:



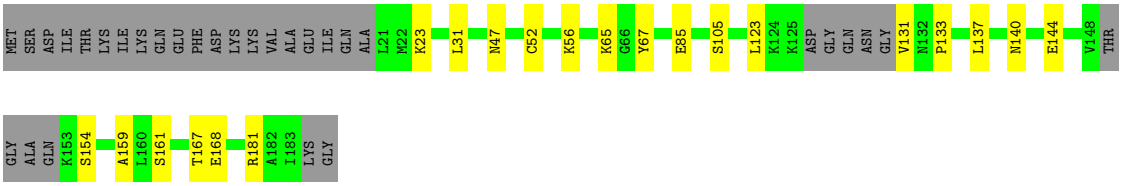
• Molecule 2: Decorator protein P03

Chain DI:

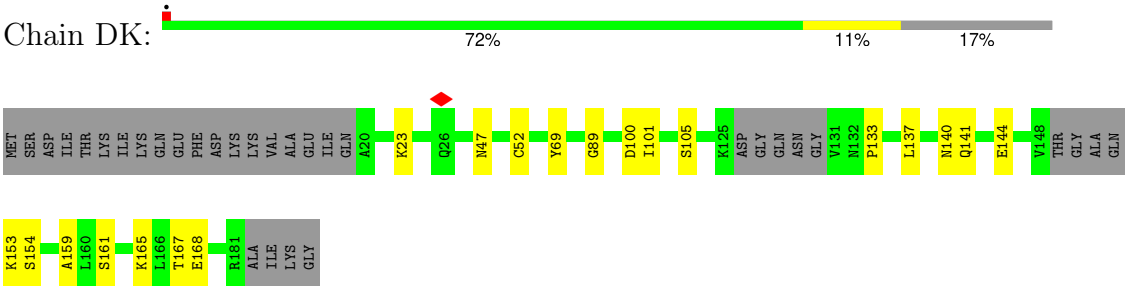


• Molecule 2: Decorator protein P03

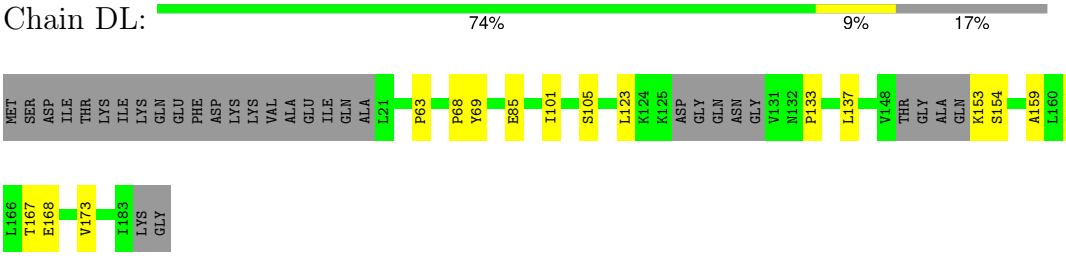
Chain DJ:



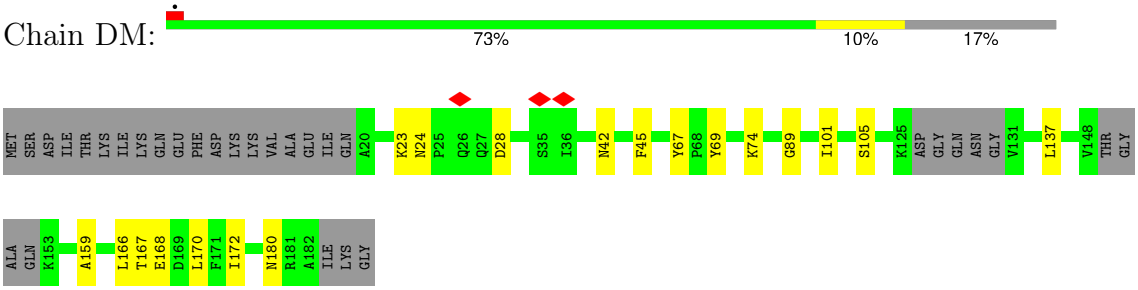
• Molecule 2: Decorator protein P03



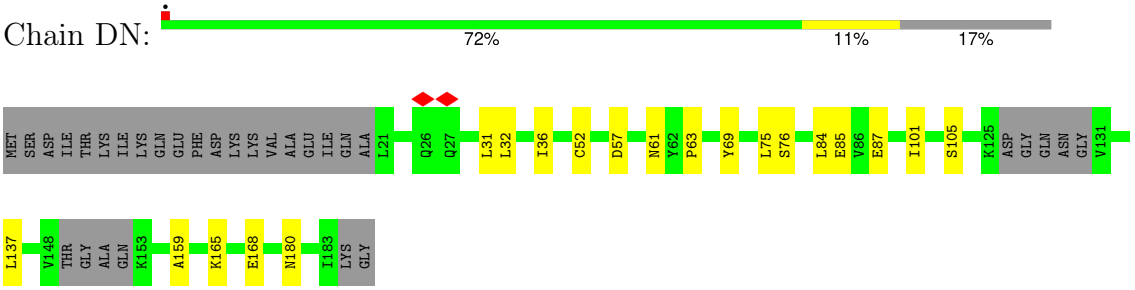
• Molecule 2: Decorator protein P03



• Molecule 2: Decorator protein P03

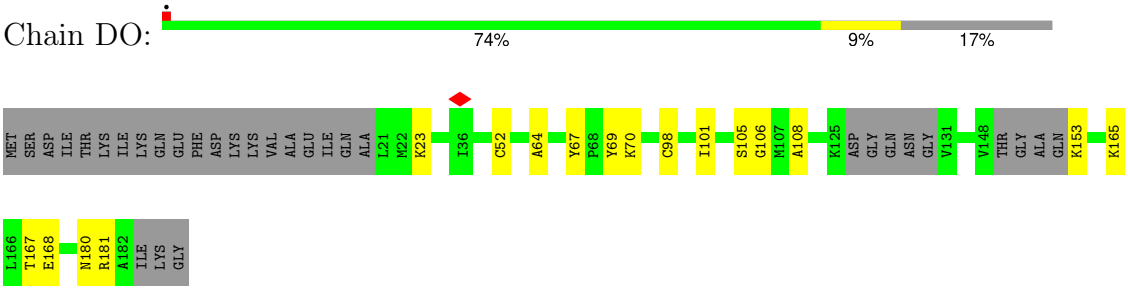


• Molecule 2: Decorator protein P03



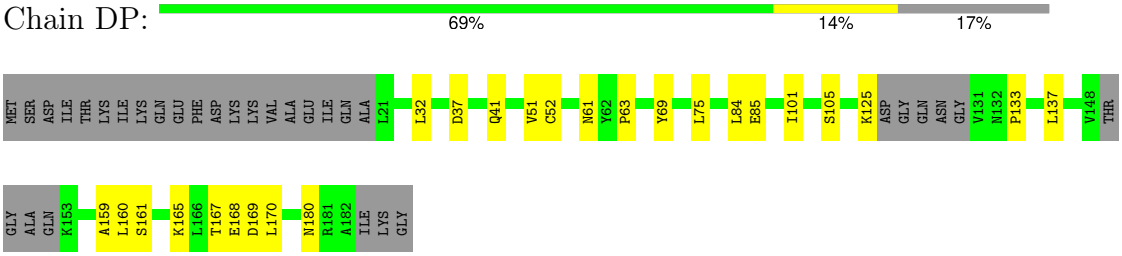
• Molecule 2: Decorator protein P03

Chain DO:



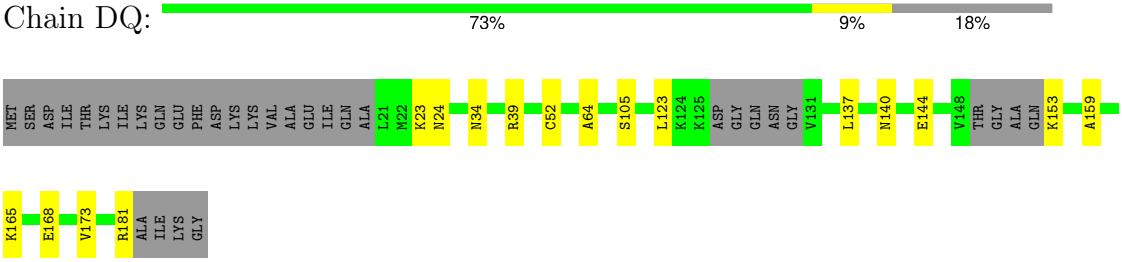
• Molecule 2: Decorator protein P03

Chain DP:



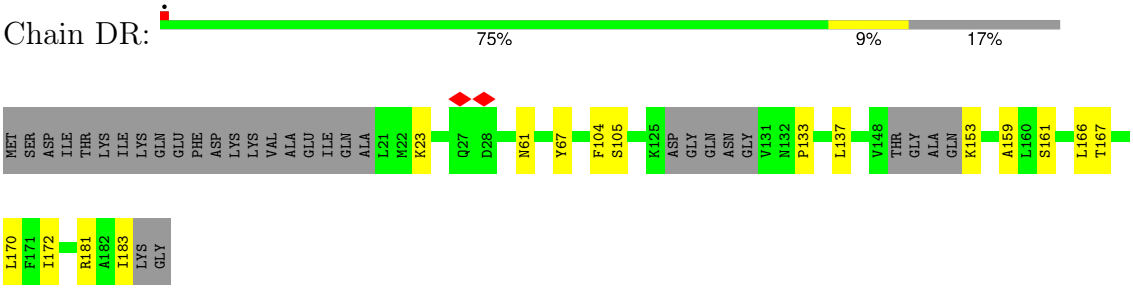
• Molecule 2: Decorator protein P03

Chain DQ:



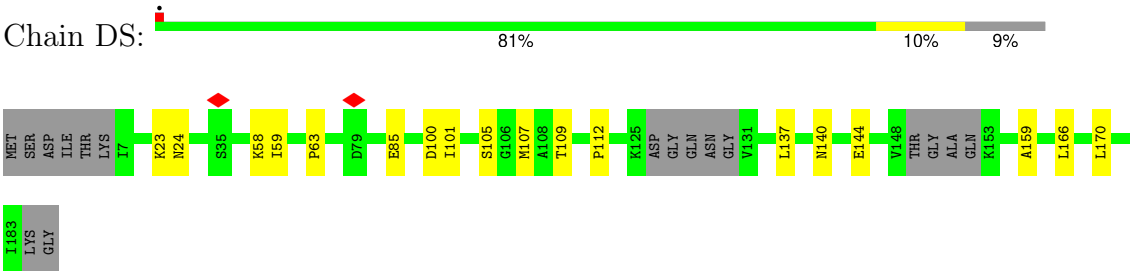
• Molecule 2: Decorator protein P03

Chain DR:



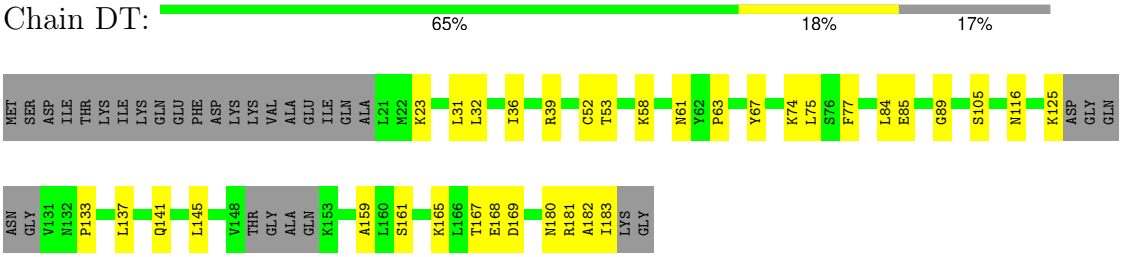
• Molecule 2: Decorator protein P03

Chain DS:



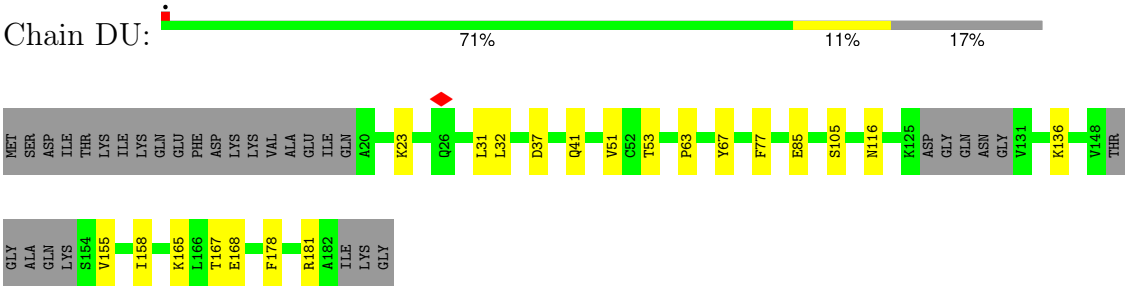
• Molecule 2: Decorator protein P03

Chain DT:



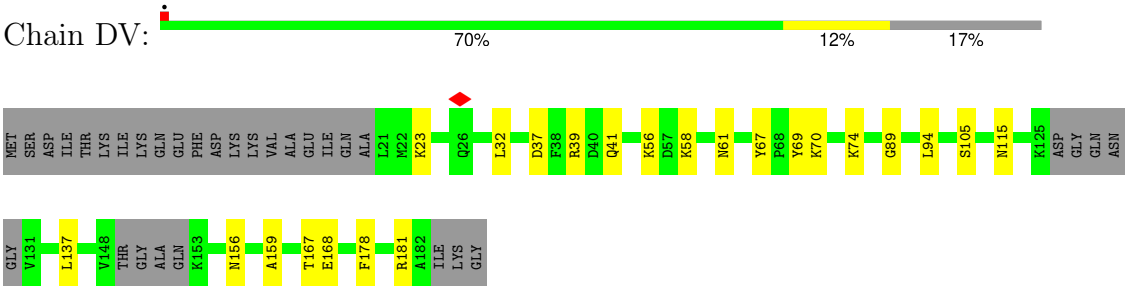
• Molecule 2: Decorator protein P03

Chain DU:



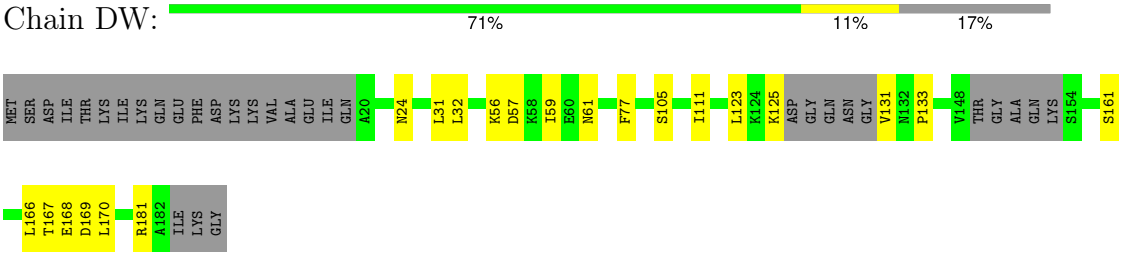
• Molecule 2: Decorator protein P03

Chain DV:



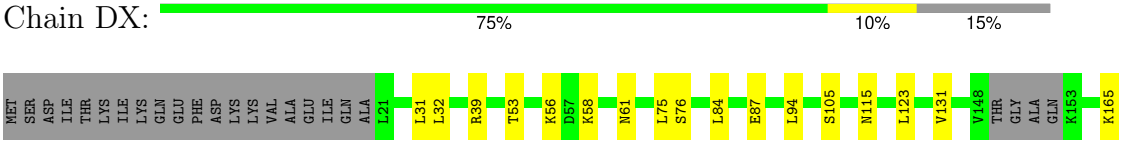
• Molecule 2: Decorator protein P03

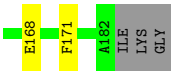
Chain DW:



• Molecule 2: Decorator protein P03

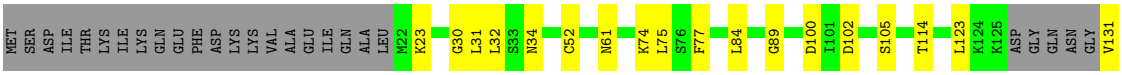
Chain DX:

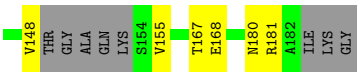




• Molecule 2: Decorator protein P03

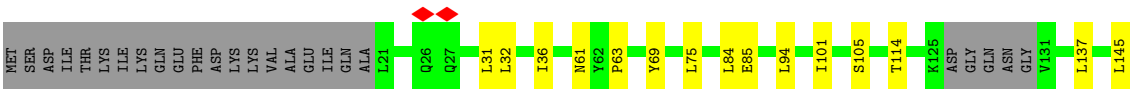
Chain DY:

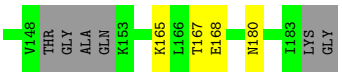




• Molecule 2: Decorator protein P03

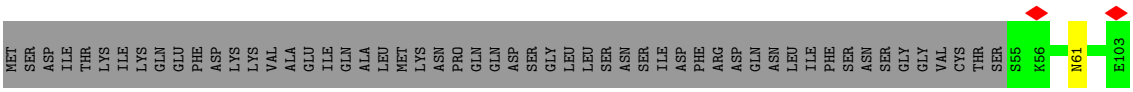
Chain DZ:

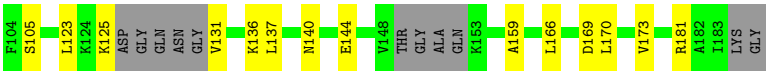




• Molecule 2: Decorator protein P03

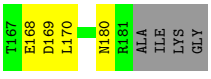
Chain EA:





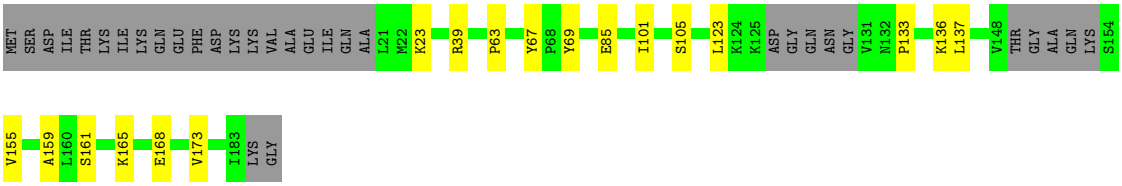
• Molecule 2: Decorator protein P03

Chain EB:



• Molecule 2: Decorator protein P03

Chain EC:

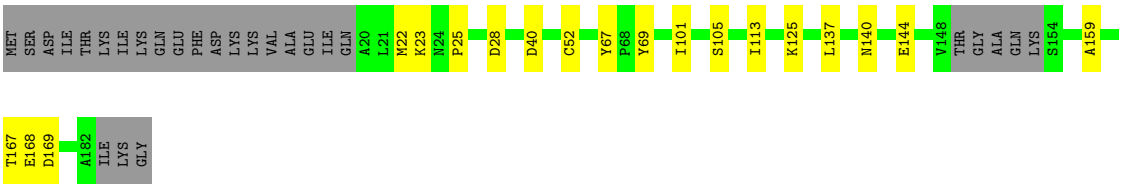


• Molecule 2: Decorator protein P03

Chain ED:

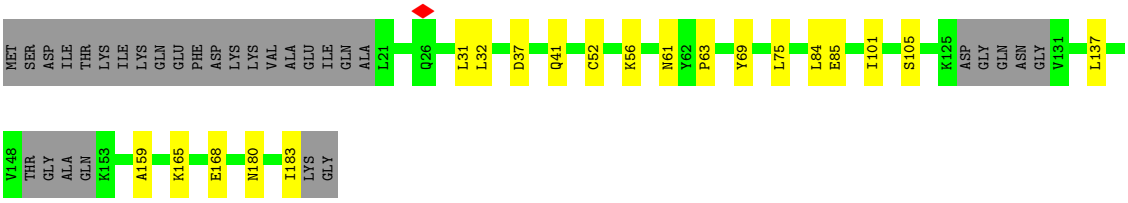
• Molecule 2: Decorator protein P03

Chain EE:



• Molecule 2: Decorator protein P03

Chain EF:

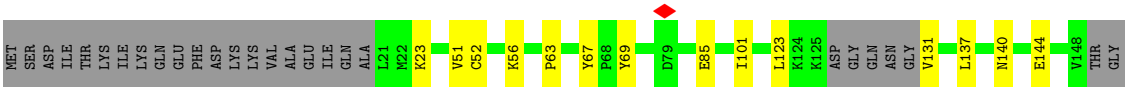


• Molecule 2: Decorator protein P03

Chain EG:

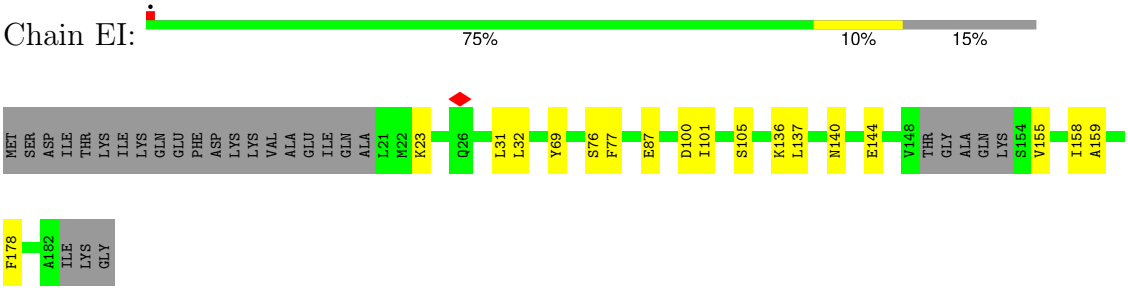
• Molecule 2: Decorator protein P03

Chain EH:



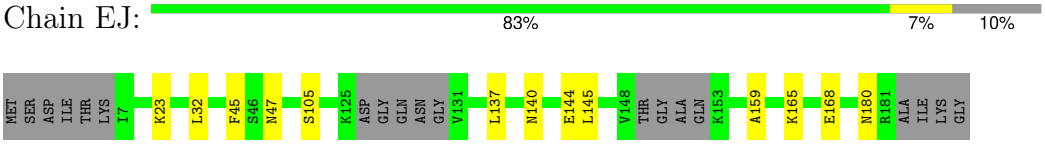
• Molecule 2: Decorator protein P03

Chain EI:



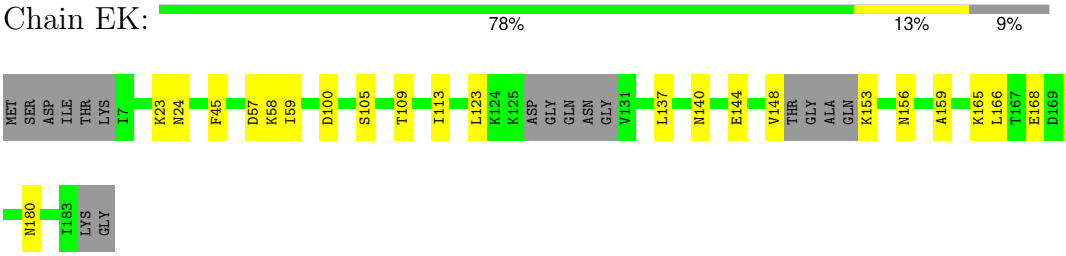
• Molecule 2: Decorator protein P03

Chain EJ:



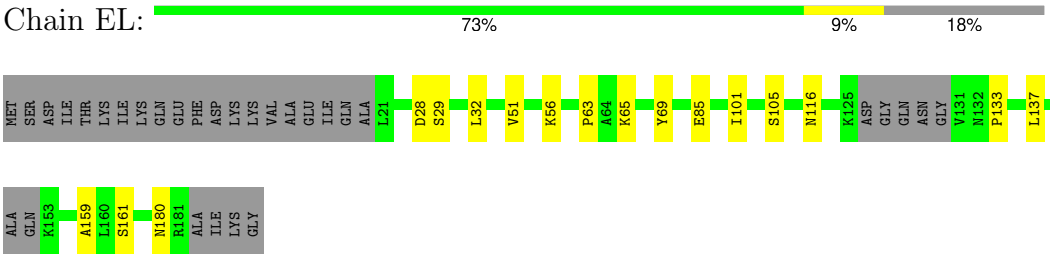
• Molecule 2: Decorator protein P03

Chain EK:



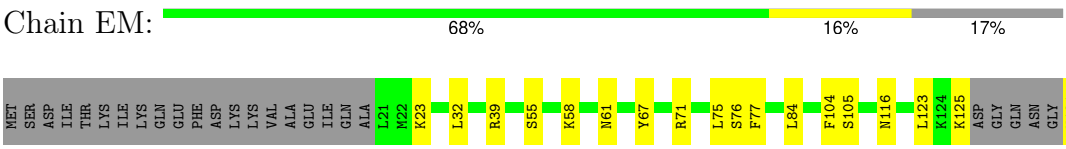
• Molecule 2: Decorator protein P03

Chain EL:



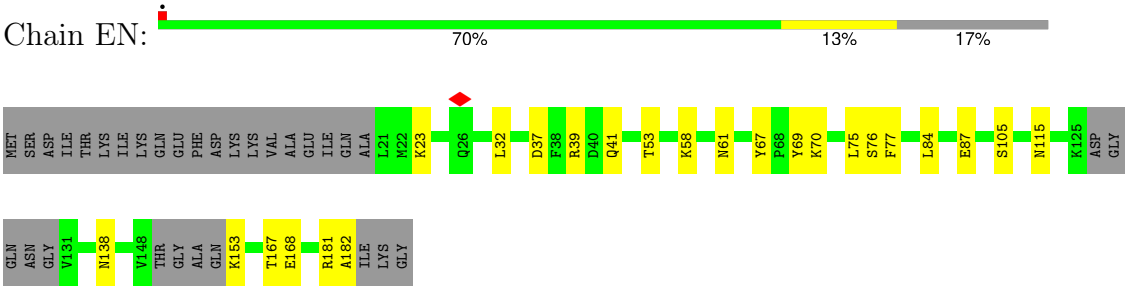
• Molecule 2: Decorator protein P03

Chain EM:



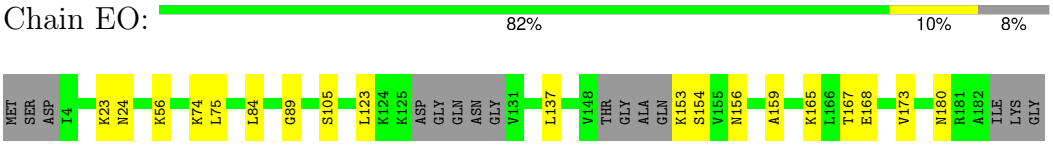
• Molecule 2: Decorator protein P03

Chain EN:



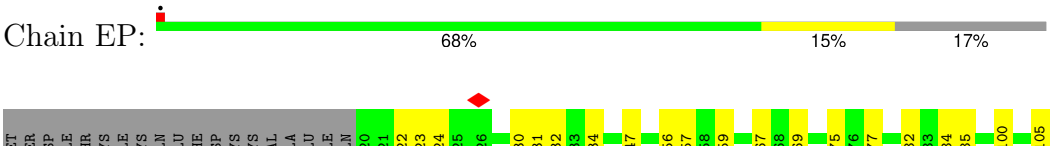
• Molecule 2: Decorator protein P03

Chain EO:



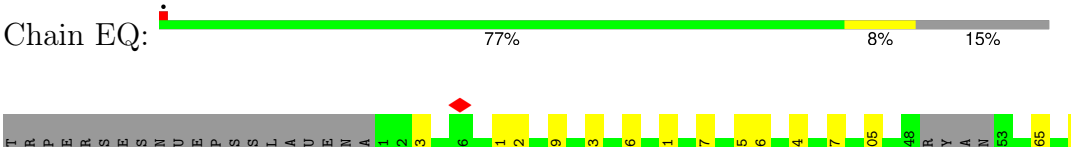
• Molecule 2: Decorator protein P03

Chain EP:



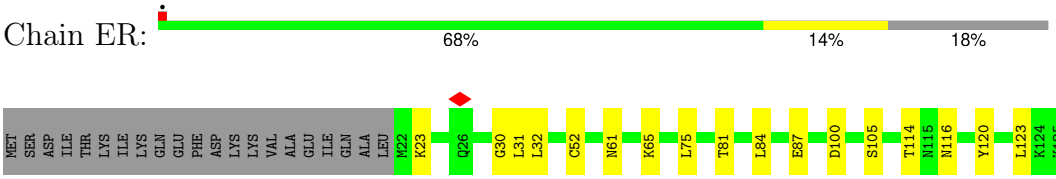
• Molecule 2: Decorator protein P03

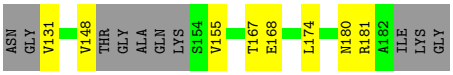
Chain EQ:



• Molecule 2: Decorator protein P03

Chain ER:





• Molecule 2: Decorator protein P03

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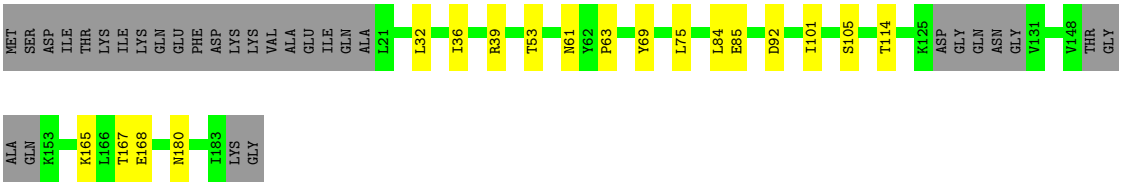

• Molecule 2: Decorator protein P03

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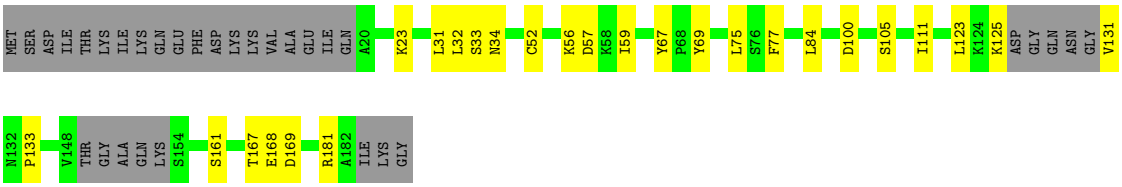

• Molecule 2: Decorator protein P03

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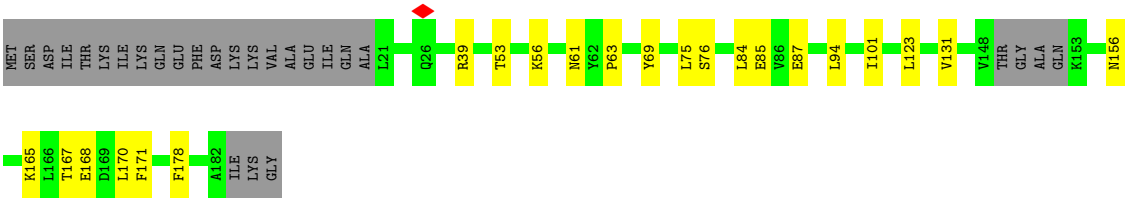
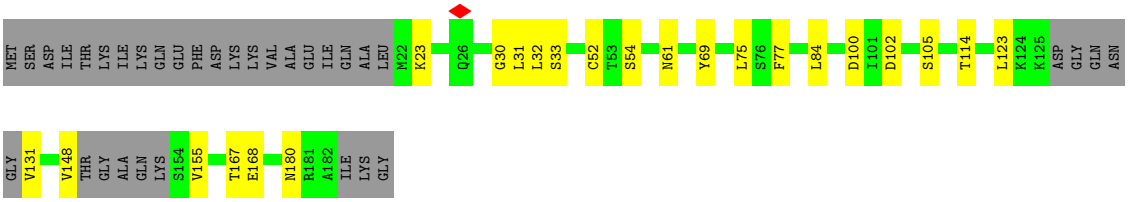


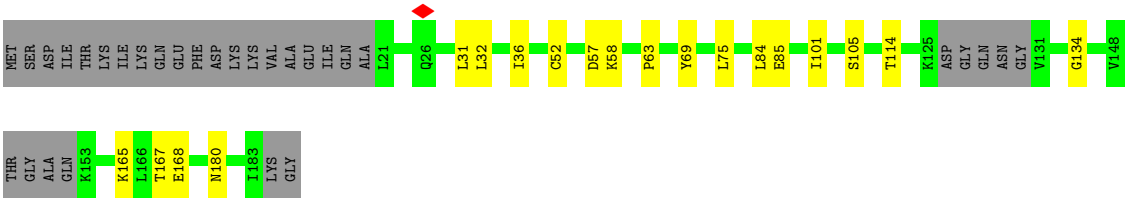
• Molecule 2: Decorator protein P03

Chain EV:



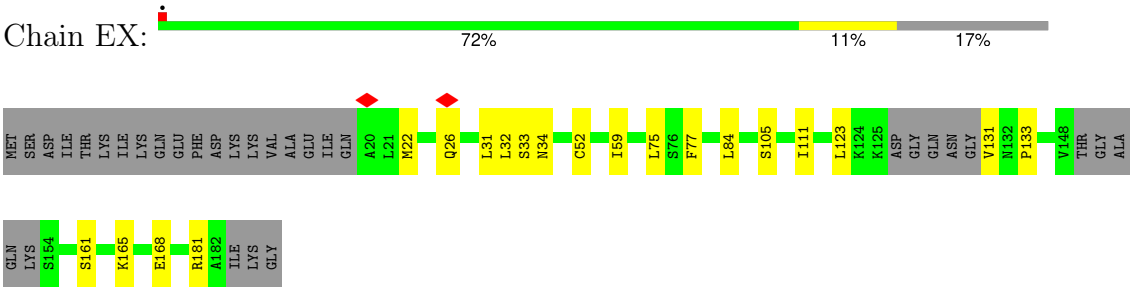
• Molecule 2: Decorator protein P03

Chain EW:



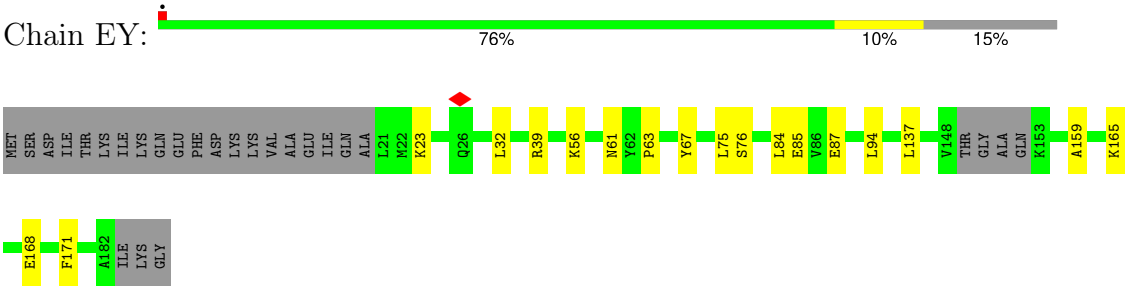
• Molecule 2: Decorator protein P03

Chain EX:



• Molecule 2: Decorator protein P03

Chain EY:



• Molecule 2: Decorator protein P03

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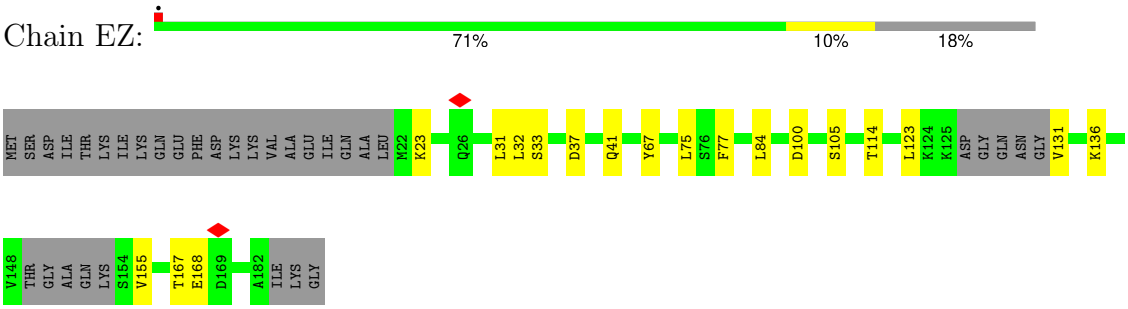

• Molecule 2: Decorator protein P03

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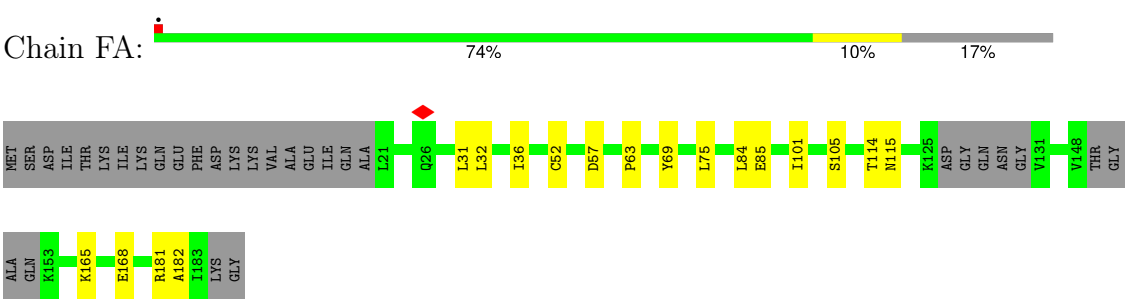
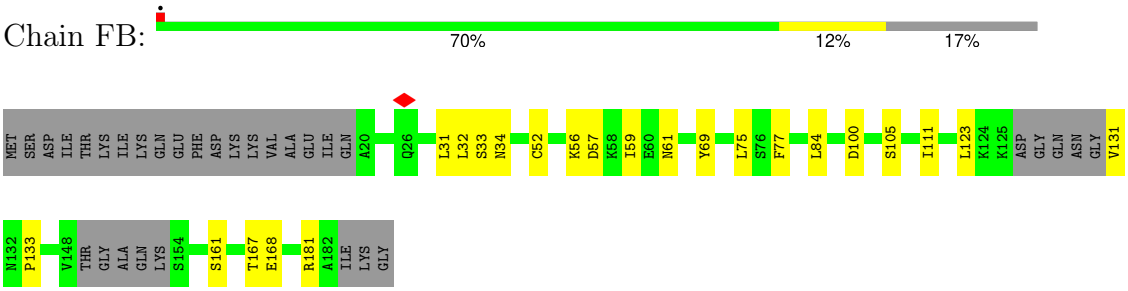


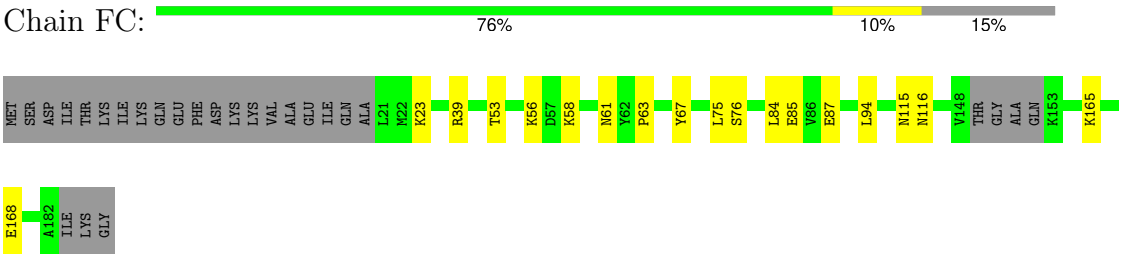
• Molecule 2: Decorator protein P03

Chain FB:



• Molecule 2: Decorator protein P03

Chain FC:



• Molecule 2: Decorator protein P03

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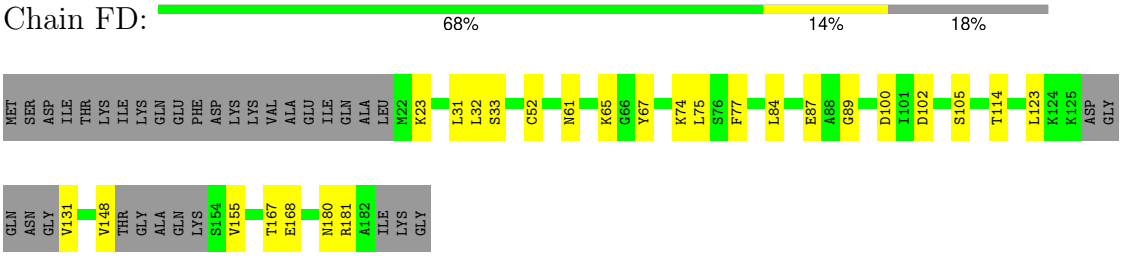

• Molecule 2: Decorator protein P03

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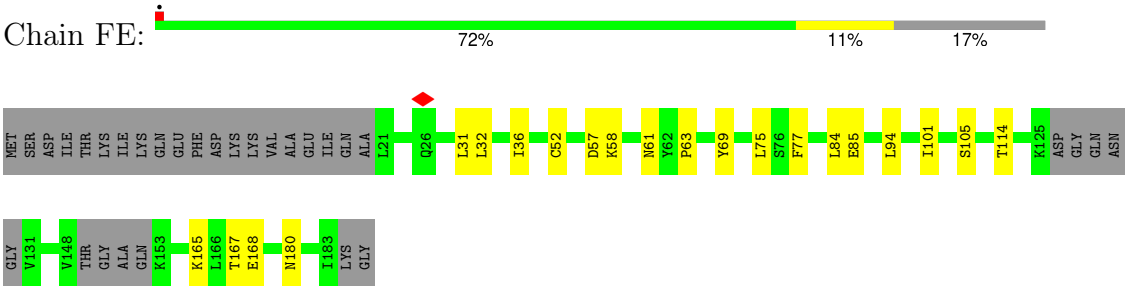

• Molecule 2: Decorator protein P03

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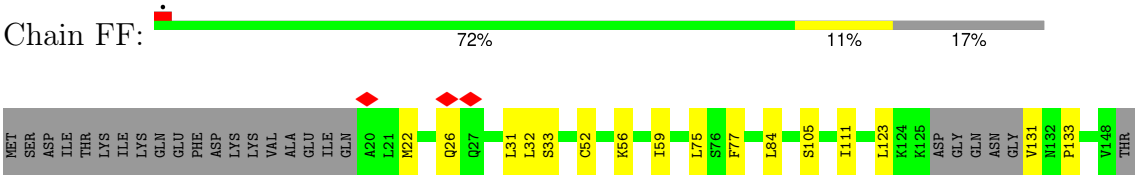

• Molecule 2: Decorator protein P03

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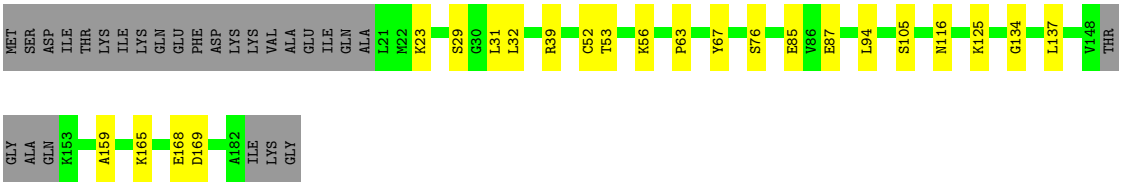

• Molecule 2: Decorator protein P03

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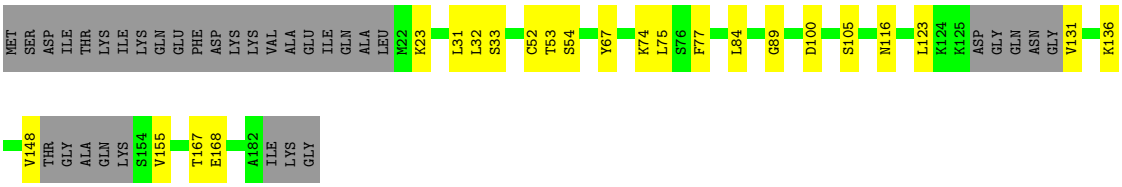

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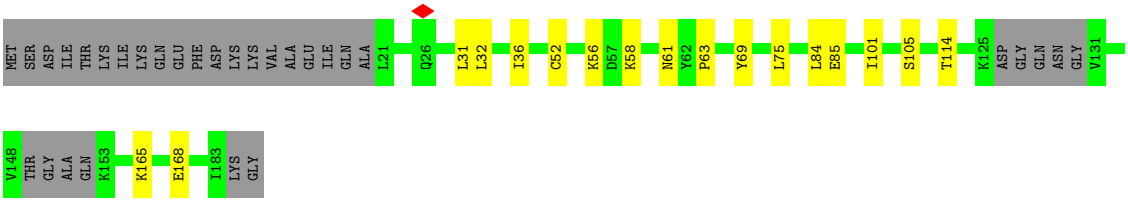
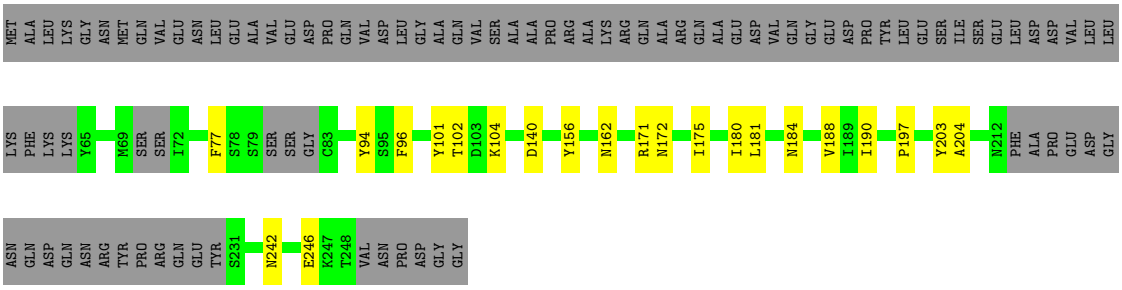


• Molecule 3: Decorator protein P04

Chain FJ:

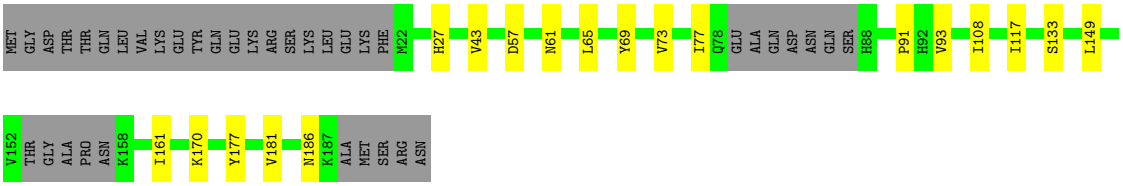


• Molecule 4: Decorator protein P05

Chain FK:

• Molecule 4: Decorator protein P05

Chain FL:



• Molecule 4: Decorator protein P05

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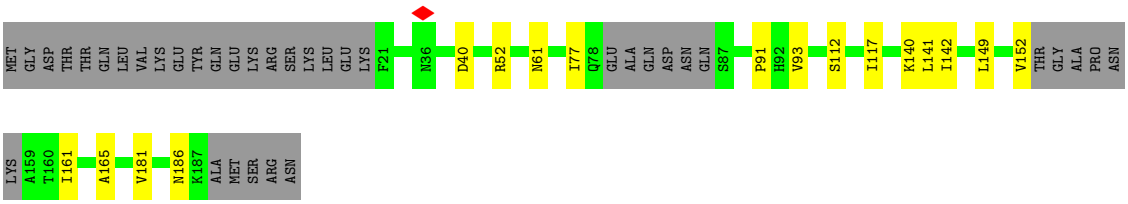

• Molecule 4: Decorator protein P05

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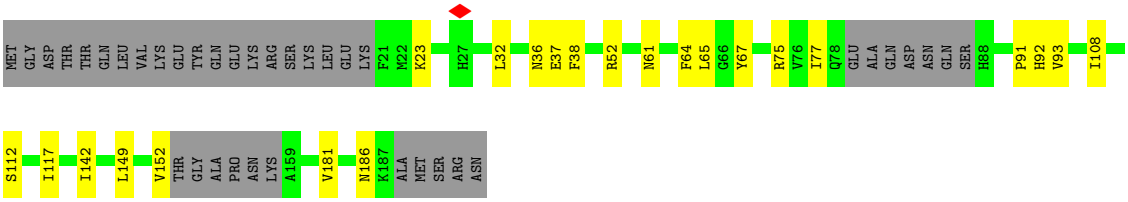

• Molecule 4: Decorator protein P05

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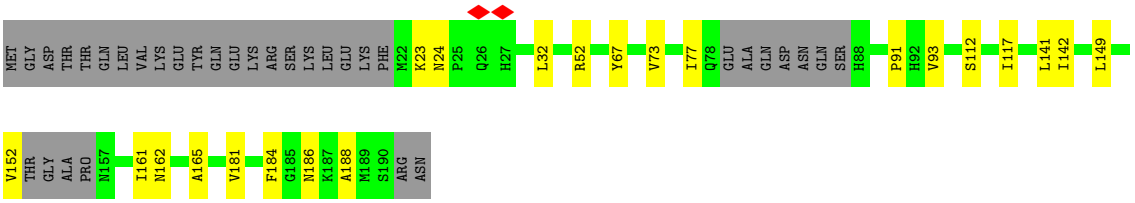

• Molecule 4: Decorator protein P05

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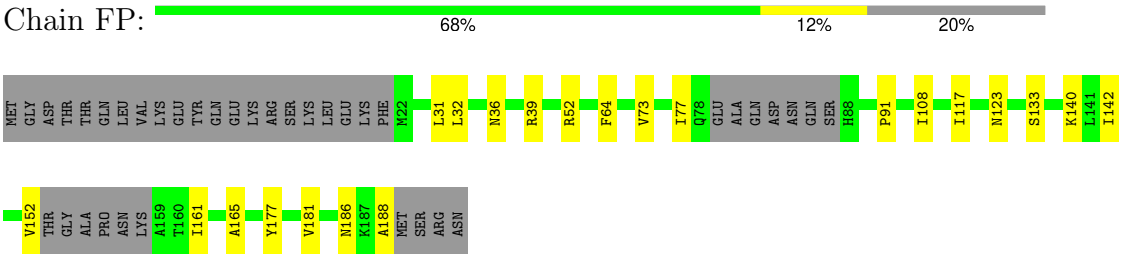

• Molecule 4: Decorator protein P05

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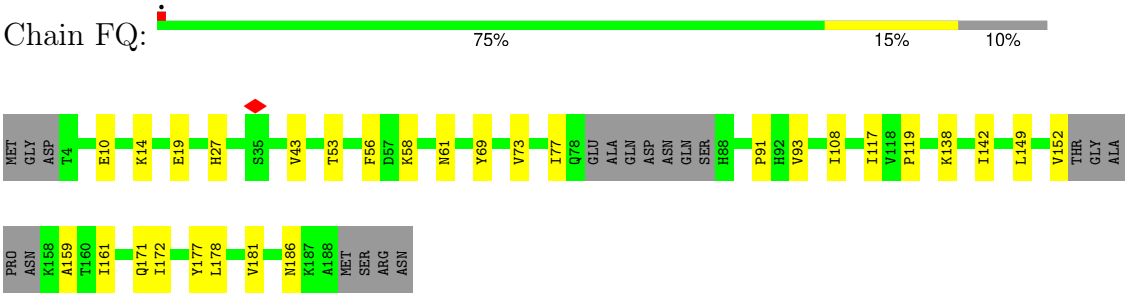

• Molecule 4: Decorator protein P05

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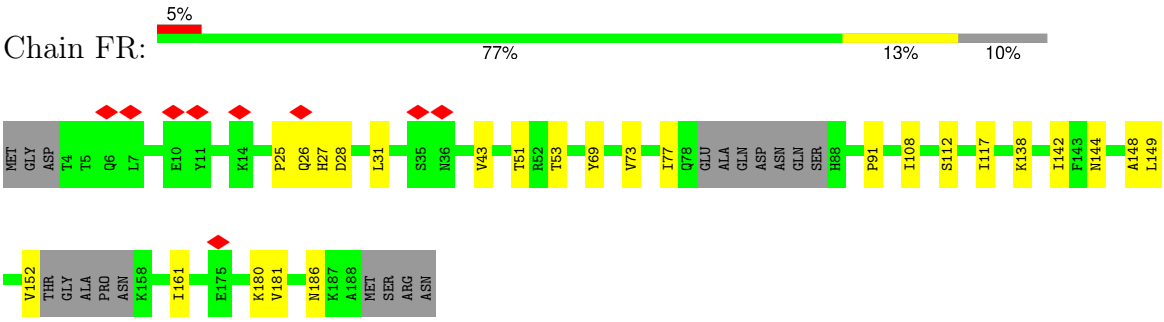

• Molecule 4: Decorator protein P05

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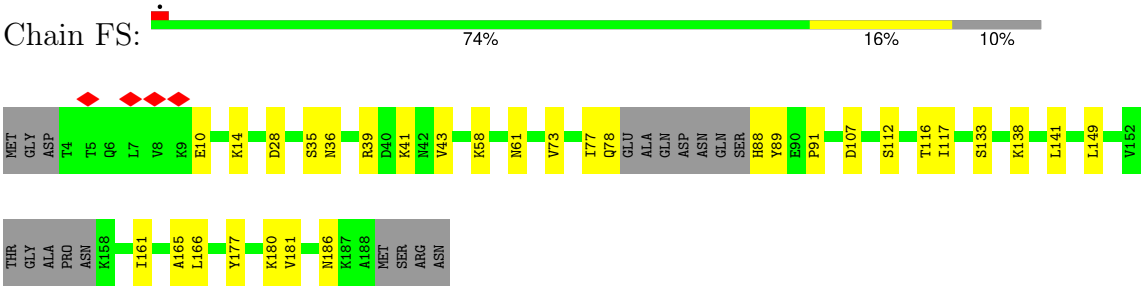

• Molecule 4: Decorator protein P05

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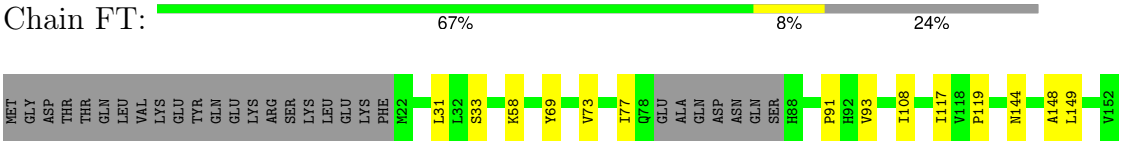

• Molecule 4: Decorator protein P05

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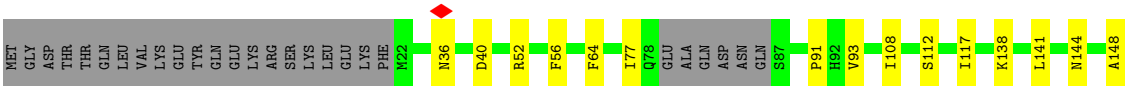

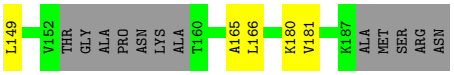

• Molecule 4: Decorator protein P05

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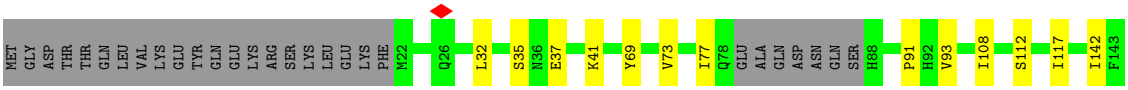

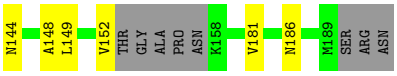

• Molecule 4: Decorator protein P05

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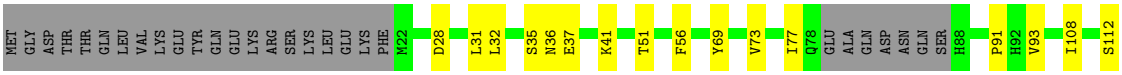

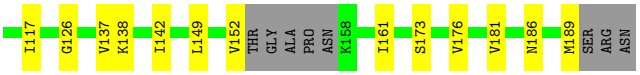

• Molecule 4: Decorator protein P05

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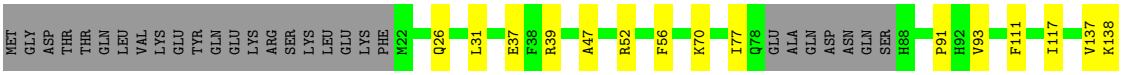

• Molecule 4: Decorator protein P05

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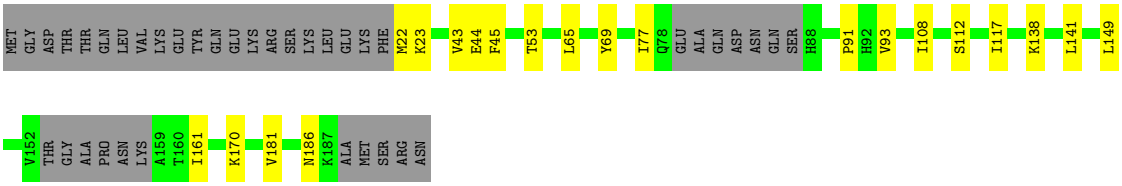

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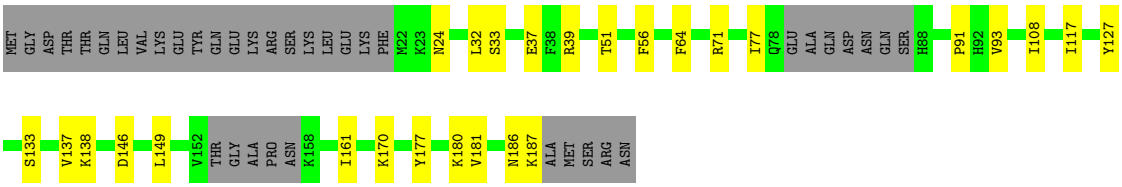
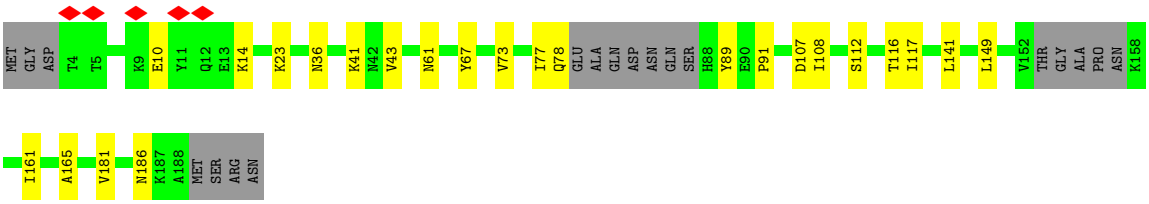


• Molecule 4: Decorator protein P05

Chain GA:

• Molecule 4: Decorator protein P05

Chain GB:

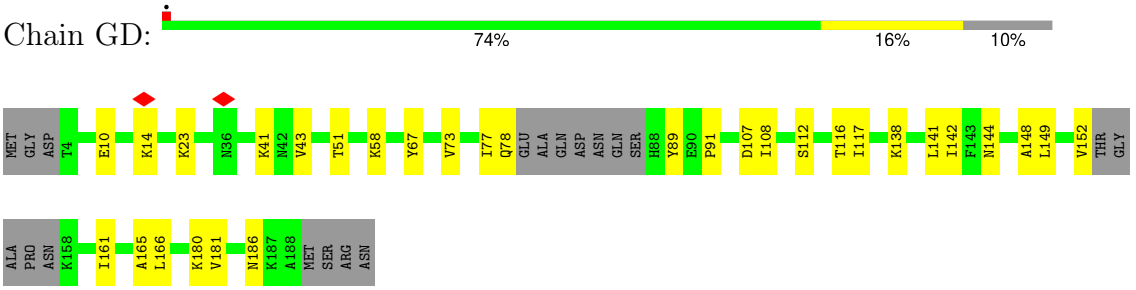


• Molecule 4: Decorator protein P05

Chain GC:

• Molecule 4: Decorator protein P05

Chain GD:



• Molecule 4: Decorator protein P05

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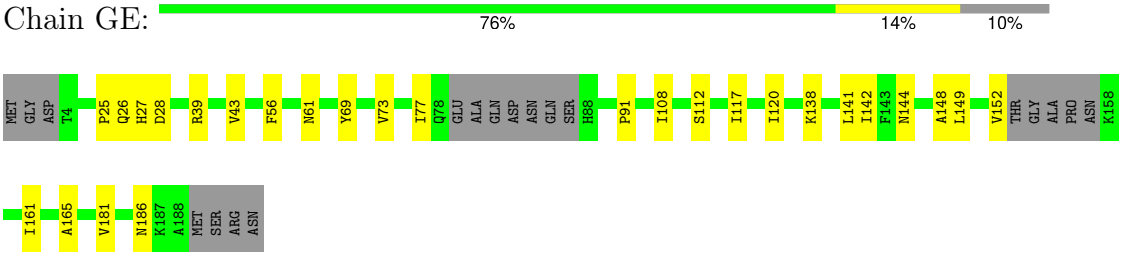

• Molecule 4: Decorator protein P05

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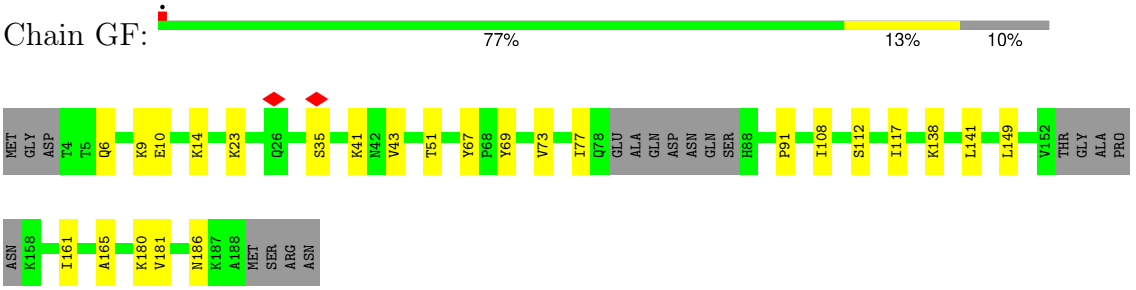

• Molecule 4: Decorator protein P05

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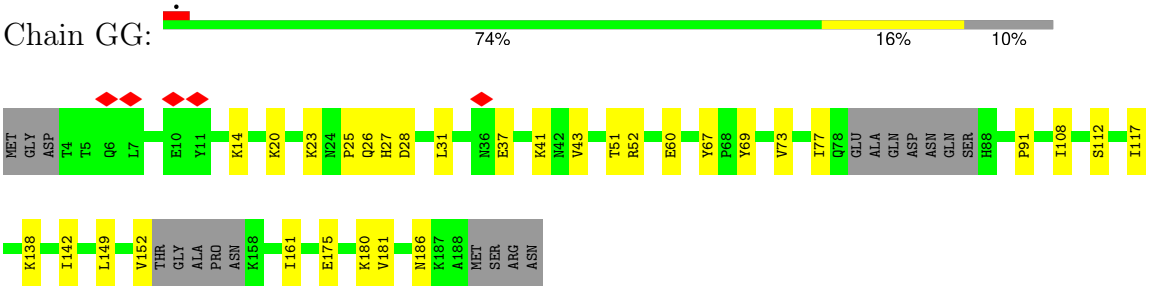

• Molecule 4: Decorator protein P05

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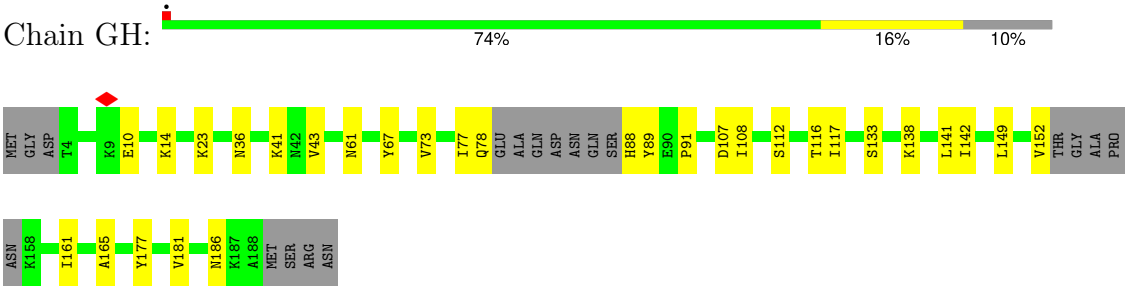

• Molecule 4: Decorator protein P05

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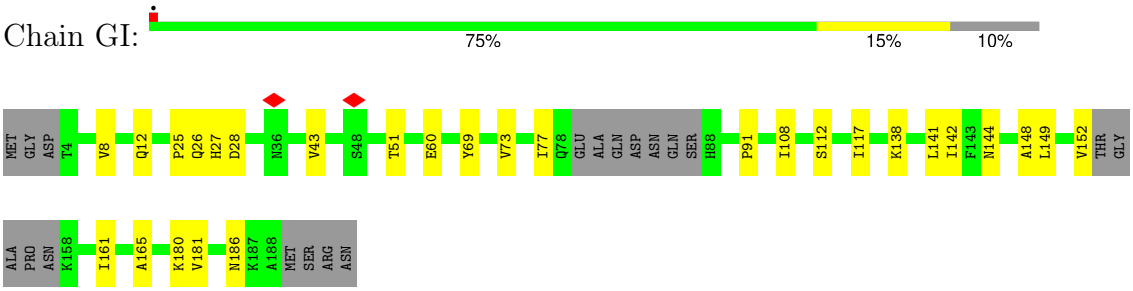

• Molecule 4: Decorator protein P05

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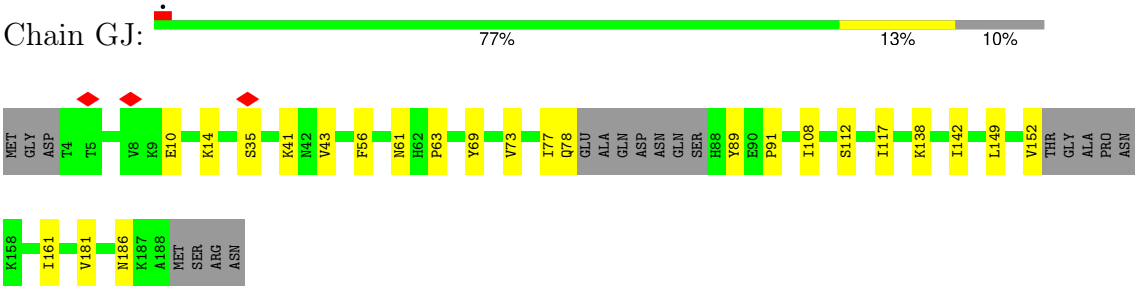
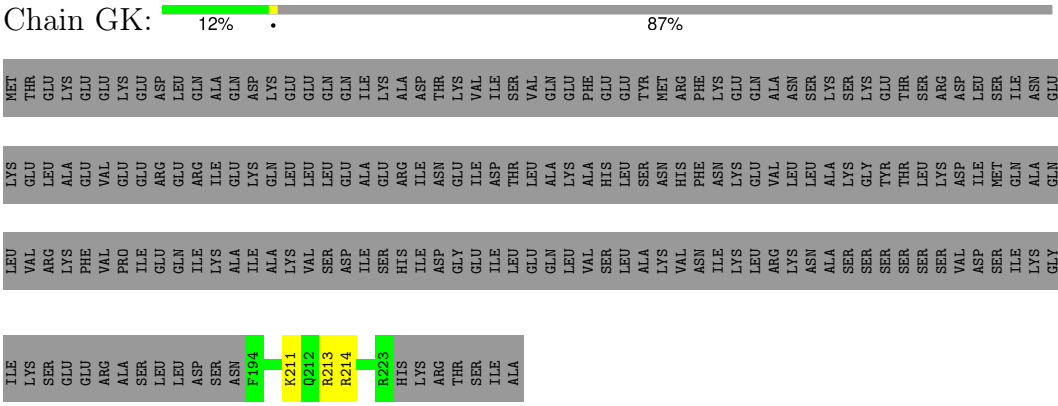


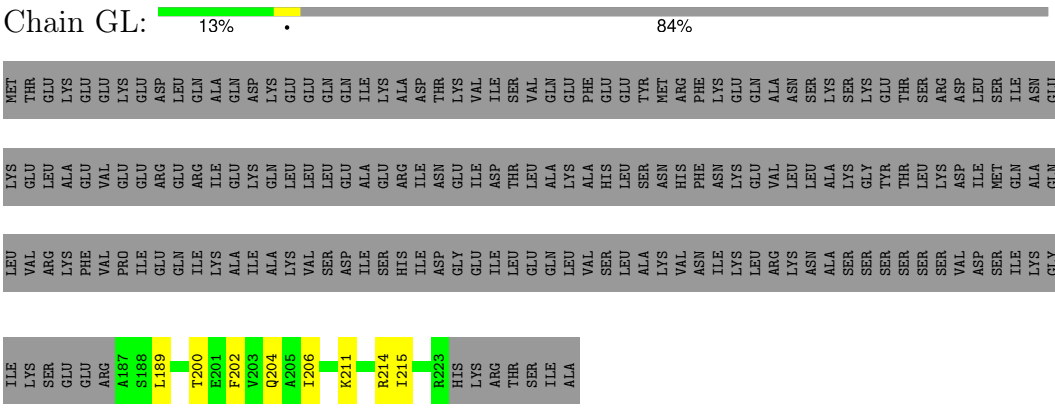
• Molecule 5: Scaffold protein

Chain GK:



• Molecule 5: Scaffold protein

Chain GL:



• Molecule 5: Scaffold protein

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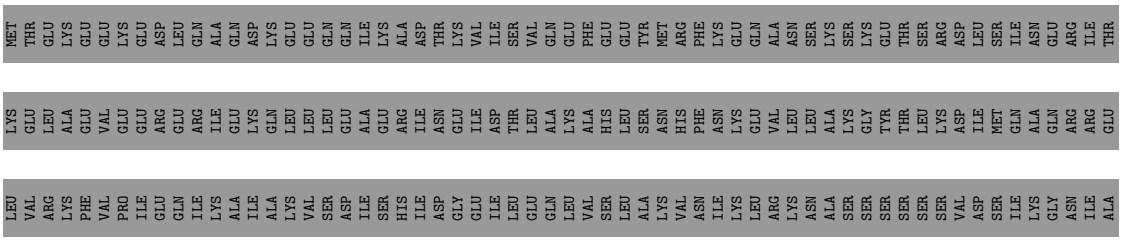

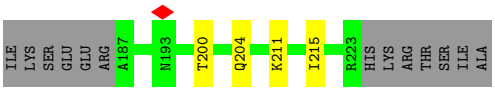

• Molecule 5: Scaffold protein

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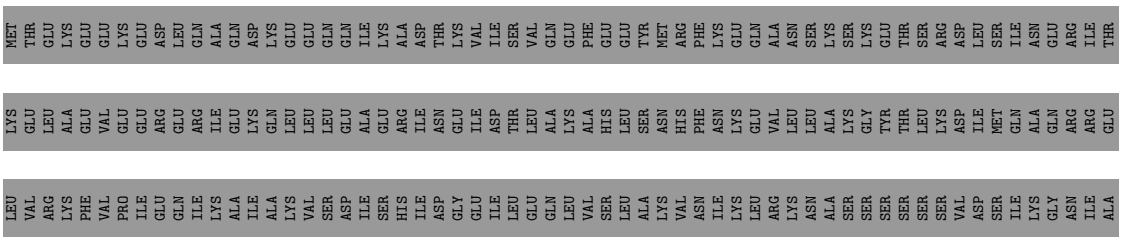

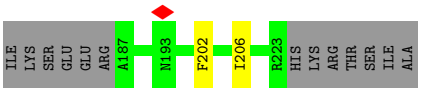

• Molecule 5: Scaffold protein

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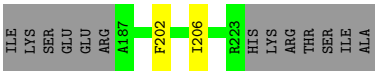

• Molecule 5: Scaffold protein

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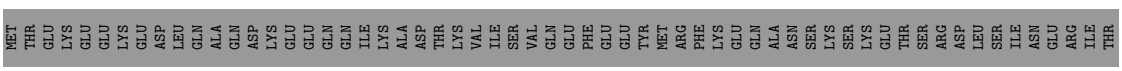

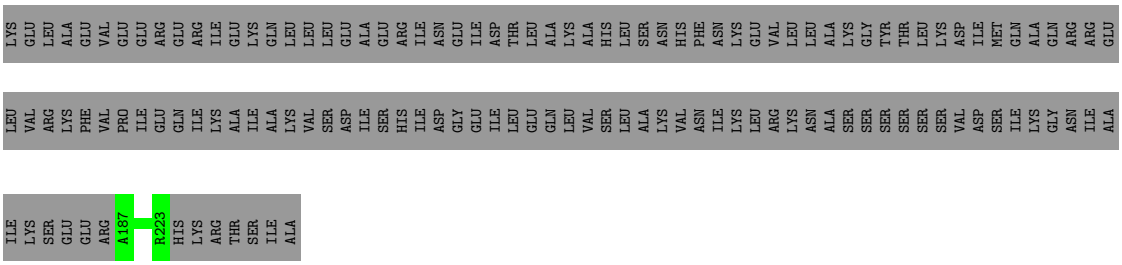

• Molecule 5: Scaffold protein

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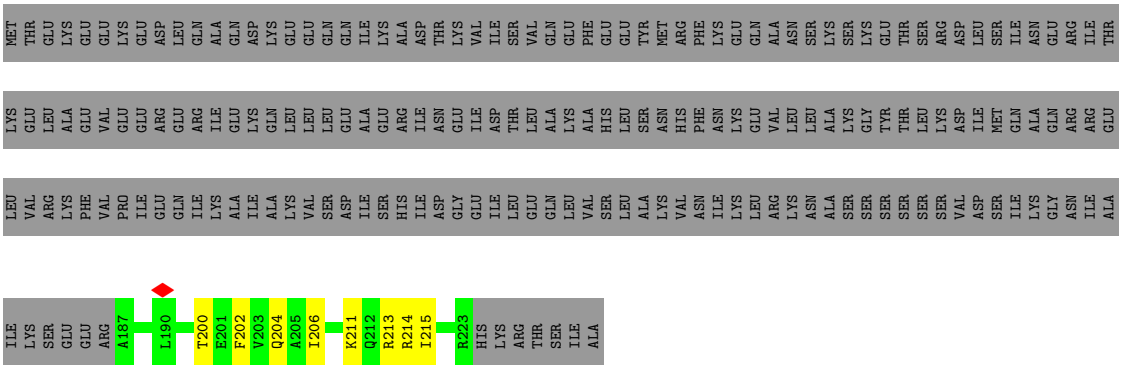
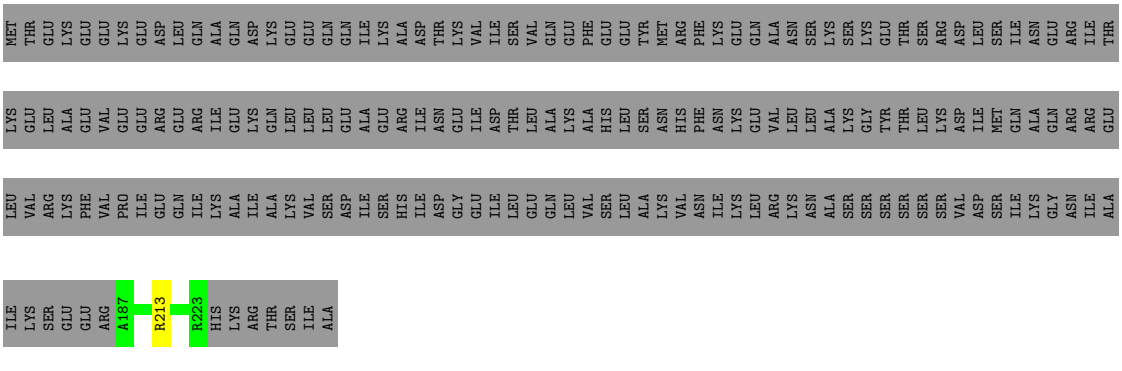


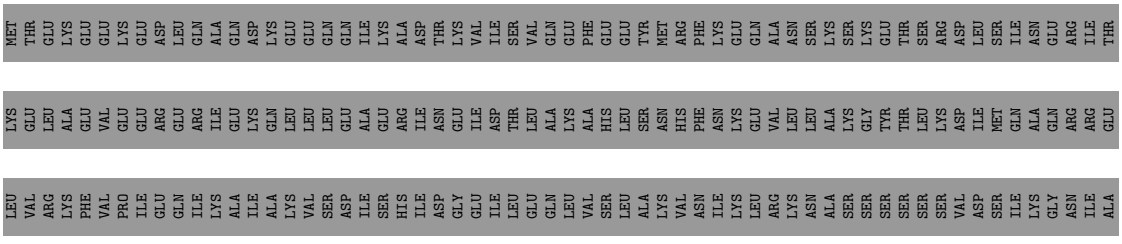
• Molecule 5: Scaffold protein

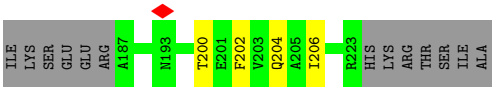
Chain GR:



• Molecule 5: Scaffold protein

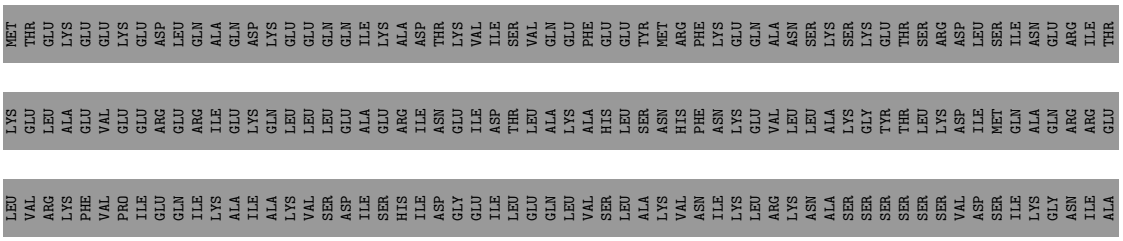
Chain GS:





• Molecule 5: Scaffold protein

Chain GT:



• Molecule 5: Scaffold protein

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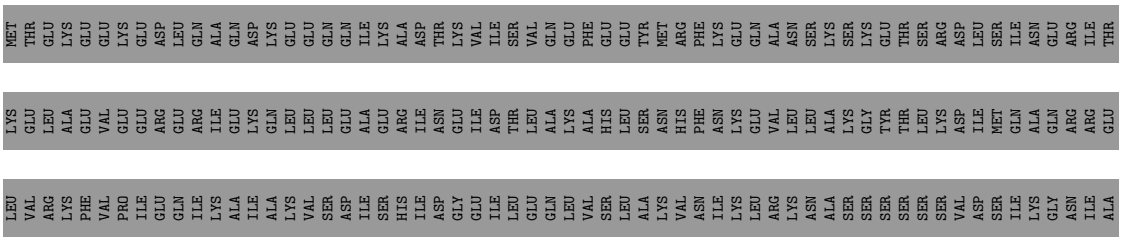
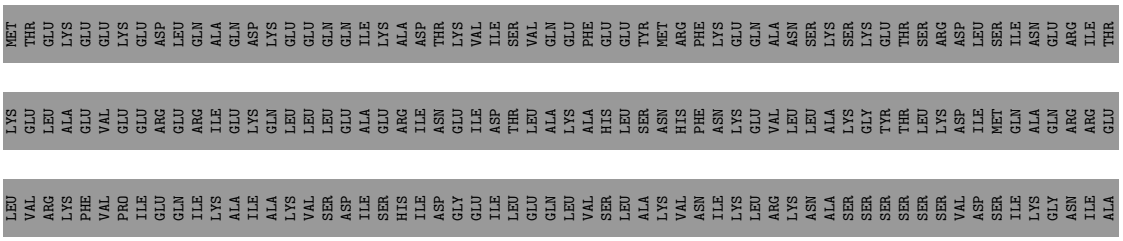


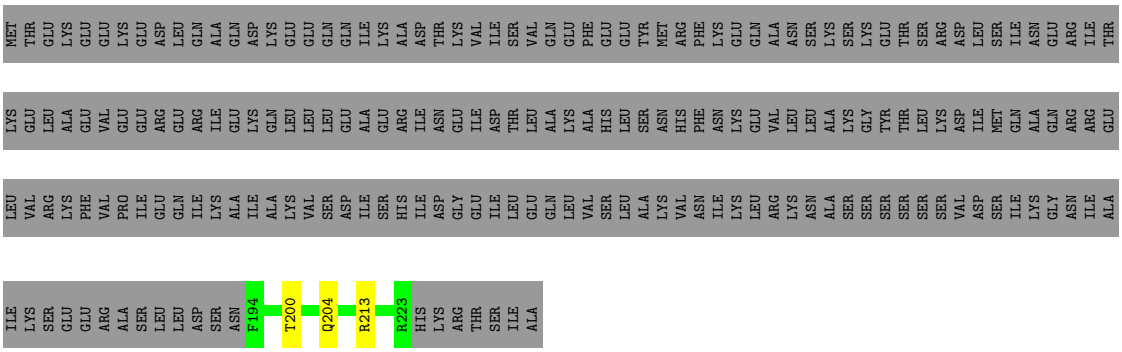
• Molecule 5: Scaffold protein

Chain GV:



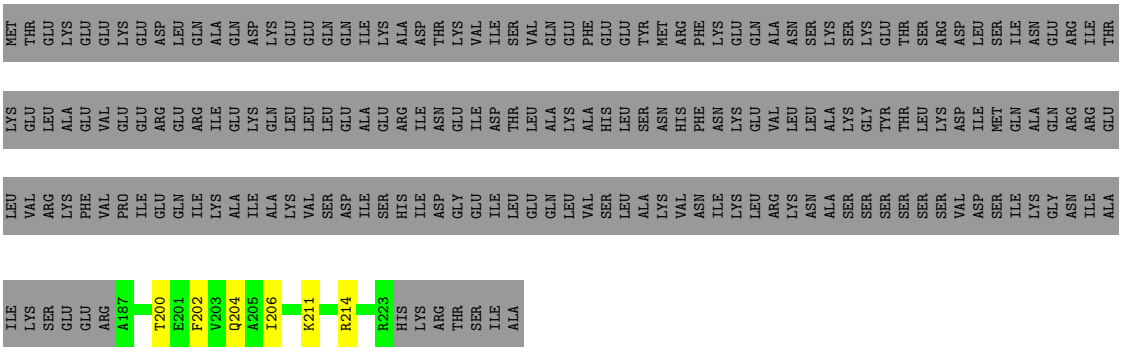
• Molecule 5: Scaffold protein

Chain GW:



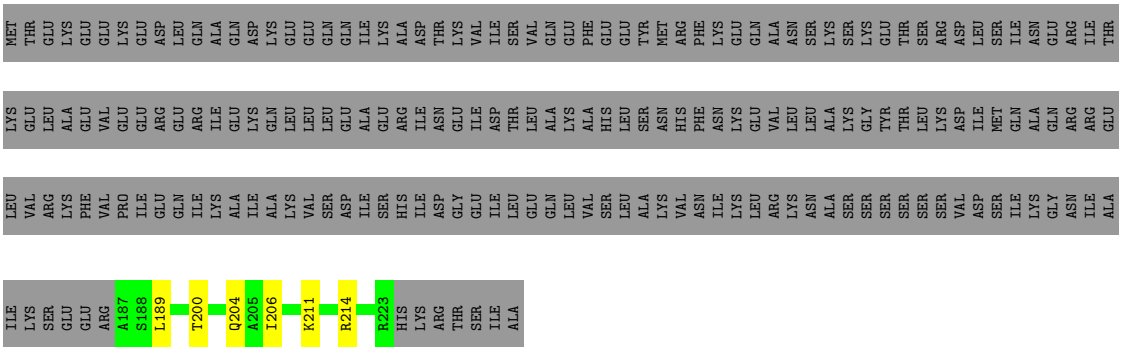
• Molecule 5: Scaffold protein

Chain GX:



• Molecule 5: Scaffold protein

Chain GY:

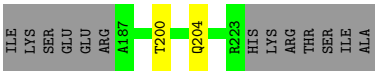


• Molecule 5: Scaffold protein

Chain GZ:

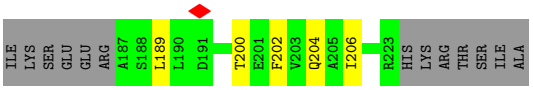
• Molecule 5: Scaffold protein

Chain HA:



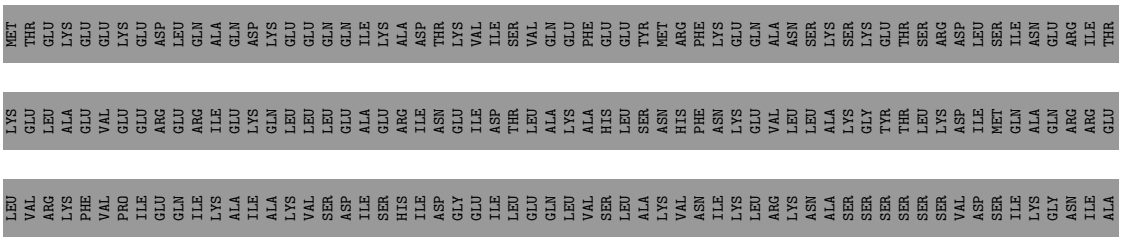
• Molecule 5: Scaffold protein

Chain HB:



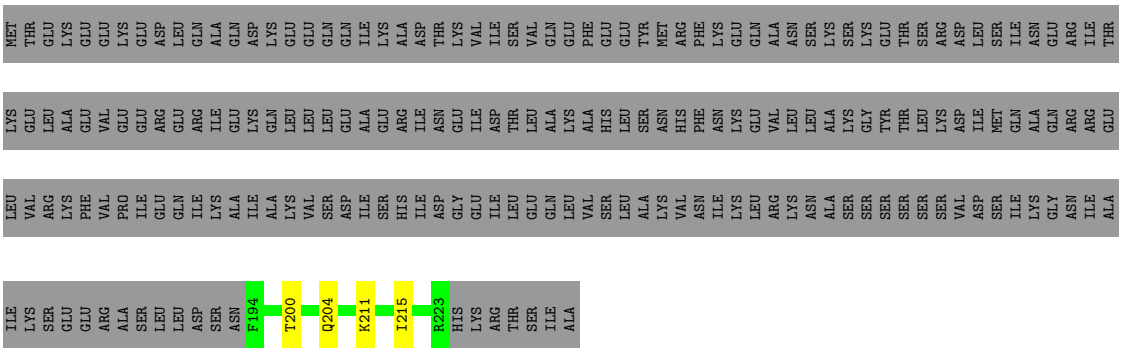
• Molecule 5: Scaffold protein

Chain HC:



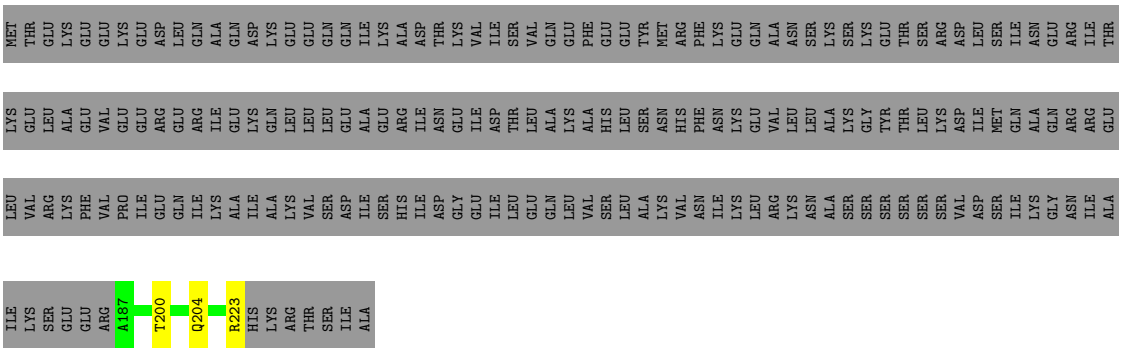
• Molecule 5: Scaffold protein

Chain HD:



• Molecule 5: Scaffold protein

Chain HE:



• Molecule 5: Scaffold protein

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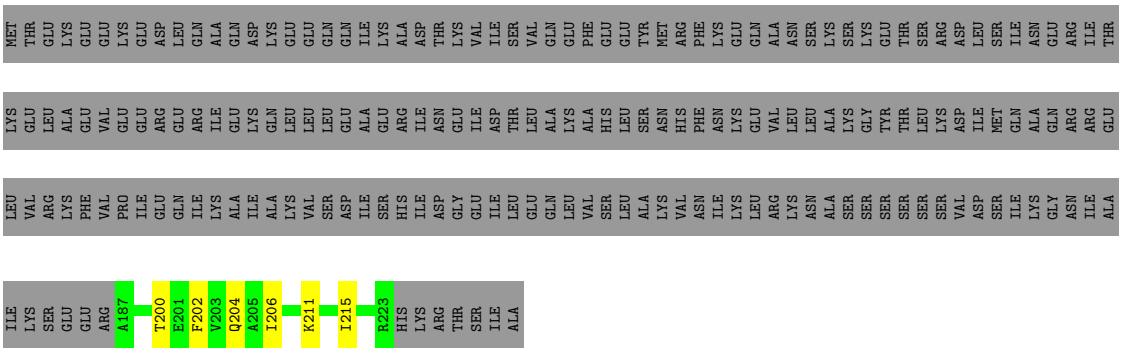

• Molecule 5: Scaffold protein

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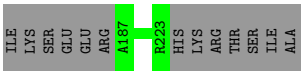

• Molecule 5: Scaffold protein

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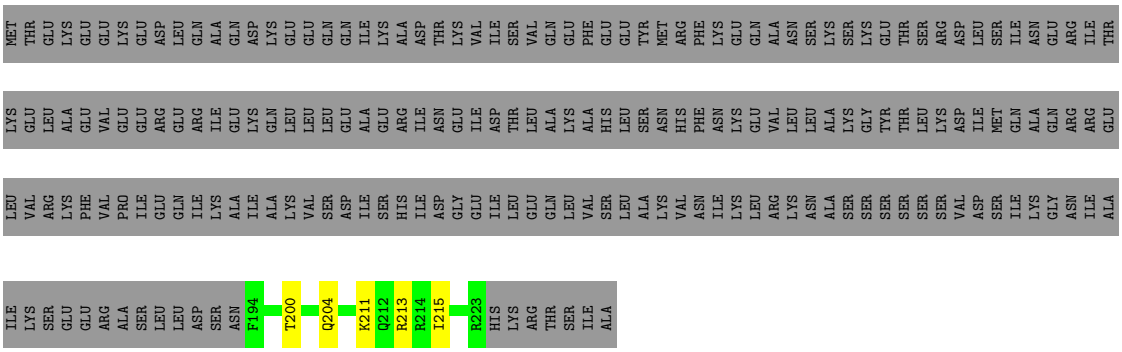

• Molecule 5: Scaffold protein

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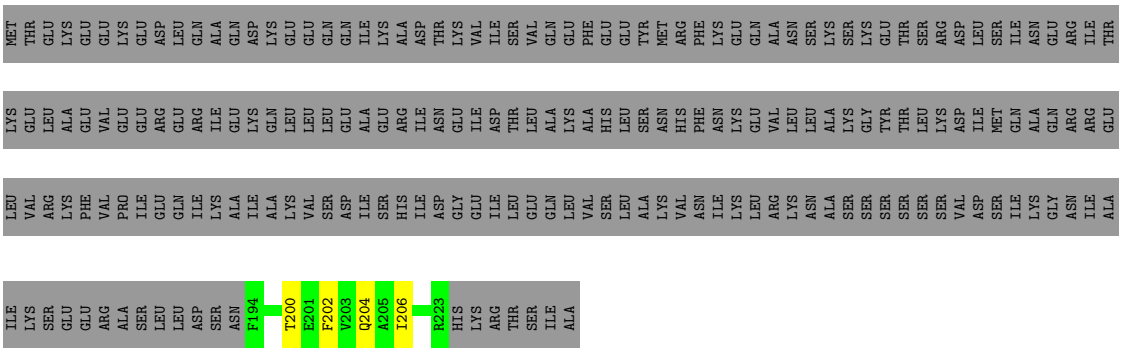

• Molecule 5: Scaffold protein

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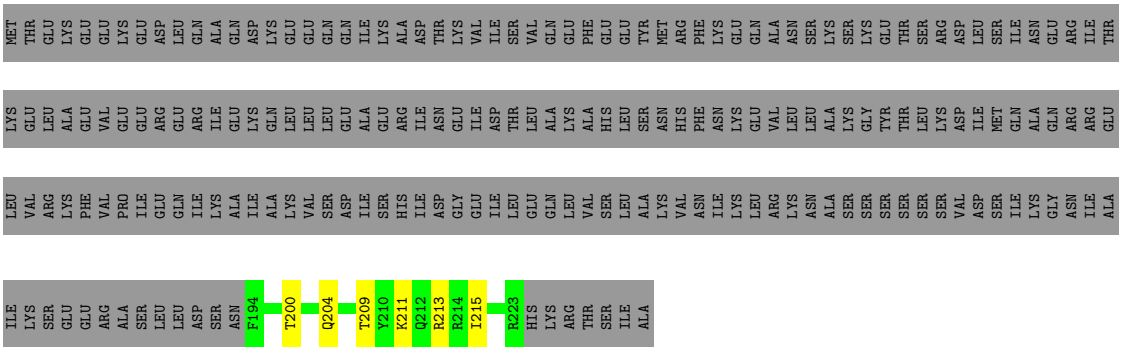

• Molecule 5: Scaffold protein

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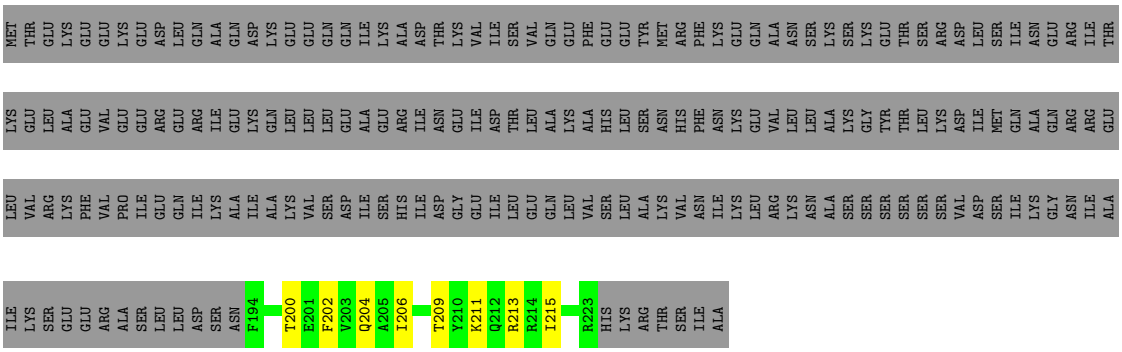

• Molecule 5: Scaffold protein

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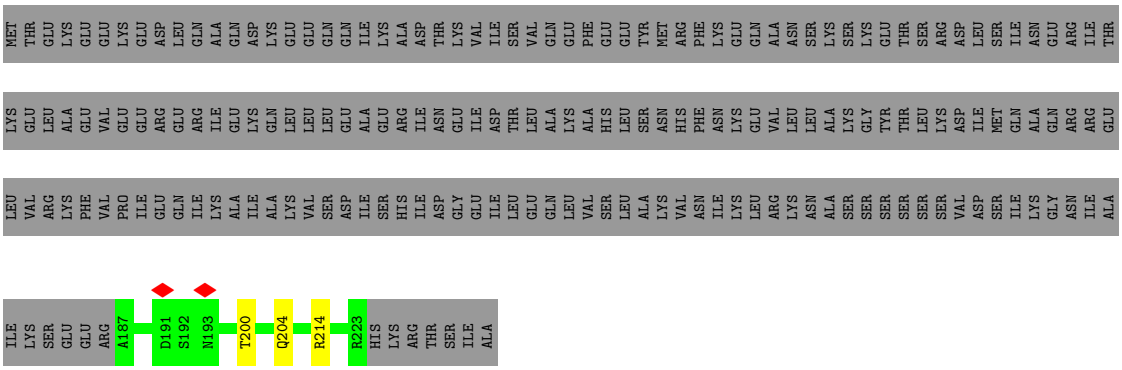
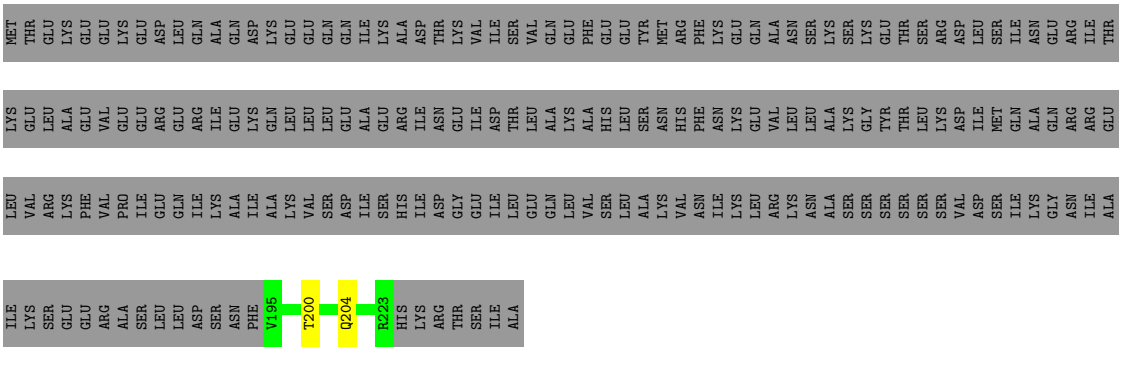


• Molecule 5: Scaffold protein

Chain HM:



• Molecule 5: Scaffold protein

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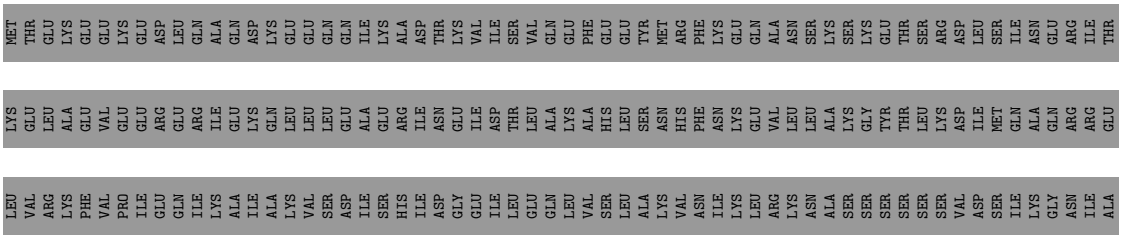

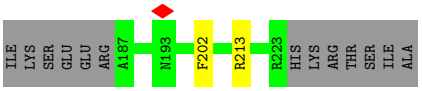

• Molecule 5: Scaffold protein

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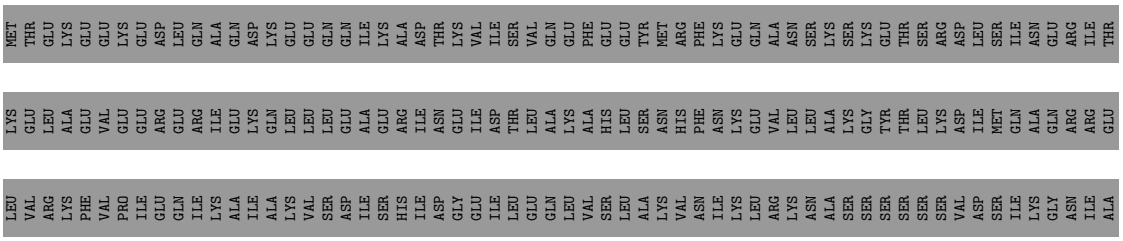

• Molecule 5: Scaffold protein

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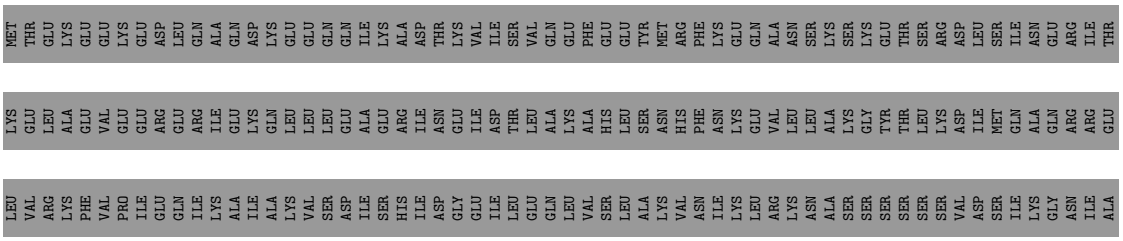

• Molecule 5: Scaffold protein

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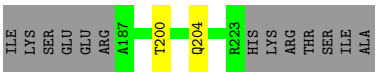

• Molecule 5: Scaffold protein

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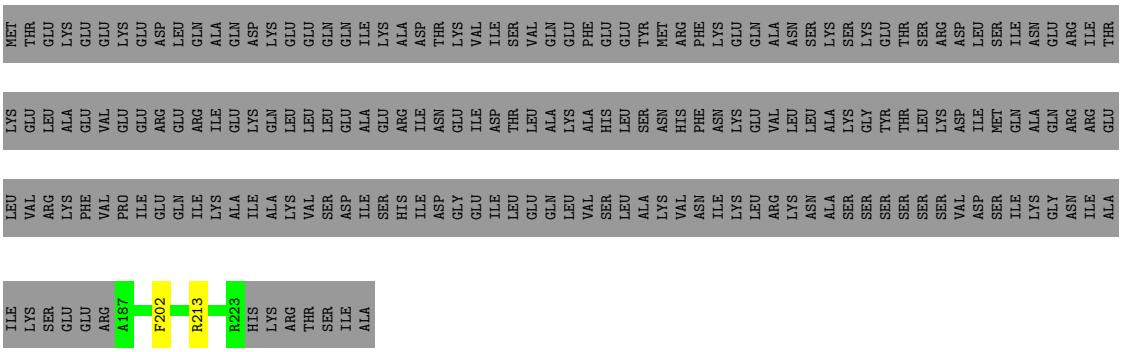

• Molecule 5: Scaffold protein

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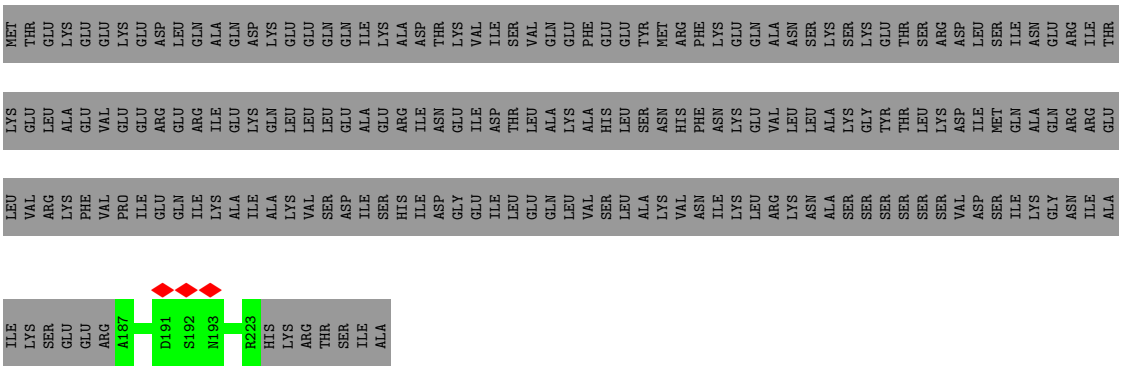

• Molecule 5: Scaffold protein

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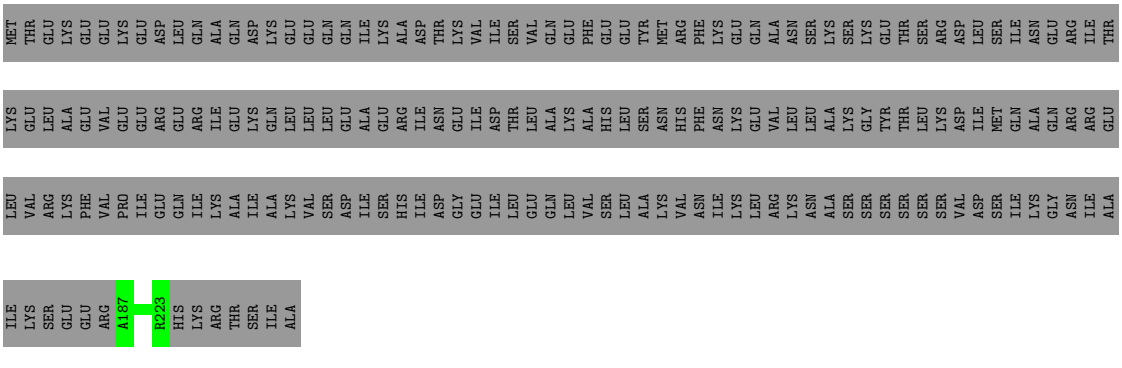

• Molecule 5: Scaffold protein

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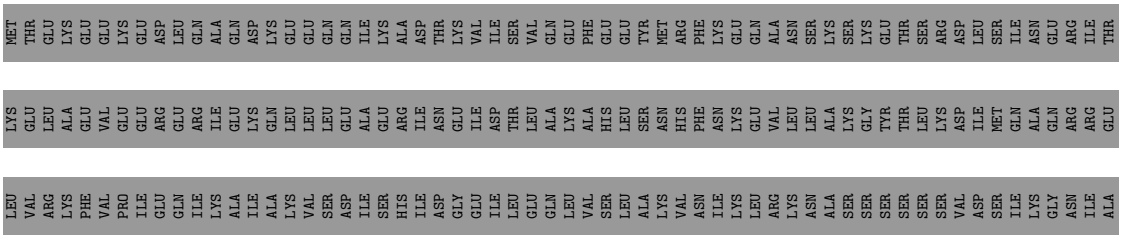

• Molecule 5: Scaffold protein

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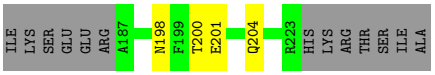

• Molecule 5: Scaffold protein

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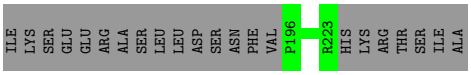

• Molecule 5: Scaffold protein

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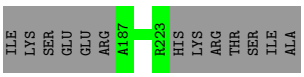

• Molecule 5: Scaffold protein

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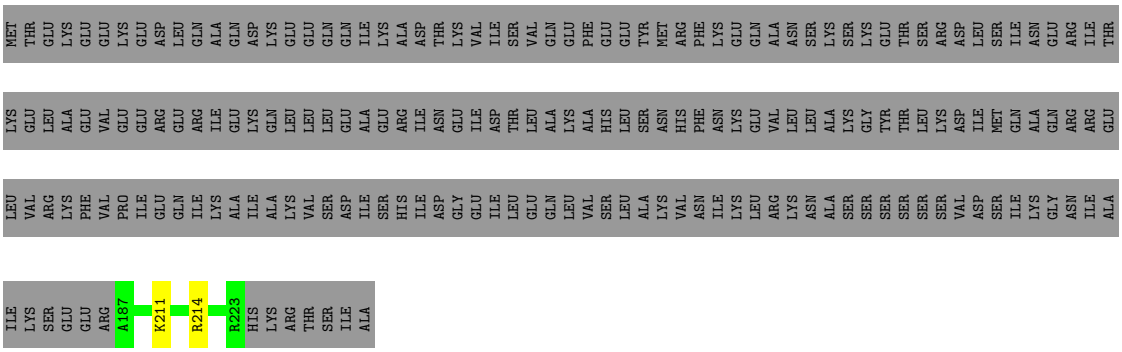

• Molecule 5: Scaffold protein

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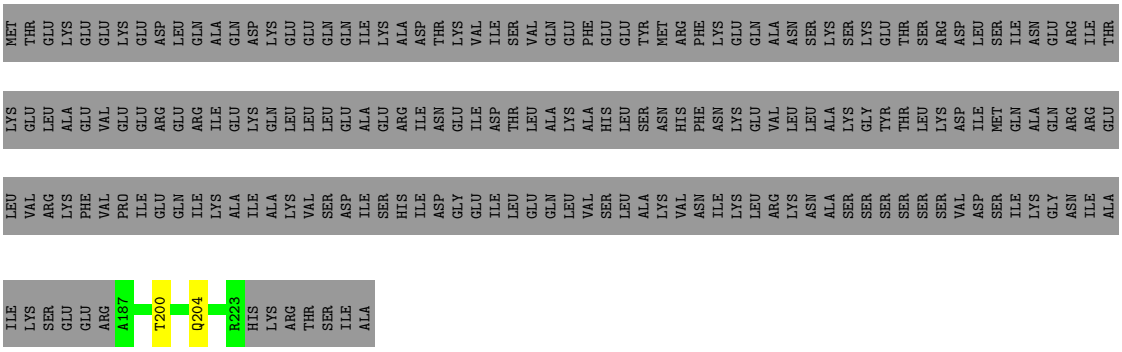
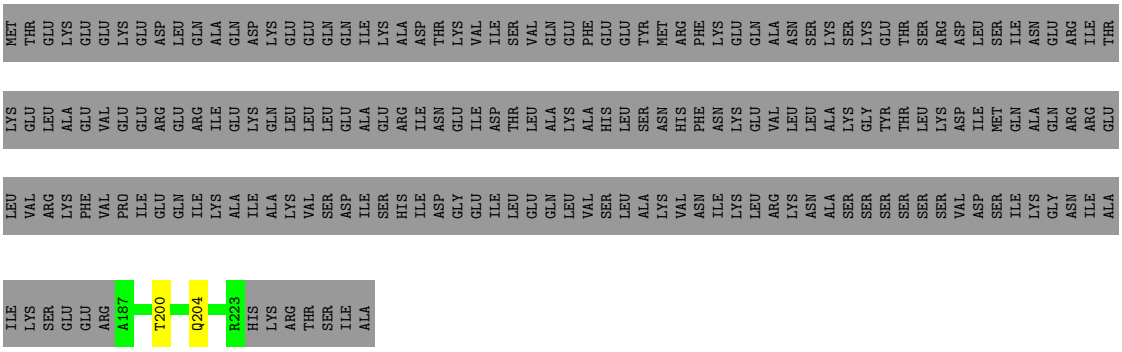


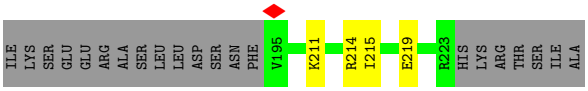
• Molecule 5: Scaffold protein

Chain IA:



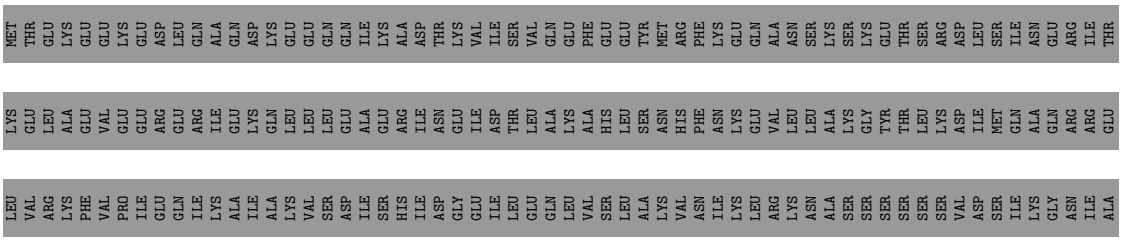
• Molecule 5: Scaffold protein

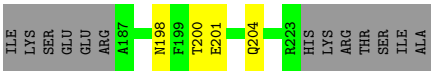
Chain IB:



• Molecule 5: Scaffold protein

Chain IC:





• Molecule 5: Scaffold protein

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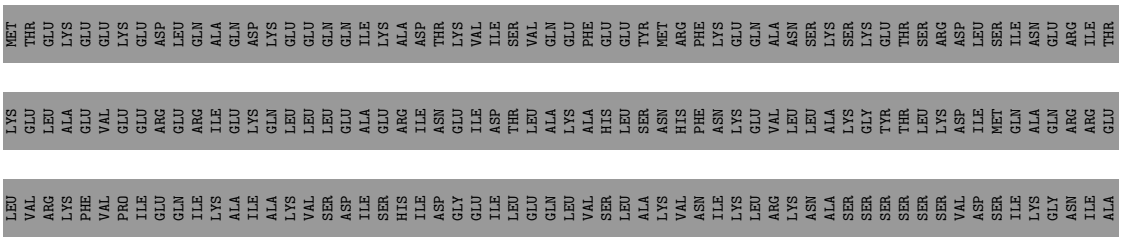
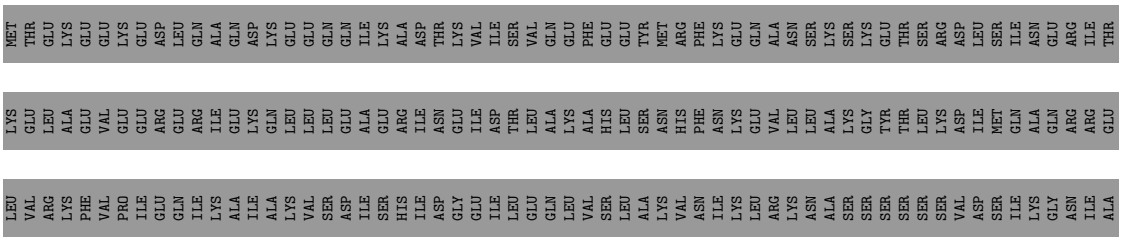
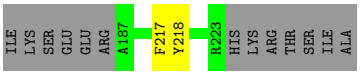


• Molecule 5: Scaffold protein

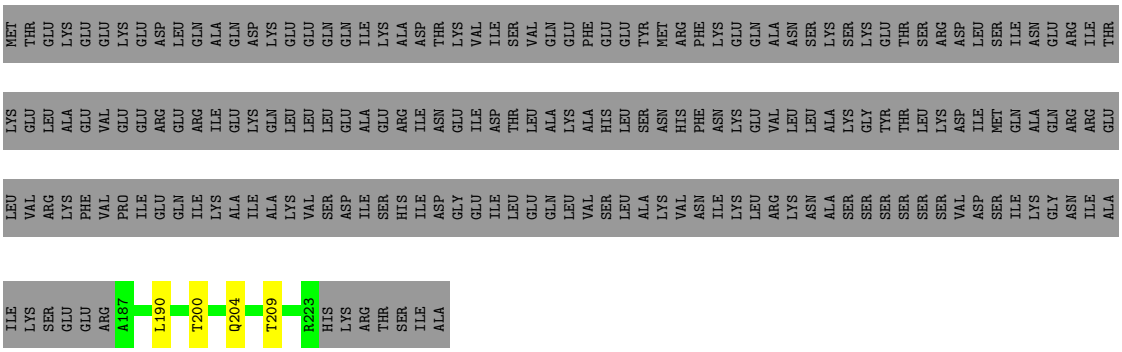
Chain IE:





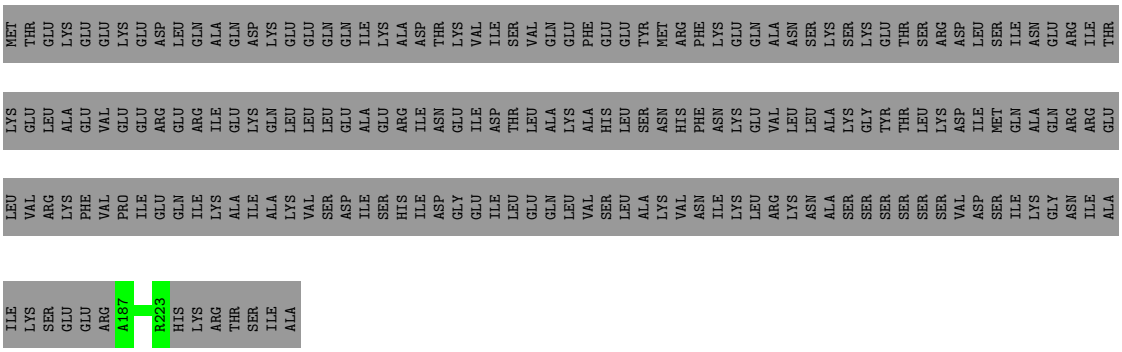
• Molecule 5: Scaffold protein

Chain IF:



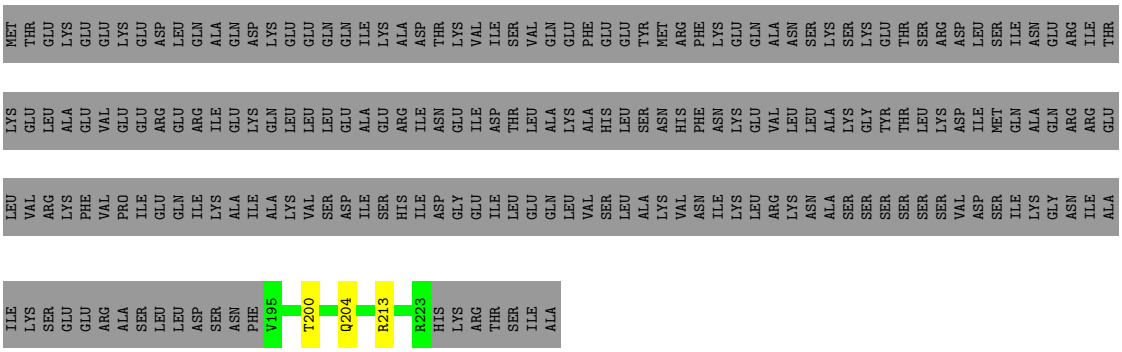
• Molecule 5: Scaffold protein

Chain IG:



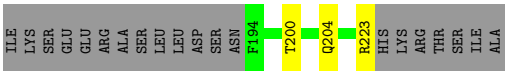
• Molecule 5: Scaffold protein

Chain IH:



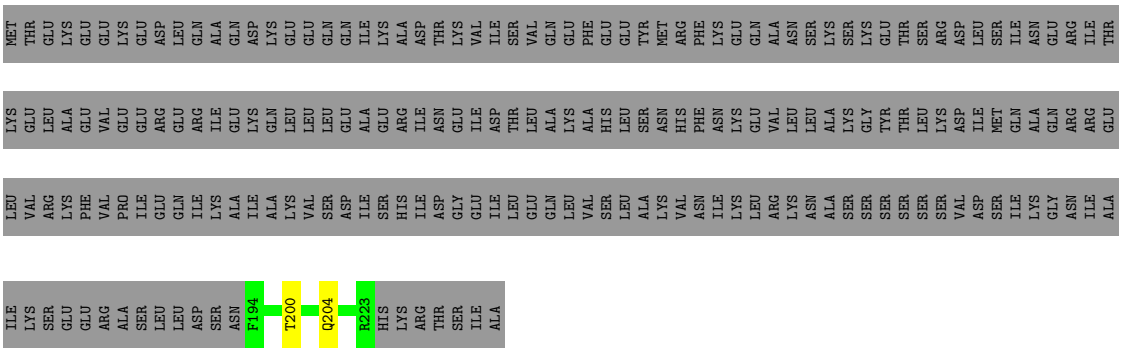
• Molecule 5: Scaffold protein

Chain II:



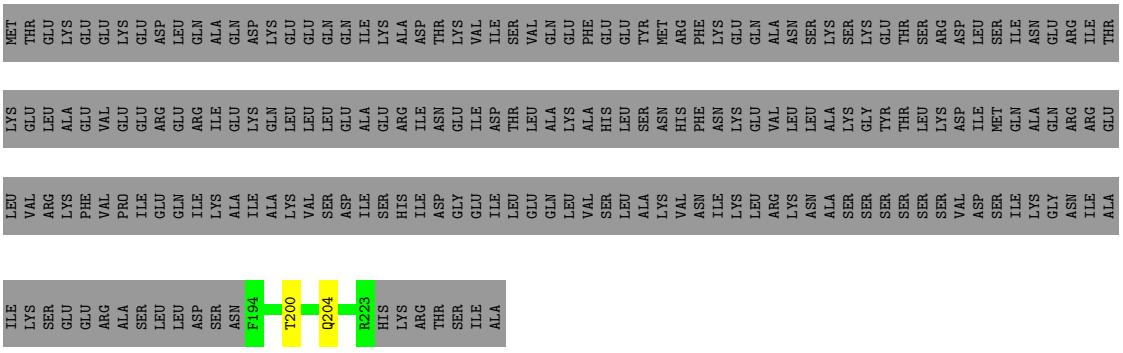
• Molecule 5: Scaffold protein

Chain IJ:



• Molecule 5: Scaffold protein

Chain IK:



• Molecule 5: Scaffold protein

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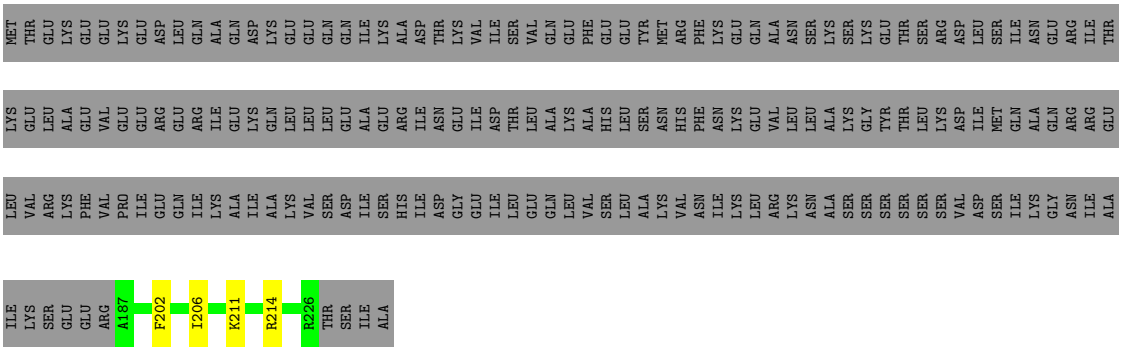

• Molecule 5: Scaffold protein

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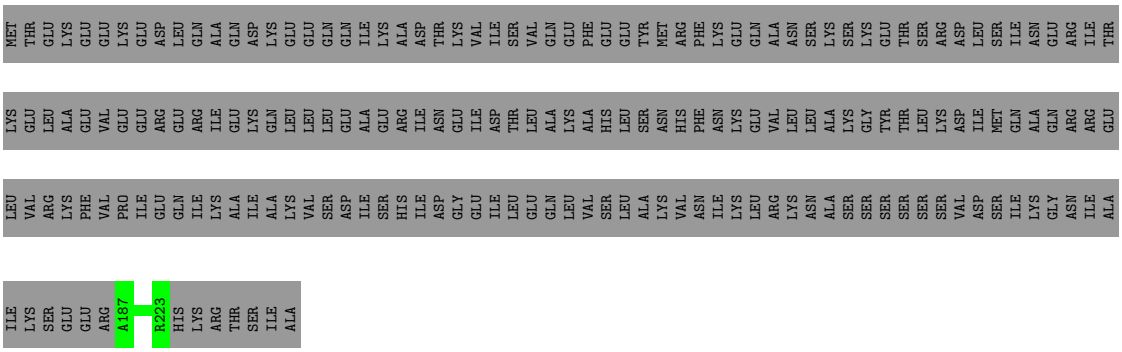
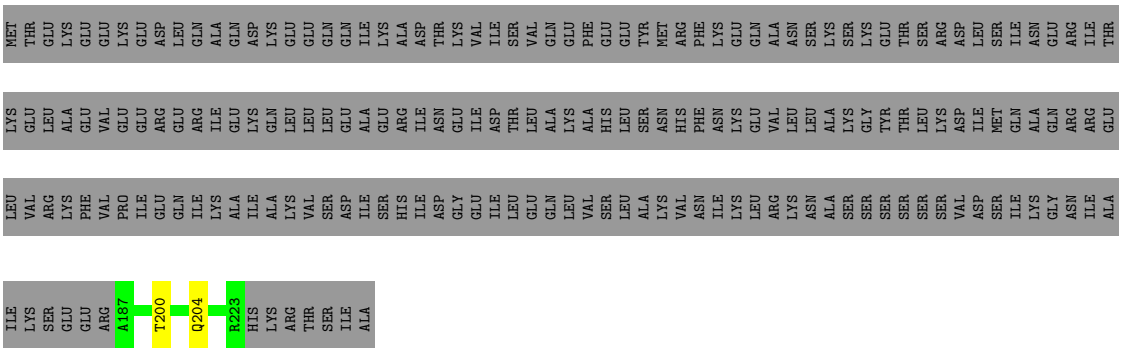


• Molecule 5: Scaffold protein

Chain IN:



• Molecule 5: Scaffold protein

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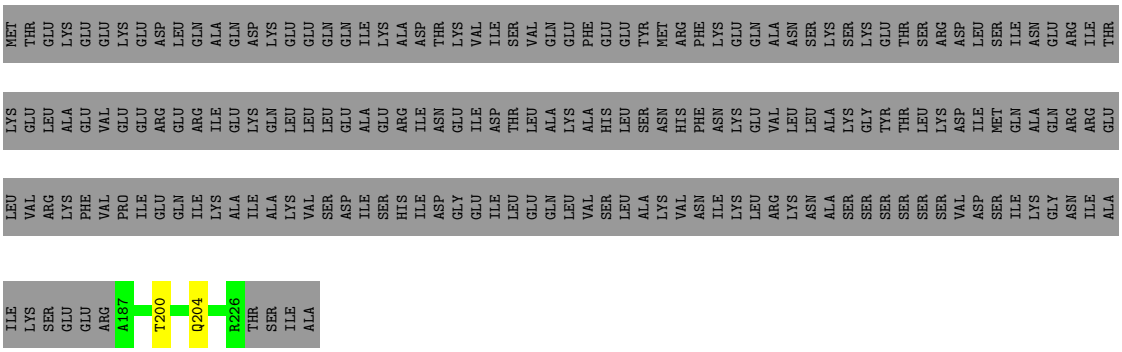

• Molecule 5: Scaffold protein

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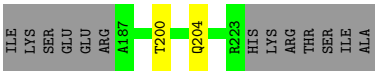

• Molecule 5: Scaffold protein

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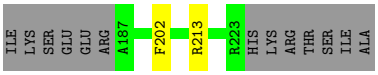
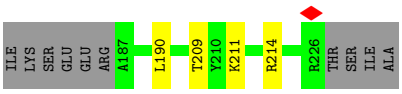


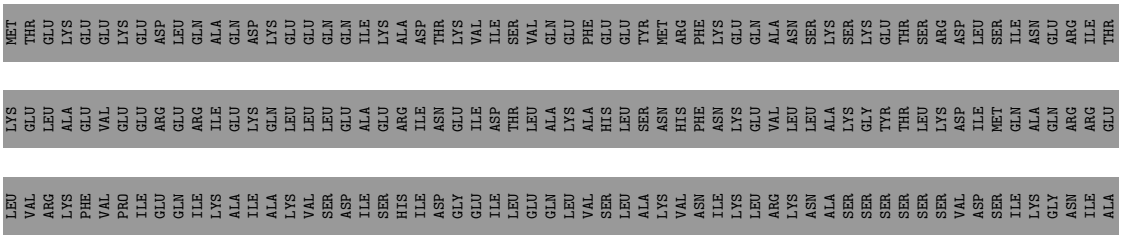
• Molecule 5: Scaffold protein

Chain IR:



• Molecule 5: Scaffold protein

Chain IS:



• Molecule 5: Scaffold protein

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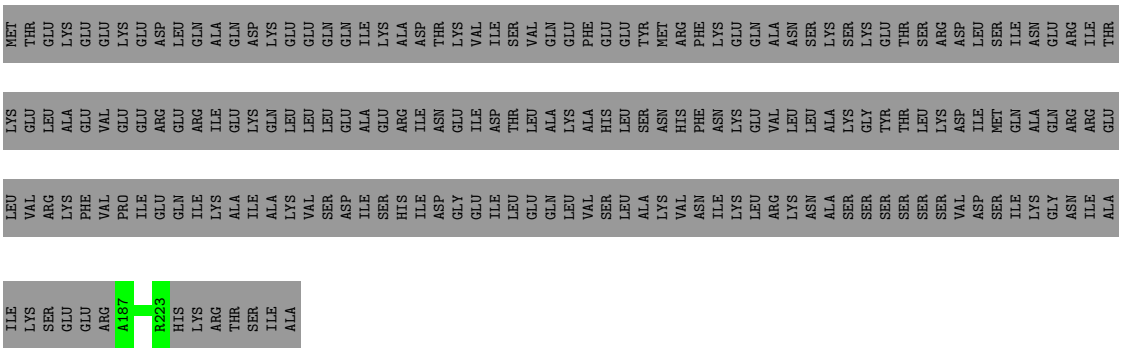
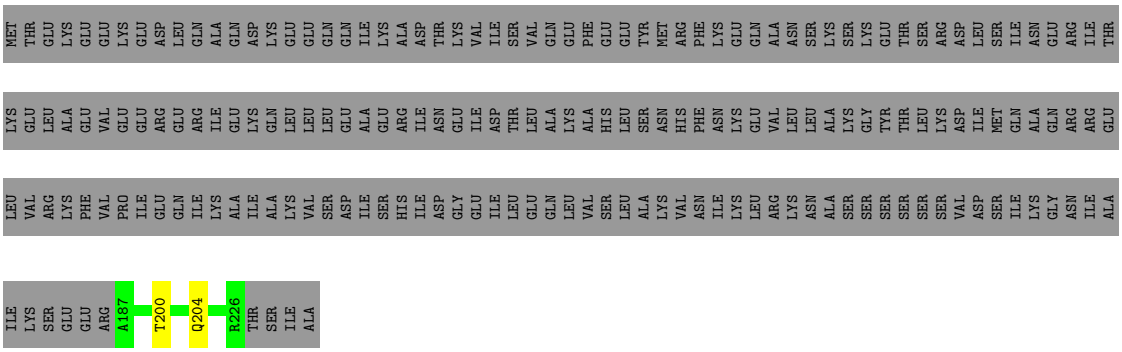


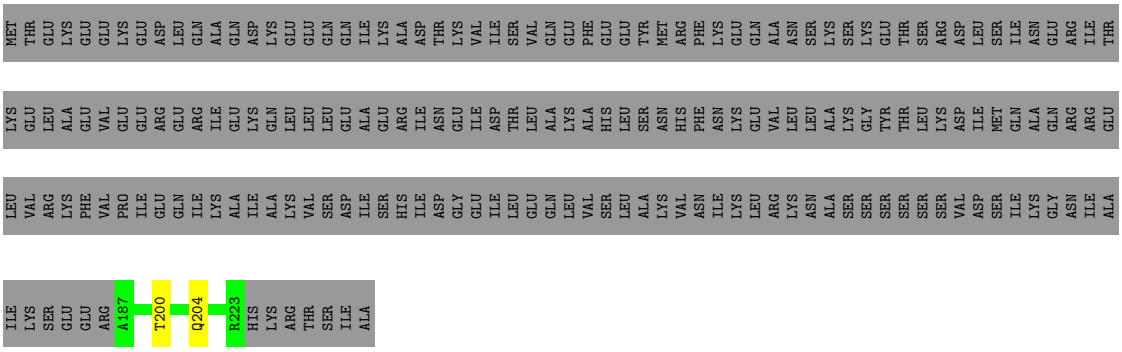
• Molecule 5: Scaffold protein

Chain IU:



• Molecule 5: Scaffold protein

Chain IV:

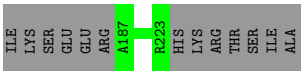


• Molecule 5: Scaffold protein

Chain IW:

• Molecule 5: Scaffold protein

Chain IX:

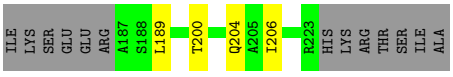


• Molecule 5: Scaffold protein

Chain IY:

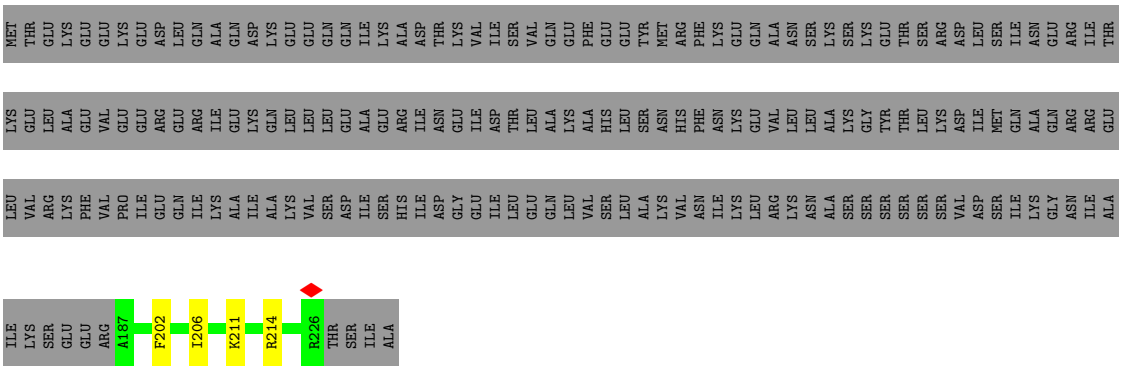
• Molecule 5: Scaffold protein

Chain IZ:



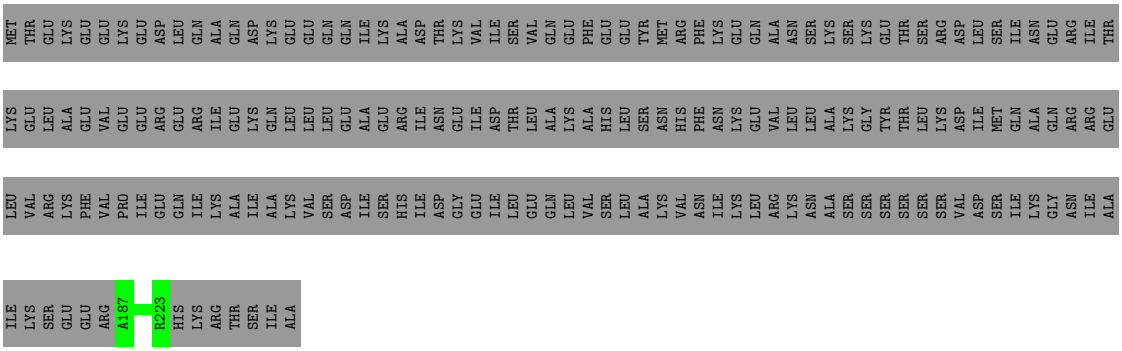
• Molecule 5: Scaffold protein

Chain JA:



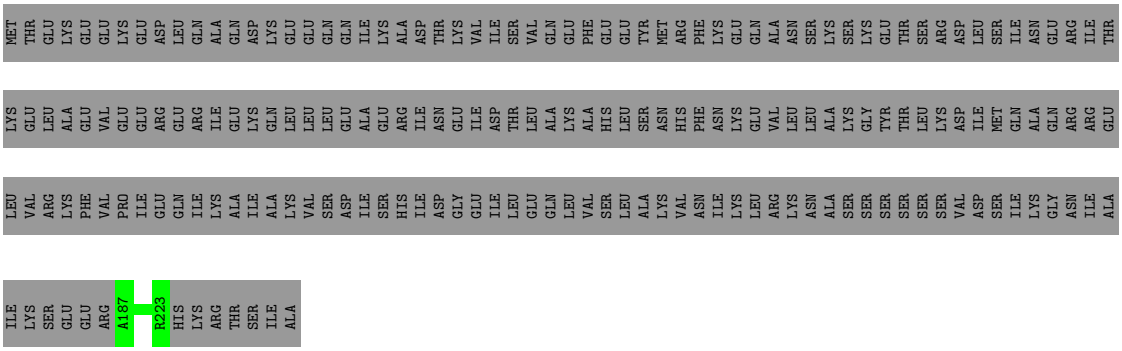
• Molecule 5: Scaffold protein

Chain JB:



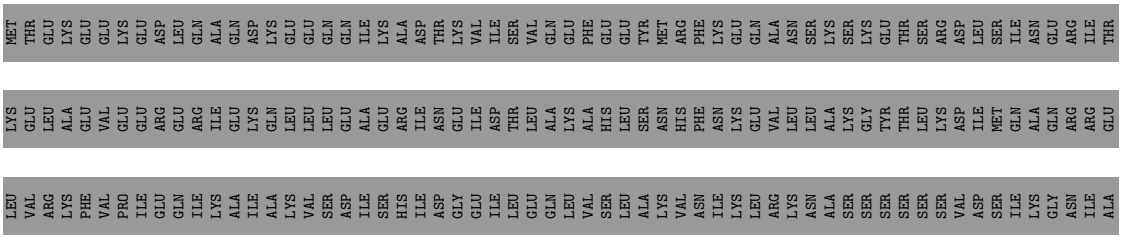
• Molecule 5: Scaffold protein

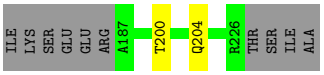
Chain JC:



• Molecule 5: Scaffold protein

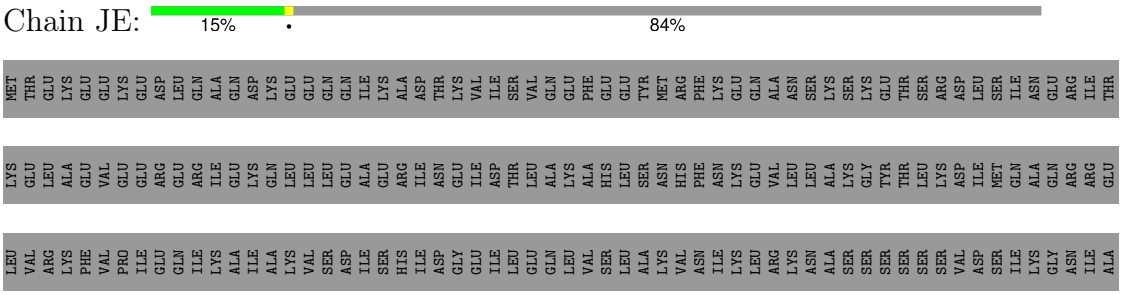
Chain JD:





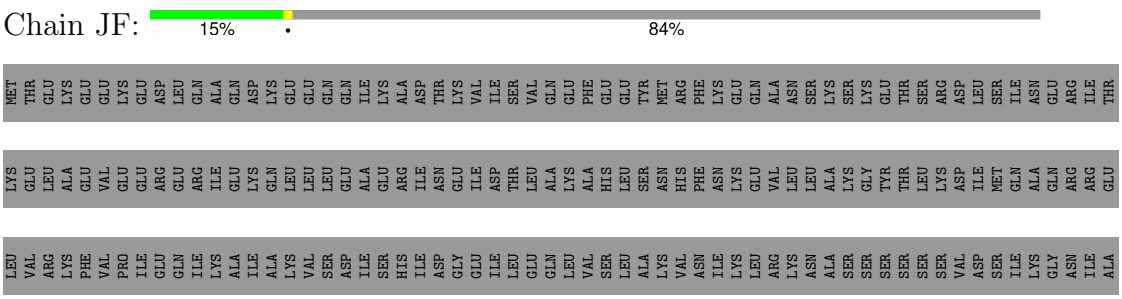
• Molecule 5: Scaffold protein

Chain JE:



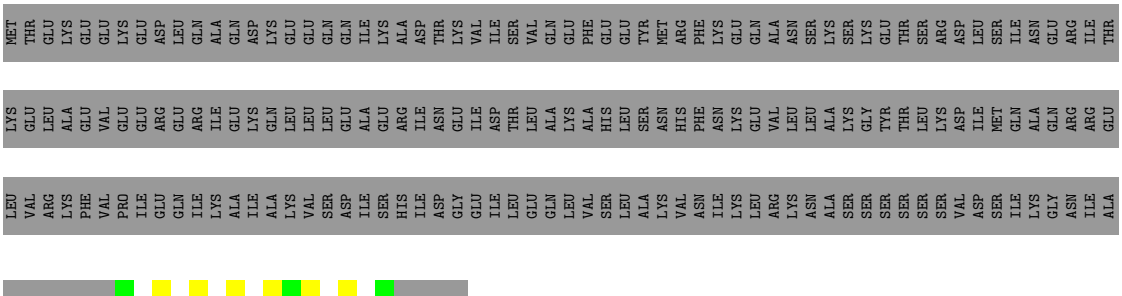
• Molecule 5: Scaffold protein

Chain JF:



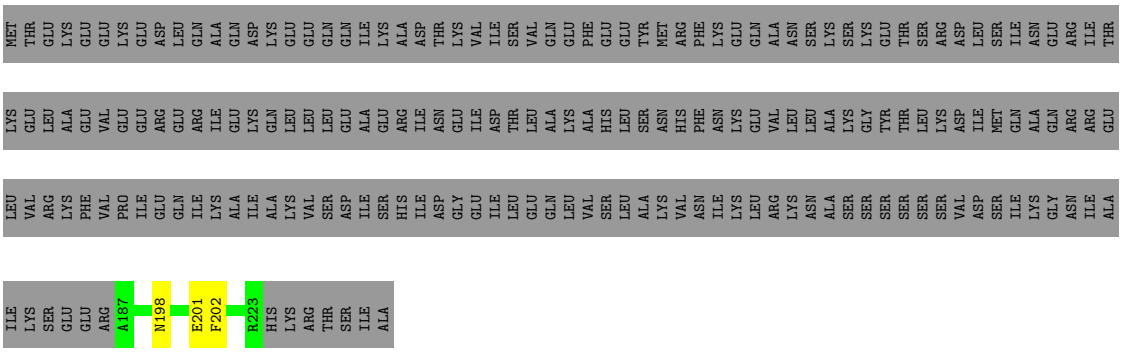
• Molecule 5: Scaffold protein

Chain JG:



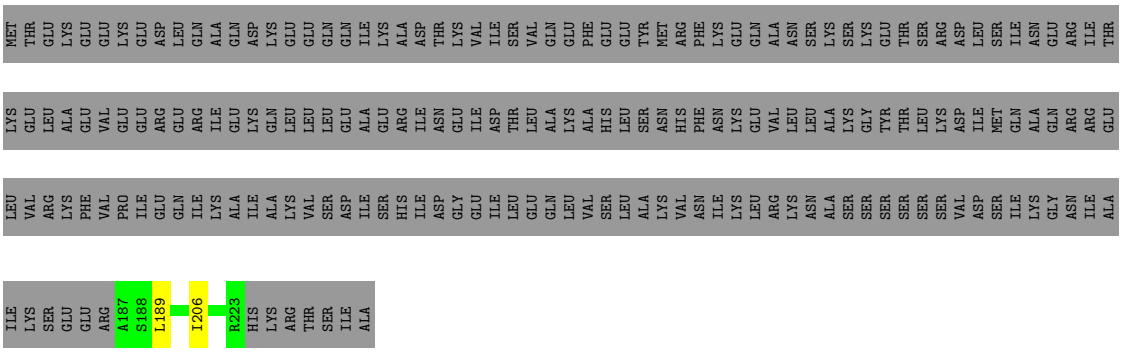
• Molecule 5: Scaffold protein

Chain JH:



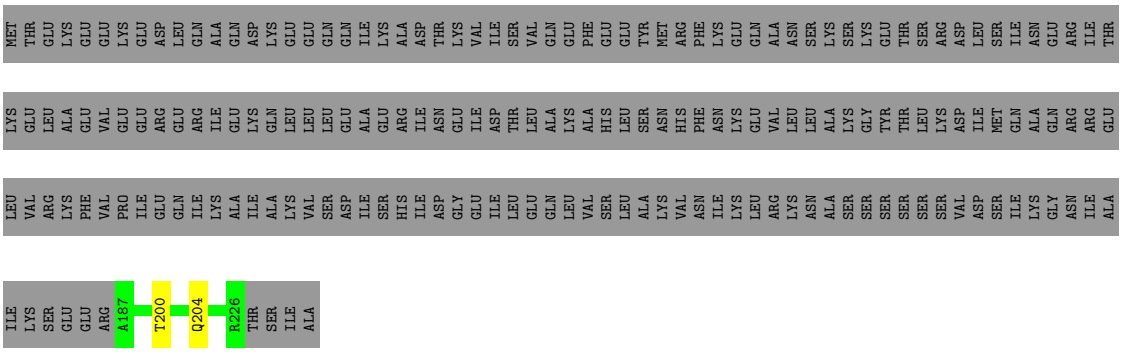
• Molecule 5: Scaffold protein

Chain JI:



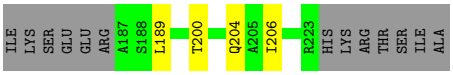
• Molecule 5: Scaffold protein

Chain JJ:



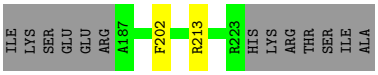
• Molecule 5: Scaffold protein

Chain JK:



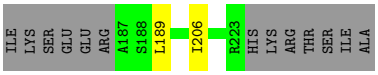
• Molecule 5: Scaffold protein

Chain JL:



• Molecule 5: Scaffold protein

Chain JM:

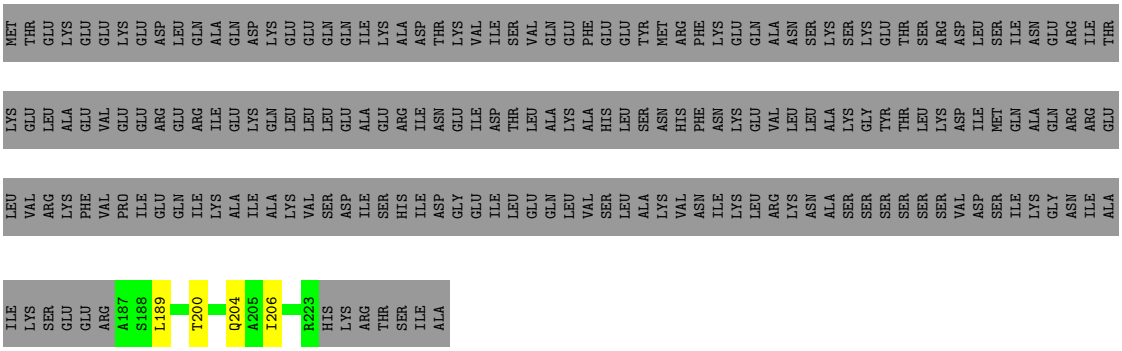


• Molecule 5: Scaffold protein

Chain JN:

• Molecule 5: Scaffold protein

Chain JO:


MET THR GLU LYS GLU GLU LYS GLU ASP LEU GLN ALA GLN ASP LYS GLU GLU GLN GLN ILE LYS ALA ASP THR LYS VAL ILE SER VAL GLN GLU PHE GLU GLU TYR MET ARG PHE LYS GLU GLN ALA ASN SER LYS SER LYS GLY TYR THR LEU LYS ASP ILE MET GLN ALA GLN ARG ARG GLU
LYS GLU LEU ALA GLU VAL GLU GLU ARG GLU ARG ILE GLU LYS GLN LEU LEU LEU GLU ALA ILE ASN GLU ILE ASP THR LEU ALA LYS ALA HIS LEU SER ASN HIS PHE ASN LYS GLU VAL LEU LEU ALA LYS GLY GLU ILE LEU GLU GLN LEU VAL SER LEU ALA LYS VAL ASN ILE LYS LEU ARG LYS ASN ALA SER SER SER SER SER SER VAL ASP SER ILE LYS GLY ASN ILE ALA
LEU VAL ARG LYS PHE VAL PRO ILE GLU GLN ILE LYS ALA ILE ALA LYS VAL SER ASP ILE SER HIS ILE ASP GLY GLU ILE LEU GLU GLN LEU VAL SER LEU ALA LYS VAL ASN ILE LYS LEU ARG LYS ASN ALA SER SER SER SER SER SER VAL ASP SER ILE LYS GLY ASN ILE ALA
ILE LYS SER GLU GLU ARG A187 S188 L189 T200 Q204 A205 I206 R223 HIS LYS ARG THR SER ILE ALA

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C5	Depositor
Number of particles used	25958	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	44	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	16500	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.098	Depositor
Minimum map value	-0.053	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	1200.384, 1200.384, 1200.384	wwPDB
Map dimensions	720, 720, 720	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.6672001, 1.6672001, 1.6672001	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	AA	0.25	0/2536	0.43	0/3428
1	AB	0.24	0/2558	0.43	0/3458
1	AC	0.25	0/2558	0.43	0/3458
1	AD	0.24	0/2536	0.43	0/3428
1	AE	0.24	0/2558	0.43	0/3458
1	AF	0.25	0/2558	0.43	0/3458
1	AG	0.25	0/2536	0.43	0/3428
1	AH	0.24	0/2558	0.43	0/3458
1	AI	0.25	0/2558	0.43	0/3458
1	AJ	0.24	0/2536	0.43	0/3428
1	AK	0.24	0/2558	0.43	0/3458
1	AL	0.24	0/2558	0.43	0/3458
1	AM	0.24	0/2536	0.43	0/3428
1	AN	0.24	0/2558	0.44	0/3458
1	AO	0.24	0/2558	0.43	0/3458
1	AP	0.25	0/2536	0.43	0/3428
1	AQ	0.24	0/2558	0.44	0/3458
1	AR	0.25	0/2558	0.43	0/3458
1	AS	0.24	0/2558	0.43	0/3458
1	AT	0.25	0/2558	0.44	0/3458
1	AU	0.24	0/2558	0.44	0/3458
1	AV	0.24	0/2558	0.44	0/3458
1	AW	0.24	0/2558	0.44	0/3458
1	AX	0.24	0/2558	0.43	0/3458
1	AY	0.24	0/2558	0.43	0/3458
1	AZ	0.24	0/2558	0.44	0/3458
1	BA	0.24	0/2558	0.43	0/3458
1	BB	0.24	0/2558	0.42	0/3458
1	BC	0.24	0/2449	0.42	0/3309
1	BD	0.24	0/2536	0.42	0/3428
1	BE	0.24	0/2558	0.42	0/3458
1	BF	0.24	0/2558	0.42	0/3458
1	BG	0.24	0/2536	0.42	0/3428
1	BH	0.24	0/2558	0.43	0/3458

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	BI	0.24	0/2558	0.43	0/3458
1	BJ	0.24	0/2536	0.43	0/3428
1	BK	0.24	0/2558	0.43	0/3458
1	BL	0.24	0/2558	0.42	0/3458
1	BM	0.24	0/2553	0.43	0/3450
1	BN	0.24	0/2558	0.43	0/3458
1	BO	0.24	0/2558	0.43	0/3458
1	BP	0.24	0/2536	0.42	0/3428
1	BQ	0.24	0/2558	0.43	0/3458
1	BR	0.25	0/2553	0.44	0/3450
1	BS	0.24	0/2558	0.42	0/3458
1	BT	0.24	0/2428	0.43	0/3281
1	BU	0.24	0/2558	0.43	0/3458
1	BV	0.24	0/2558	0.43	0/3458
1	BW	0.24	0/2558	0.43	0/3458
1	BX	0.24	0/2428	0.43	0/3281
1	BY	0.24	0/2558	0.43	0/3458
1	BZ	0.24	0/2558	0.42	0/3458
1	CA	0.24	0/2558	0.42	0/3458
1	CB	0.24	0/2558	0.43	0/3458
1	CC	0.24	0/2558	0.43	0/3458
1	CD	0.24	0/2558	0.42	0/3458
1	CE	0.24	0/2558	0.42	0/3458
1	CF	0.24	0/2558	0.42	0/3458
1	CG	0.24	0/2558	0.43	0/3458
1	CH	0.24	0/2558	0.43	0/3458
1	CI	0.24	0/2558	0.43	0/3458
1	CJ	0.24	0/2558	0.43	0/3458
1	CK	0.24	0/2558	0.43	0/3458
1	CL	0.24	0/2558	0.42	0/3458
1	CM	0.24	0/2558	0.43	0/3458
1	CN	0.24	0/2558	0.43	0/3458
1	CO	0.24	0/2558	0.42	0/3458
1	CP	0.24	0/2558	0.42	0/3458
1	CQ	0.24	0/2558	0.42	0/3458
1	CR	0.24	0/2558	0.43	0/3458
1	CS	0.24	0/2558	0.43	0/3458
1	CT	0.24	0/2558	0.42	0/3458
1	CU	0.24	0/2558	0.42	0/3458
1	CV	0.24	0/2558	0.42	0/3458
1	CW	0.24	0/2558	0.43	0/3458
1	CX	0.24	0/2558	0.43	0/3458
1	CY	0.24	0/2558	0.42	0/3458

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	CZ	0.24	0/2558	0.42	0/3458
1	DA	0.24	0/2558	0.42	0/3458
1	DB	0.24	0/2558	0.42	0/3458
1	DC	0.24	0/2558	0.43	0/3458
1	DD	0.24	0/2558	0.42	0/3458
1	DE	0.24	0/2558	0.42	0/3458
2	DF	0.25	0/1195	0.46	0/1608
2	DG	0.25	0/1177	0.44	0/1583
2	DH	0.24	0/1190	0.44	0/1601
2	DI	0.25	0/1182	0.46	0/1590
2	DJ	0.25	0/1190	0.45	0/1601
2	DK	0.24	0/1182	0.45	0/1590
2	DL	0.25	0/1190	0.46	0/1601
2	DM	0.25	0/1187	0.45	0/1597
2	DN	0.25	0/1190	0.45	0/1601
2	DO	0.25	0/1182	0.46	0/1590
2	DP	0.24	0/1182	0.44	0/1590
2	DQ	0.25	0/1177	0.45	0/1583
2	DR	0.24	0/1190	0.45	0/1601
2	DS	0.26	0/1306	0.46	0/1755
2	DT	0.25	0/1190	0.45	0/1601
2	DU	0.25	0/1178	0.44	0/1586
2	DV	0.24	0/1182	0.43	0/1590
2	DW	0.24	0/1178	0.44	0/1586
2	DX	0.25	0/1216	0.44	0/1637
2	DY	0.24	0/1165	0.43	0/1568
2	DZ	0.25	0/1190	0.45	0/1601
2	EA	0.24	0/931	0.44	0/1252
2	EB	0.25	0/1216	0.45	0/1637
2	EC	0.25	0/1181	0.44	0/1590
2	ED	0.25	0/1229	0.46	0/1655
2	EE	0.25	0/1212	0.45	0/1633
2	EF	0.24	0/1190	0.44	0/1601
2	EG	0.25	0/1356	0.44	0/1823
2	EH	0.25	0/1182	0.45	0/1590
2	EI	0.24	0/1207	0.44	0/1626
2	EJ	0.24	0/1293	0.44	0/1737
2	EK	0.24	0/1306	0.44	0/1755
2	EL	0.25	0/1177	0.44	0/1583
2	EM	0.24	0/1190	0.45	0/1601
2	EN	0.25	0/1182	0.44	0/1590
2	EO	0.24	0/1322	0.44	0/1776
2	EP	0.24	0/1178	0.44	0/1586

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
2	EQ	0.24	0/1216	0.44	0/1637
2	ER	0.25	0/1165	0.43	0/1568
2	ES	0.25	0/1190	0.44	0/1601
2	ET	0.24	0/1178	0.44	0/1586
2	EU	0.24	0/1216	0.44	0/1637
2	EV	0.25	0/1165	0.43	0/1568
2	EW	0.24	0/1190	0.45	0/1601
2	EX	0.24	0/1178	0.45	0/1586
2	EY	0.24	0/1216	0.44	0/1637
2	EZ	0.25	0/1165	0.44	0/1568
2	FA	0.24	0/1190	0.44	0/1601
2	FB	0.25	0/1178	0.45	0/1586
2	FC	0.25	0/1216	0.44	0/1637
2	FD	0.24	0/1165	0.43	0/1568
2	FE	0.24	0/1190	0.45	0/1601
2	FF	0.25	0/1178	0.45	0/1586
2	FG	0.24	0/1216	0.44	0/1637
2	FH	0.25	0/1165	0.44	0/1568
2	FI	0.25	0/1190	0.45	0/1601
3	FJ	0.26	0/1274	0.46	0/1721
4	FK	0.25	0/1216	0.46	0/1636
4	FL	0.25	0/1216	0.46	0/1636
4	FM	0.25	0/1225	0.46	0/1649
4	FN	0.25	0/1219	0.46	0/1641
4	FO	0.25	0/1243	0.47	0/1672
4	FP	0.24	0/1212	0.46	0/1632
4	FQ	0.24	0/1381	0.45	0/1855
4	FR	0.24	0/1381	0.45	0/1855
4	FS	0.24	0/1381	0.45	0/1855
4	FT	0.24	0/1158	0.44	0/1559
4	FU	0.25	0/1208	0.45	0/1626
4	FV	0.24	0/1229	0.45	0/1653
4	FW	0.25	0/1229	0.46	0/1653
4	FX	0.25	0/1207	0.45	0/1625
4	FY	0.24	0/1207	0.45	0/1625
4	FZ	0.24	0/1216	0.45	0/1636
4	GA	0.24	0/1381	0.45	0/1855
4	GB	0.24	0/1381	0.44	0/1855
4	GC	0.24	0/1381	0.44	0/1855
4	GD	0.24	0/1381	0.44	0/1855
4	GE	0.24	0/1381	0.44	0/1855
4	GF	0.24	0/1381	0.44	0/1855
4	GG	0.24	0/1381	0.44	0/1855

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
4	GH	0.24	0/1381	0.45	0/1855
4	GI	0.24	0/1381	0.45	0/1855
4	GJ	0.24	0/1381	0.45	0/1855
5	GK	0.26	0/272	0.46	0/365
5	GL	0.26	0/321	0.45	0/432
5	GM	0.26	0/321	0.45	0/432
5	GN	0.26	0/321	0.44	0/432
5	GO	0.26	0/321	0.44	0/432
5	GP	0.26	0/321	0.44	0/432
5	GQ	0.25	0/321	0.44	0/432
5	GR	0.26	0/321	0.45	0/432
5	GS	0.26	0/321	0.44	0/432
5	GT	0.26	0/321	0.45	0/432
5	GU	0.26	0/321	0.45	0/432
5	GV	0.26	0/321	0.44	0/432
5	GW	0.26	0/272	0.46	0/365
5	GX	0.26	0/321	0.46	0/432
5	GY	0.26	0/321	0.46	0/432
5	GZ	0.26	0/321	0.45	0/432
5	HA	0.26	0/321	0.45	0/432
5	HB	0.25	0/321	0.45	0/432
5	HC	0.26	0/321	0.44	0/432
5	HD	0.27	0/272	0.47	0/365
5	HE	0.25	0/321	0.44	0/432
5	HF	0.25	0/321	0.45	0/432
5	HG	0.26	0/321	0.45	0/432
5	HH	0.26	0/272	0.47	0/365
5	HI	0.26	0/272	0.47	0/365
5	HJ	0.26	0/272	0.49	0/365
5	HK	0.26	0/272	0.46	0/365
5	HL	0.25	0/321	0.43	0/432
5	HM	0.25	0/260	0.45	0/349
5	HN	0.25	0/321	0.43	0/432
5	HO	0.25	0/321	0.43	0/432
5	HP	0.25	0/321	0.43	0/432
5	HQ	0.25	0/321	0.43	0/432
5	HR	0.25	0/321	0.43	0/432
5	HS	0.25	0/321	0.43	0/432
5	HT	0.25	0/321	0.44	0/432
5	HU	0.26	0/321	0.44	0/432
5	HV	0.25	0/321	0.43	0/432
5	HW	0.25	0/253	0.45	0/338
5	HX	0.25	0/321	0.44	0/432

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
5	HY	0.25	0/321	0.44	0/432
5	HZ	0.25	0/321	0.43	0/432
5	IA	0.25	0/321	0.43	0/432
5	IB	0.25	0/260	0.45	0/349
5	IC	0.26	0/321	0.43	0/432
5	ID	0.25	0/260	0.45	0/349
5	IE	0.25	0/321	0.43	0/432
5	IF	0.25	0/321	0.44	0/432
5	IG	0.25	0/321	0.43	0/432
5	IH	0.26	0/260	0.46	0/349
5	II	0.26	0/272	0.45	0/365
5	IJ	0.26	0/272	0.47	0/365
5	IK	0.25	0/272	0.45	0/365
5	IL	0.25	0/352	0.46	0/472
5	IM	0.26	0/321	0.43	0/432
5	IN	0.25	0/321	0.43	0/432
5	IO	0.25	0/352	0.45	0/472
5	IP	0.25	0/321	0.43	0/432
5	IQ	0.26	0/321	0.44	0/432
5	IR	0.25	0/352	0.46	0/472
5	IS	0.26	0/321	0.43	0/432
5	IT	0.25	0/321	0.43	0/432
5	IU	0.25	0/352	0.46	0/472
5	IV	0.25	0/321	0.43	0/432
5	IW	0.25	0/321	0.43	0/432
5	IX	0.25	0/321	0.43	0/432
5	IY	0.25	0/352	0.47	0/472
5	IZ	0.25	0/321	0.43	0/432
5	JA	0.25	0/352	0.46	0/472
5	JB	0.25	0/321	0.43	0/432
5	JC	0.25	0/321	0.42	0/432
5	JD	0.25	0/352	0.45	0/472
5	JE	0.25	0/321	0.43	0/432
5	JF	0.25	0/321	0.43	0/432
5	JG	0.25	0/352	0.47	0/472
5	JH	0.26	0/321	0.43	0/432
5	JI	0.25	0/321	0.43	0/432
5	JJ	0.25	0/352	0.46	0/472
5	JK	0.25	0/321	0.43	0/432
5	JL	0.25	0/321	0.44	0/432
5	JM	0.26	0/321	0.43	0/432
5	JN	0.25	0/352	0.46	0/472
5	JO	0.25	0/321	0.43	0/432

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
All	All	0.24	0/339816	0.43	0/458503

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	AA	2488	0	2527	23	0
1	AB	2510	0	2547	23	0
1	AC	2510	0	2547	27	0
1	AD	2488	0	2527	24	0
1	AE	2510	0	2547	25	0
1	AF	2510	0	2547	31	0
1	AG	2488	0	2527	32	0
1	AH	2510	0	2547	30	0
1	AI	2510	0	2547	20	0
1	AJ	2488	0	2527	30	0
1	AK	2510	0	2547	31	0
1	AL	2510	0	2547	29	0
1	AM	2488	0	2527	29	0
1	AN	2510	0	2547	32	0
1	AO	2510	0	2547	37	0
1	AP	2488	0	2527	33	0
1	AQ	2510	0	2547	24	0
1	AR	2510	0	2547	30	0
1	AS	2510	0	2547	43	0
1	AT	2510	0	2547	33	0
1	AU	2510	0	2547	35	0
1	AV	2510	0	2547	37	0
1	AW	2510	0	2547	26	0
1	AX	2510	0	2547	37	0
1	AY	2510	0	2547	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AZ	2510	0	2547	38	0
1	BA	2510	0	2547	39	0
1	BB	2510	0	2547	25	0
1	BC	2405	0	2453	23	0
1	BD	2488	0	2527	26	0
1	BE	2510	0	2547	22	0
1	BF	2510	0	2547	25	0
1	BG	2488	0	2527	27	0
1	BH	2510	0	2547	26	0
1	BI	2510	0	2547	23	0
1	BJ	2488	0	2527	31	0
1	BK	2510	0	2547	35	0
1	BL	2510	0	2547	25	0
1	BM	2505	0	2545	27	0
1	BN	2510	0	2547	22	0
1	BO	2510	0	2547	32	0
1	BP	2488	0	2527	33	0
1	BQ	2510	0	2547	24	0
1	BR	2505	0	2545	26	0
1	BS	2510	0	2547	34	0
1	BT	2383	0	2425	24	0
1	BU	2510	0	2547	34	0
1	BV	2510	0	2547	32	0
1	BW	2510	0	2547	24	0
1	BX	2383	0	2425	26	0
1	BY	2510	0	2547	42	0
1	BZ	2510	0	2547	32	0
1	CA	2510	0	2547	38	0
1	CB	2510	0	2547	29	0
1	CC	2510	0	2547	28	0
1	CD	2510	0	2547	29	0
1	CE	2510	0	2547	30	0
1	CF	2510	0	2547	39	0
1	CG	2510	0	2547	33	0
1	CH	2510	0	2547	35	0
1	CI	2510	0	2547	22	0
1	CJ	2510	0	2547	25	0
1	CK	2510	0	2547	38	0
1	CL	2510	0	2547	39	0
1	CM	2510	0	2547	29	0
1	CN	2510	0	2547	28	0
1	CO	2510	0	2547	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CP	2510	0	2547	35	0
1	CQ	2510	0	2547	25	0
1	CR	2510	0	2547	29	0
1	CS	2510	0	2547	35	0
1	CT	2510	0	2547	35	0
1	CU	2510	0	2547	41	0
1	CV	2510	0	2547	40	0
1	CW	2510	0	2547	37	0
1	CX	2510	0	2547	24	0
1	CY	2510	0	2547	24	0
1	CZ	2510	0	2547	36	0
1	DA	2510	0	2547	36	0
1	DB	2510	0	2547	28	0
1	DC	2510	0	2547	34	0
1	DD	2510	0	2547	43	0
1	DE	2510	0	2547	31	0
2	DF	1178	0	1163	6	0
2	DG	1160	0	1142	9	0
2	DH	1173	0	1158	10	0
2	DI	1165	0	1147	9	0
2	DJ	1173	0	1158	13	0
2	DK	1165	0	1147	12	0
2	DL	1173	0	1158	10	0
2	DM	1170	0	1152	12	0
2	DN	1173	0	1158	16	0
2	DO	1165	0	1147	12	0
2	DP	1165	0	1147	17	0
2	DQ	1160	0	1142	12	0
2	DR	1173	0	1158	10	0
2	DS	1288	0	1279	13	0
2	DT	1173	0	1158	31	0
2	DU	1161	0	1139	15	0
2	DV	1165	0	1147	17	0
2	DW	1161	0	1139	17	0
2	DX	1198	0	1172	17	0
2	DY	1148	0	1123	19	0
2	DZ	1173	0	1158	15	0
2	EA	917	0	912	9	0
2	EB	1198	0	1172	18	0
2	EC	1164	0	1145	10	0
2	ED	1211	0	1188	9	0
2	EE	1194	0	1164	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	EF	1173	0	1158	15	0
2	EG	1337	0	1324	15	0
2	EH	1165	0	1147	11	0
2	EI	1189	0	1159	11	0
2	EJ	1275	0	1263	9	0
2	EK	1288	0	1279	17	0
2	EL	1160	0	1142	14	0
2	EM	1173	0	1158	22	0
2	EN	1165	0	1147	17	0
2	EO	1304	0	1299	12	0
2	EP	1161	0	1139	21	0
2	EQ	1198	0	1172	13	0
2	ER	1148	0	1123	18	0
2	ES	1173	0	1158	16	0
2	ET	1161	0	1139	18	0
2	EU	1198	0	1172	14	0
2	EV	1148	0	1123	18	0
2	EW	1173	0	1158	18	0
2	EX	1161	0	1139	15	0
2	EY	1198	0	1172	14	0
2	EZ	1148	0	1123	13	0
2	FA	1173	0	1158	13	0
2	FB	1161	0	1139	19	0
2	FC	1198	0	1172	12	0
2	FD	1148	0	1123	19	0
2	FE	1173	0	1158	19	0
2	FF	1161	0	1139	15	0
2	FG	1198	0	1172	18	0
2	FH	1148	0	1123	17	0
2	FI	1173	0	1158	15	0
3	FJ	1252	0	1235	17	0
4	FK	1195	0	1189	12	0
4	FL	1195	0	1189	12	0
4	FM	1203	0	1190	11	0
4	FN	1197	0	1185	15	0
4	FO	1222	0	1214	14	0
4	FP	1191	0	1181	17	0
4	FQ	1358	0	1361	19	0
4	FR	1358	0	1361	16	0
4	FS	1358	0	1361	21	0
4	FT	1137	0	1125	10	0
4	FU	1187	0	1176	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	FV	1208	0	1203	12	0
4	FW	1208	0	1203	20	0
4	FX	1186	0	1176	12	0
4	FY	1186	0	1176	15	0
4	FZ	1195	0	1189	18	0
4	GA	1358	0	1361	15	0
4	GB	1358	0	1361	15	0
4	GC	1358	0	1361	19	0
4	GD	1358	0	1361	23	0
4	GE	1358	0	1361	18	0
4	GF	1358	0	1361	14	0
4	GG	1358	0	1361	20	0
4	GH	1358	0	1361	20	0
4	GI	1358	0	1361	18	0
4	GJ	1358	0	1361	15	0
5	GK	266	0	265	3	0
5	GL	315	0	312	5	0
5	GM	315	0	312	2	0
5	GN	315	0	312	1	0
5	GO	315	0	312	1	0
5	GP	315	0	312	0	0
5	GQ	315	0	312	5	0
5	GR	315	0	312	1	0
5	GS	315	0	312	2	0
5	GT	315	0	312	1	0
5	GU	315	0	312	3	0
5	GV	315	0	312	2	0
5	GW	266	0	265	2	0
5	GX	315	0	312	4	0
5	GY	315	0	312	4	0
5	GZ	315	0	312	4	0
5	HA	315	0	312	1	0
5	HB	315	0	312	4	0
5	HC	315	0	312	5	0
5	HD	266	0	265	2	0
5	HE	315	0	312	2	0
5	HF	315	0	312	3	0
5	HG	315	0	312	0	0
5	HH	266	0	265	3	0
5	HI	266	0	265	2	0
5	HJ	266	0	265	4	0
5	HK	266	0	265	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	HL	315	0	312	2	0
5	HM	255	0	256	1	0
5	HN	315	0	312	2	0
5	HO	315	0	312	1	0
5	HP	315	0	312	1	0
5	HQ	315	0	312	1	0
5	HR	315	0	312	2	0
5	HS	315	0	312	0	0
5	HT	315	0	312	0	0
5	HU	315	0	312	1	0
5	HV	315	0	312	2	0
5	HW	248	0	248	0	0
5	HX	315	0	312	0	0
5	HY	315	0	312	1	0
5	HZ	315	0	312	1	0
5	IA	315	0	312	1	0
5	IB	255	0	256	2	0
5	IC	315	0	312	2	0
5	ID	255	0	256	0	0
5	IE	315	0	312	2	0
5	IF	315	0	312	2	0
5	IG	315	0	312	0	0
5	IH	255	0	256	3	0
5	II	266	0	265	2	0
5	IJ	266	0	265	1	0
5	IK	266	0	265	1	0
5	IL	345	0	345	2	0
5	IM	315	0	312	0	0
5	IN	315	0	312	1	0
5	IO	345	0	345	1	0
5	IP	315	0	312	1	0
5	IQ	315	0	312	2	0
5	IR	345	0	345	2	0
5	IS	315	0	312	2	0
5	IT	315	0	312	0	0
5	IU	345	0	345	1	0
5	IV	315	0	312	1	0
5	IW	315	0	312	1	0
5	IX	315	0	312	0	0
5	IY	345	0	345	1	0
5	IZ	315	0	312	2	0
5	JA	345	0	345	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	JB	315	0	312	0	0
5	JC	315	0	312	0	0
5	JD	345	0	345	1	0
5	JE	315	0	312	1	0
5	JF	315	0	312	2	0
5	JG	345	0	345	3	0
5	JH	315	0	312	2	0
5	JI	315	0	312	1	0
5	JJ	345	0	345	1	0
5	JK	315	0	312	2	0
5	JL	315	0	312	2	0
5	JM	315	0	312	1	0
5	JN	345	0	345	2	0
5	JO	315	0	312	2	0
All	All	333778	0	335560	3234	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 5.

All (3234) 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:BY:165:ILE:HD13	1:BY:191:LEU:HD23	1.62	0.79
1:CF:165:ILE:HD13	1:CF:191:LEU:HD23	1.64	0.79
4:FX:77:ILE:HG13	4:FX:91:PRO:HB3	1.66	0.77
1:CU:165:ILE:HD13	1:CU:191:LEU:HD23	1.64	0.77
1:CP:165:ILE:HD13	1:CP:191:LEU:HD23	1.67	0.76
1:DE:165:ILE:HD13	1:DE:191:LEU:HD23	1.64	0.76
4:FQ:77:ILE:HG13	4:FQ:91:PRO:HB3	1.68	0.75
4:FT:77:ILE:HG13	4:FT:91:PRO:HB3	1.68	0.75
1:AJ:261:ILE:HD12	1:AJ:312:LEU:HD23	1.67	0.75
1:DD:165:ILE:HD13	1:DD:191:LEU:HD23	1.69	0.75
4:FM:77:ILE:HG13	4:FM:91:PRO:HB3	1.69	0.74
4:GD:73:VAL:HG21	4:GD:117:ILE:HD13	1.70	0.74
1:CB:165:ILE:HD13	1:CB:191:LEU:HD23	1.70	0.74
1:BY:150:ARG:NH1	2:EP:85:GLU:OE1	2.21	0.73
1:CL:165:ILE:HD13	1:CL:191:LEU:HD23	1.69	0.73
1:AW:165:ILE:HD13	1:AW:191:LEU:HD23	1.70	0.73
1:DA:165:ILE:HD13	1:DA:191:LEU:HD23	1.68	0.73
4:GB:73:VAL:HG21	4:GB:117:ILE:HD13	1.71	0.73
1:AH:165:ILE:HD13	1:AH:191:LEU:HD23	1.69	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AY:261:ILE:HD12	1:AY:312:LEU:HD23	1.70	0.73
1:CO:165:ILE:HD13	1:CO:191:LEU:HD23	1.68	0.73
1:AD:210:SER:HB3	1:AG:244:ARG:HH12	1.53	0.72
1:AX:261:ILE:HD12	1:AX:312:LEU:HD23	1.70	0.72
1:AZ:165:ILE:HD13	1:AZ:191:LEU:HD23	1.71	0.72
1:BK:152:LEU:HD21	4:FW:112:SER:HA	1.70	0.72
1:CQ:165:ILE:HD13	1:CQ:191:LEU:HD23	1.70	0.72
1:CA:165:ILE:HD13	1:CA:191:LEU:HD23	1.70	0.72
1:BN:79:LEU:HD11	1:BN:305:LEU:HB2	1.72	0.72
4:GH:73:VAL:HG21	4:GH:117:ILE:HD13	1.71	0.72
1:AU:261:ILE:HD12	1:AU:312:LEU:HD23	1.72	0.72
4:FS:73:VAL:HG21	4:FS:117:ILE:HD13	1.70	0.72
1:AB:215:LYS:HE2	1:AF:181:PHE:HE2	1.55	0.71
1:CL:261:ILE:HD12	1:CL:312:LEU:HD23	1.72	0.71
1:CN:261:ILE:HD12	1:CN:312:LEU:HD23	1.72	0.71
4:GI:77:ILE:HG13	4:GI:91:PRO:HB3	1.71	0.71
1:CE:261:ILE:HD12	1:CE:312:LEU:HD23	1.73	0.71
1:AH:261:ILE:HD12	1:AH:312:LEU:HD23	1.71	0.71
1:CU:261:ILE:HD12	1:CU:312:LEU:HD23	1.71	0.71
1:CW:165:ILE:HD13	1:CW:191:LEU:HD23	1.71	0.71
1:AE:261:ILE:HD12	1:AE:312:LEU:HD23	1.72	0.71
1:AR:261:ILE:HD12	1:AR:312:LEU:HD23	1.72	0.71
1:DC:261:ILE:HD12	1:DC:312:LEU:HD23	1.71	0.71
4:FR:73:VAL:HG21	4:FR:117:ILE:HG12	1.73	0.71
1:BW:165:ILE:HD13	1:BW:191:LEU:HD23	1.72	0.71
1:CT:261:ILE:HD12	1:CT:312:LEU:HD23	1.72	0.70
1:BS:261:ILE:HD12	1:BS:312:LEU:HD23	1.74	0.70
1:CB:261:ILE:HD12	1:CB:312:LEU:HD23	1.73	0.70
1:AS:192:GLU:HB3	2:DZ:36:ILE:HD11	1.72	0.70
1:AA:261:ILE:HD12	1:AA:312:LEU:HD23	1.73	0.70
1:AC:165:ILE:HD13	1:AC:191:LEU:HD23	1.73	0.70
1:BW:261:ILE:HD12	1:BW:312:LEU:HD23	1.74	0.70
1:CK:261:ILE:HD12	1:CK:312:LEU:HD23	1.74	0.70
1:CF:261:ILE:HD12	1:CF:312:LEU:HD23	1.72	0.70
1:CH:165:ILE:HD13	1:CH:191:LEU:HD23	1.73	0.69
1:CH:192:GLU:HB3	2:EW:36:ILE:HD11	1.74	0.69
1:CL:48:LYS:NZ	2:ET:33:SER:O	2.25	0.69
1:BE:261:ILE:HD12	1:BE:312:LEU:HD23	1.75	0.69
1:BH:92:LYS:NZ	1:BH:288:ASP:O	2.25	0.69
1:BY:261:ILE:HD12	1:BY:312:LEU:HD23	1.74	0.69
1:BA:261:ILE:HD12	1:BA:312:LEU:HD23	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DE:77:VAL:HG21	2:FF:32:LEU:HD23	1.74	0.69
1:AD:165:ILE:HD13	1:AD:191:LEU:HD23	1.74	0.69
1:BJ:261:ILE:HD12	1:BJ:312:LEU:HD23	1.74	0.69
1:CE:165:ILE:HD13	1:CE:191:LEU:HD23	1.73	0.69
1:CM:199:THR:HG21	1:CM:265:ASN:HB2	1.75	0.69
1:CW:261:ILE:HD12	1:CW:312:LEU:HD23	1.75	0.69
1:AB:165:ILE:HD13	1:AB:191:LEU:HD23	1.75	0.69
1:BE:165:ILE:HD13	1:BE:191:LEU:HD23	1.75	0.69
1:CH:261:ILE:HD12	1:CH:312:LEU:HD23	1.75	0.69
1:DD:192:GLU:HB3	2:FI:36:ILE:HD11	1.75	0.69
1:DE:261:ILE:HD12	1:DE:312:LEU:HD23	1.73	0.69
2:DW:123:LEU:HD21	2:DW:131:VAL:HG21	1.74	0.69
2:EC:63:PRO:HB2	2:EC:85:GLU:HG2	1.72	0.69
4:FN:77:ILE:HG13	4:FN:91:PRO:HB3	1.75	0.69
1:BS:152:LEU:HD21	2:EM:105:SER:HA	1.75	0.69
1:DA:48:LYS:NZ	2:FB:33:SER:O	2.26	0.69
2:DO:180:ASN:O	2:DP:180:ASN:ND2	2.25	0.69
1:BU:261:ILE:HD12	1:BU:312:LEU:HD23	1.73	0.68
1:AG:261:ILE:HD12	1:AG:312:LEU:HD23	1.73	0.68
1:BZ:165:ILE:HD13	1:BZ:191:LEU:HD23	1.75	0.68
1:BS:164:GLN:HE22	1:BS:308:ARG:HA	1.58	0.68
1:BT:261:ILE:HD12	1:BT:312:LEU:HD23	1.73	0.68
1:BV:261:ILE:HD12	1:BV:312:LEU:HD23	1.75	0.68
1:CV:199:THR:HG21	1:CV:265:ASN:HB2	1.75	0.68
1:CZ:165:ILE:HD13	1:CZ:191:LEU:HD23	1.74	0.68
1:AU:165:ILE:HD13	1:AU:191:LEU:HD23	1.76	0.68
1:BL:261:ILE:HD12	1:BL:312:LEU:HD23	1.75	0.68
1:DE:48:LYS:NZ	2:FF:33:SER:O	2.26	0.68
4:GA:73:VAL:HG21	4:GA:117:ILE:HG12	1.74	0.68
1:AV:165:ILE:HD13	1:AV:191:LEU:HD23	1.74	0.68
1:AZ:261:ILE:HD12	1:AZ:312:LEU:HD23	1.76	0.68
2:FA:57:ASP:OD1	2:FA:115:ASN:ND2	2.26	0.68
1:AO:261:ILE:HD12	1:AO:312:LEU:HD23	1.76	0.68
1:BU:199:THR:HG21	1:BU:265:ASN:HB2	1.75	0.68
1:CP:48:LYS:NZ	2:EX:33:SER:O	2.26	0.68
1:DD:261:ILE:HD12	1:DD:312:LEU:HD23	1.74	0.68
1:CO:261:ILE:HD12	1:CO:312:LEU:HD23	1.76	0.68
1:CP:261:ILE:HD12	1:CP:312:LEU:HD23	1.73	0.68
1:CQ:261:ILE:HD12	1:CQ:312:LEU:HD23	1.75	0.68
1:CP:77:VAL:HG21	2:EX:32:LEU:HD23	1.74	0.68
1:AP:152:LEU:HD21	2:DQ:105:SER:HA	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CZ:261:ILE:HD12	1:CZ:312:LEU:HD23	1.74	0.68
2:EI:140:ASN:HD21	2:EI:144:GLU:HB2	1.57	0.68
4:FY:161:ILE:HA	4:FY:186:ASN:HA	1.76	0.68
1:AL:261:ILE:HD12	1:AL:312:LEU:HD23	1.76	0.67
1:AW:39:LEU:HD11	1:AW:81:TYR:HD2	1.59	0.67
1:CN:152:LEU:HD21	4:GA:112:SER:HA	1.76	0.67
4:GE:73:VAL:HG21	4:GE:117:ILE:HG12	1.76	0.67
1:CG:199:THR:HG21	1:CG:265:ASN:HB2	1.76	0.67
1:CW:192:GLU:HB3	2:FE:36:ILE:HD11	1.74	0.67
1:BV:164:GLN:HE22	1:BV:308:ARG:HA	1.57	0.67
1:BY:89:ARG:HH21	1:BY:112:LEU:HD21	1.60	0.67
1:BB:317:LYS:NZ	1:BB:319:SER:OXT	2.27	0.67
4:FU:77:ILE:HG12	4:FU:91:PRO:HB3	1.76	0.67
1:AN:165:ILE:HD13	1:AN:191:LEU:HD23	1.75	0.67
1:CX:261:ILE:HD12	1:CX:312:LEU:HD23	1.76	0.67
1:AB:261:ILE:HD12	1:AB:312:LEU:HD23	1.77	0.67
1:AW:261:ILE:HD12	1:AW:312:LEU:HD23	1.76	0.67
4:GG:73:VAL:HG21	4:GG:117:ILE:HG12	1.77	0.67
1:CJ:143:LYS:HA	4:GE:39:ARG:HE	1.60	0.67
1:CN:59:THR:O	2:ER:61:ASN:ND2	2.28	0.67
4:GC:73:VAL:HG21	4:GC:117:ILE:HG12	1.77	0.67
4:GE:77:ILE:HG13	4:GE:91:PRO:HB3	1.77	0.67
1:AS:165:ILE:HD13	1:AS:191:LEU:HD23	1.77	0.67
1:AV:261:ILE:HD12	1:AV:312:LEU:HD23	1.76	0.67
1:CT:77:VAL:HG21	2:FG:32:LEU:HD23	1.76	0.67
2:FB:123:LEU:HD21	2:FB:131:VAL:HG21	1.77	0.67
4:FR:77:ILE:HG13	4:FR:91:PRO:HB3	1.75	0.67
1:DC:152:LEU:HD21	4:FR:112:SER:HA	1.76	0.67
1:CJ:261:ILE:HD12	1:CJ:312:LEU:HD23	1.77	0.66
1:CR:152:LEU:HD21	4:GG:112:SER:HA	1.76	0.66
1:CU:48:LYS:NZ	2:EV:33:SER:O	2.27	0.66
1:AR:165:ILE:HD13	1:AR:191:LEU:HD23	1.76	0.66
1:AT:110:ASN:OD1	1:BA:62:ASN:ND2	2.28	0.66
1:BH:261:ILE:HD12	1:BH:312:LEU:HD23	1.78	0.66
1:BZ:261:ILE:HD12	1:BZ:312:LEU:HD23	1.77	0.66
1:DA:261:ILE:HD12	1:DA:312:LEU:HD23	1.77	0.66
1:DB:199:THR:HG21	1:DB:265:ASN:HB2	1.76	0.66
1:AB:317:LYS:NZ	1:AB:319:SER:OXT	2.28	0.66
1:AT:261:ILE:HD12	1:AT:312:LEU:HD23	1.75	0.66
1:BT:152:LEU:HD21	2:EL:105:SER:HA	1.77	0.66
1:CF:48:LYS:NZ	2:FD:33:SER:O	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CT:165:ILE:HD13	1:CT:191:LEU:HD23	1.77	0.66
1:CV:261:ILE:HD12	1:CV:312:LEU:HD23	1.78	0.66
1:CW:59:THR:O	4:GH:61:ASN:ND2	2.28	0.66
1:CX:152:LEU:HD21	4:GI:112:SER:HA	1.77	0.66
2:FF:77:PHE:HB2	4:GI:138:LYS:HE2	1.77	0.66
1:DC:59:THR:O	2:DY:61:ASN:ND2	2.29	0.66
1:AP:261:ILE:HD12	1:AP:312:LEU:HD23	1.77	0.66
1:AS:240:ALA:HB2	1:AZ:214:VAL:HG11	1.78	0.66
1:BA:165:ILE:HD13	1:BA:191:LEU:HD23	1.76	0.66
1:BD:92:LYS:NZ	1:BD:94:THR:OG1	2.28	0.66
4:FQ:142:ILE:HG12	4:FQ:159:ALA:HB2	1.78	0.66
1:BH:165:ILE:HD13	1:BH:191:LEU:HD23	1.76	0.66
1:CD:261:ILE:HD12	1:CD:312:LEU:HD23	1.78	0.65
1:CG:261:ILE:HD12	1:CG:312:LEU:HD23	1.78	0.65
1:CO:192:GLU:HB3	2:FA:36:ILE:HD11	1.78	0.65
2:ES:63:PRO:HB2	2:ES:85:GLU:HG2	1.78	0.65
1:AD:261:ILE:HD12	1:AD:312:LEU:HD23	1.77	0.65
1:CI:261:ILE:HD12	1:CI:312:LEU:HD23	1.77	0.65
2:ER:123:LEU:HD21	2:ER:131:VAL:HG21	1.78	0.65
1:BS:192:GLU:HB3	2:ES:36:ILE:HD11	1.79	0.65
1:CC:152:LEU:HD21	4:GC:112:SER:HA	1.78	0.65
1:CC:261:ILE:HD12	1:CC:312:LEU:HD23	1.78	0.65
1:CK:212:LYS:HA	1:CK:215:LYS:HE3	1.77	0.65
1:CY:261:ILE:HD12	1:CY:312:LEU:HD23	1.77	0.65
2:DH:165:LYS:HE3	2:DH:168:GLU:HA	1.78	0.65
1:AI:261:ILE:HD12	1:AI:312:LEU:HD23	1.79	0.65
1:CO:164:GLN:HE22	1:CO:308:ARG:HA	1.60	0.65
1:CR:261:ILE:HD12	1:CR:312:LEU:HD23	1.77	0.65
1:AH:174:LYS:HE2	1:AH:318:GLN:HE21	1.61	0.65
1:AY:41:MET:HE2	1:AY:83:LYS:H	1.61	0.65
1:AC:261:ILE:HD12	1:AC:312:LEU:HD23	1.79	0.65
1:CZ:212:LYS:HA	1:CZ:215:LYS:HE3	1.80	0.64
4:GG:77:ILE:HG13	4:GG:91:PRO:HB3	1.79	0.64
4:GJ:161:ILE:HA	4:GJ:186:ASN:HA	1.79	0.64
4:FP:77:ILE:HG12	4:FP:91:PRO:HB3	1.79	0.64
1:CF:66:THR:OG1	2:FE:58:LYS:NZ	2.30	0.64
2:FF:123:LEU:HD21	2:FF:131:VAL:HG21	1.79	0.64
1:BH:317:LYS:NZ	1:BH:319:SER:OXT	2.31	0.64
1:CH:77:VAL:HG21	2:EW:32:LEU:HD23	1.80	0.64
2:DF:136:LYS:HD3	2:DF:181:ARG:HH12	1.62	0.64
1:BP:305:LEU:HD11	2:EG:32:LEU:HG	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BR:227:CYS:SG	1:BR:228:GLU:N	2.69	0.64
1:CF:77:VAL:HG21	2:FD:32:LEU:HD23	1.79	0.64
1:CQ:164:GLN:HE22	1:CQ:308:ARG:HA	1.62	0.64
1:AM:20:VAL:O	5:GW:213:ARG:NH2	2.28	0.64
1:BW:143:LYS:HA	2:EN:39:ARG:HE	1.62	0.64
1:CC:59:THR:O	2:EV:61:ASN:ND2	2.31	0.64
4:FW:161:ILE:HA	4:FW:186:ASN:HA	1.79	0.64
1:BM:163:GLU:HB2	4:FW:31:LEU:HD22	1.80	0.64
1:BC:261:ILE:HD12	1:BC:312:LEU:HD23	1.79	0.64
1:CK:165:ILE:HD13	1:CK:191:LEU:HD23	1.79	0.64
1:CN:13:VAL:HG11	1:CN:281:PRO:HG3	1.80	0.64
4:FO:73:VAL:HG21	4:FO:117:ILE:HD13	1.79	0.64
1:AE:59:THR:O	4:FL:61:ASN:ND2	2.31	0.63
1:AT:100:THR:HG22	1:AT:105:ILE:HG23	1.78	0.63
2:FB:77:PHE:HB2	4:GG:138:LYS:HE2	1.79	0.63
4:FK:161:ILE:HA	4:FK:186:ASN:HA	1.79	0.63
1:AH:92:LYS:NZ	1:AH:288:ASP:O	2.31	0.63
1:BV:308:ARG:HH21	2:EF:31:LEU:HB2	1.62	0.63
1:CA:261:ILE:HD12	1:CA:312:LEU:HD23	1.79	0.63
4:FZ:161:ILE:HA	4:FZ:186:ASN:HA	1.81	0.63
1:AM:261:ILE:HD12	1:AM:312:LEU:HD23	1.81	0.63
1:CR:143:LYS:HA	2:FC:39:ARG:HE	1.62	0.63
4:FY:69:TYR:HB2	4:FY:108:ILE:HD12	1.81	0.63
1:AQ:261:ILE:HD12	1:AQ:312:LEU:HD23	1.80	0.63
1:BB:166:LYS:HG2	1:BB:313:GLN:HE21	1.63	0.63
1:BI:261:ILE:HD12	1:BI:312:LEU:HD23	1.81	0.63
1:CL:286:ASP:HB2	1:CL:294:HIS:HB2	1.80	0.63
1:BF:165:ILE:HD13	1:BF:191:LEU:HD23	1.81	0.63
2:DN:63:PRO:HB2	2:DN:85:GLU:HG2	1.80	0.63
2:EB:125:LYS:HD2	2:EB:169:ASP:HA	1.80	0.63
4:FO:161:ILE:HA	4:FO:186:ASN:HA	1.79	0.63
1:BQ:152:LEU:HD21	2:EI:105:SER:HA	1.80	0.63
1:DC:13:VAL:HG11	1:DC:281:PRO:HG3	1.80	0.63
1:CA:152:LEU:HD21	2:ES:105:SER:HA	1.80	0.63
1:CE:77:VAL:HG21	2:EY:32:LEU:HD23	1.79	0.63
1:CX:13:VAL:HG11	1:CX:281:PRO:HG3	1.80	0.63
2:EJ:180:ASN:O	4:FY:186:ASN:ND2	2.32	0.63
1:CM:13:VAL:HG11	1:CM:281:PRO:HG3	1.80	0.62
1:CV:65:ASN:ND2	2:FB:57:ASP:O	2.32	0.62
1:DB:261:ILE:HD12	1:DB:312:LEU:HD23	1.81	0.62
4:FQ:73:VAL:HG21	4:FQ:117:ILE:HD13	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CS:48:LYS:NZ	2:FH:33:SER:O	2.32	0.62
1:CD:143:LYS:HA	4:GC:39:ARG:HE	1.64	0.62
1:DC:165:ILE:HD13	1:DC:191:LEU:HD23	1.81	0.62
4:GI:73:VAL:HG21	4:GI:117:ILE:HG12	1.81	0.62
1:BZ:110:ASN:ND2	1:CJ:62:ASN:OD1	2.32	0.62
1:AU:199:THR:HG21	1:AU:265:ASN:HB2	1.80	0.62
1:CM:261:ILE:HD12	1:CM:312:LEU:HD23	1.82	0.62
4:FY:43:VAL:HG11	4:FY:170:LYS:HD3	1.82	0.62
1:AT:164:GLN:HE22	1:AT:308:ARG:HA	1.65	0.62
1:DD:77:VAL:HG21	2:FI:32:LEU:HD23	1.81	0.62
1:AL:77:VAL:HG21	2:DV:32:LEU:HD23	1.81	0.62
1:AN:261:ILE:HD12	1:AN:312:LEU:HD23	1.82	0.62
1:BX:261:ILE:HD12	1:BX:312:LEU:HD23	1.81	0.62
1:CS:107:ASP:OD2	1:CS:110:ASN:ND2	2.31	0.62
2:ET:123:LEU:HD21	2:ET:131:VAL:HG21	1.82	0.62
4:GA:77:ILE:HG13	4:GA:91:PRO:HB3	1.82	0.62
1:BZ:87:LYS:NZ	2:ES:53:THR:O	2.28	0.62
1:AE:165:ILE:HD13	1:AE:191:LEU:HD23	1.80	0.61
1:BO:261:ILE:HD12	1:BO:312:LEU:HD23	1.82	0.61
2:EK:100:ASP:HB3	2:EK:109:THR:HB	1.82	0.61
2:ER:167:THR:HG22	2:ER:168:GLU:H	1.65	0.61
4:FZ:77:ILE:HG13	4:FZ:91:PRO:HB3	1.82	0.61
1:BK:286:ASP:HB2	1:BK:294:HIS:HB2	1.83	0.61
1:BT:75:GLU:HG2	4:FX:26:GLN:HB3	1.82	0.61
1:BT:100:THR:HG22	1:BT:105:ILE:HG23	1.82	0.61
2:DP:63:PRO:HB2	2:DP:85:GLU:HG2	1.83	0.61
1:CR:13:VAL:HG11	1:CR:281:PRO:HG3	1.82	0.61
1:BY:110:ASN:ND2	1:CK:62:ASN:OD1	2.34	0.61
2:FH:54:SER:HB2	2:FI:58:LYS:HZ3	1.64	0.61
4:GA:26:GLN:NE2	4:GA:28:ASP:OD1	2.33	0.61
1:AX:165:ILE:HD13	1:AX:191:LEU:HD12	1.83	0.61
1:CS:261:ILE:HD12	1:CS:312:LEU:HD23	1.82	0.61
3:FJ:197:PRO:HB2	3:FJ:246:GLU:HB3	1.83	0.61
1:BC:286:ASP:HB2	1:BC:294:HIS:HB2	1.83	0.61
1:AH:317:LYS:NZ	1:AH:319:SER:OXT	2.34	0.61
1:BU:89:ARG:HH21	1:BU:112:LEU:HD21	1.66	0.61
1:CS:214:VAL:HG11	1:CV:240:ALA:HB2	1.83	0.61
2:EA:137:LEU:HD11	2:EA:159:ALA:HB2	1.83	0.61
2:EU:165:LYS:HE3	2:EU:168:GLU:HA	1.83	0.61
2:EV:167:THR:HG22	2:EV:168:GLU:H	1.66	0.61
4:FW:69:TYR:HB2	4:FW:108:ILE:HD12	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:FZ:93:VAL:HG21	4:FZ:117:ILE:HD11	1.82	0.61
1:CC:55:ALA:HB2	4:GD:51:THR:HB	1.82	0.61
1:CH:16:ILE:HD12	1:CH:116:ALA:HB1	1.82	0.61
1:CI:143:LYS:HA	2:EY:39:ARG:HE	1.66	0.61
4:FR:69:TYR:HB2	4:FR:108:ILE:HD12	1.83	0.61
4:FS:77:ILE:HG13	4:FS:91:PRO:HB3	1.81	0.61
1:AS:77:VAL:HG21	2:DZ:32:LEU:HD23	1.82	0.61
1:CC:13:VAL:HG11	1:CC:281:PRO:HG3	1.83	0.61
1:AK:13:VAL:HG11	1:AK:281:PRO:HG2	1.82	0.60
1:AS:261:ILE:HD12	1:AS:312:LEU:HD23	1.82	0.60
1:AT:165:ILE:HD13	1:AT:191:LEU:HD23	1.83	0.60
2:DY:167:THR:HG22	2:DY:168:GLU:H	1.65	0.60
2:EN:37:ASP:O	2:EN:41:GLN:NE2	2.34	0.60
1:AV:308:ARG:HH21	2:DN:31:LEU:HB2	1.65	0.60
1:BG:261:ILE:HD12	1:BG:312:LEU:HD23	1.83	0.60
1:CI:13:VAL:HG11	1:CI:281:PRO:HG3	1.83	0.60
1:DC:87:LYS:NZ	2:DX:53:THR:O	2.31	0.60
1:AH:152:LEU:HD21	2:DK:105:SER:HA	1.83	0.60
1:CI:152:LEU:HD21	4:GE:112:SER:HA	1.81	0.60
1:CU:135:LEU:HD21	1:CU:255:LEU:HG	1.83	0.60
2:DW:77:PHE:HB2	4:FR:138:LYS:HE2	1.84	0.60
1:CT:164:GLN:HE22	1:CT:308:ARG:HA	1.66	0.60
4:GJ:73:VAL:HG21	4:GJ:117:ILE:HD13	1.82	0.60
1:AW:143:LYS:HA	2:DV:39:ARG:HE	1.65	0.60
1:BX:77:VAL:HG21	2:EP:32:LEU:HD23	1.83	0.60
1:CB:164:GLN:HE22	1:CB:308:ARG:HA	1.66	0.60
1:CW:16:ILE:HD12	1:CW:116:ALA:HB1	1.84	0.60
1:CZ:162:PRO:HG2	2:DX:31:LEU:HD11	1.82	0.60
2:DU:77:PHE:HB2	4:FQ:138:LYS:HE2	1.83	0.60
4:GE:26:GLN:NE2	4:GE:28:ASP:OD1	2.34	0.60
1:CF:286:ASP:HB2	1:CF:294:HIS:HB2	1.82	0.60
1:DC:143:LYS:HA	2:DX:39:ARG:HE	1.66	0.60
2:EM:75:LEU:HB3	2:EM:84:LEU:HD11	1.82	0.60
2:FH:167:THR:HG22	2:FH:168:GLU:H	1.67	0.60
1:AM:59:THR:O	4:FM:61:ASN:ND2	2.34	0.60
1:AS:62:ASN:OD1	1:DE:110:ASN:ND2	2.34	0.60
1:BH:59:THR:O	2:EF:61:ASN:ND2	2.35	0.60
1:CL:77:VAL:HG21	2:ET:32:LEU:HD23	1.83	0.60
2:EF:137:LEU:HD11	2:EF:159:ALA:HB2	1.83	0.60
2:FD:167:THR:HG22	2:FD:168:GLU:H	1.66	0.60
1:BD:261:ILE:HD12	1:BD:312:LEU:HD23	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BH:13:VAL:HG11	1:BH:281:PRO:HG2	1.84	0.60
1:CD:214:VAL:HG11	1:CG:240:ALA:HB2	1.82	0.60
1:CW:77:VAL:HG21	2:FE:32:LEU:HD23	1.83	0.60
4:GD:77:ILE:HG13	4:GD:91:PRO:HB3	1.83	0.60
1:AS:13:VAL:HG11	1:AS:281:PRO:HG2	1.83	0.60
1:CK:77:VAL:HG21	2:EQ:32:LEU:HD23	1.83	0.60
1:DD:164:GLN:HE22	1:DD:308:ARG:HA	1.66	0.60
4:FZ:161:ILE:O	4:FZ:187:LYS:NZ	2.35	0.60
1:BK:21:LYS:NZ	1:BV:195:ASP:OD2	2.35	0.60
4:GC:77:ILE:HG13	4:GC:91:PRO:HB3	1.84	0.60
1:AO:165:ILE:HD13	1:AO:191:LEU:HD23	1.84	0.59
1:BX:225:SER:HB2	1:CO:224:ALA:HB3	1.82	0.59
1:CA:164:GLN:HE22	1:CA:308:ARG:HA	1.65	0.59
1:AY:110:ASN:ND2	1:CZ:62:ASN:OD1	2.35	0.59
1:BK:261:ILE:HD12	1:BK:312:LEU:HD23	1.84	0.59
1:CX:143:LYS:HA	2:FG:39:ARG:HE	1.67	0.59
2:DZ:63:PRO:HB2	2:DZ:85:GLU:HG2	1.83	0.59
1:DD:59:THR:O	4:GJ:61:ASN:ND2	2.35	0.59
2:EM:23:LYS:N	2:EM:67:TYR:OH	2.35	0.59
1:BK:289:SER:HB2	1:BL:85:GLN:HE22	1.67	0.59
1:BM:174:LYS:O	1:BM:212:LYS:NZ	2.36	0.59
2:DV:37:ASP:O	2:DV:41:GLN:NE2	2.34	0.59
2:FF:181:ARG:HH12	2:FG:94:LEU:HB3	1.67	0.59
1:AX:77:VAL:HG21	2:DW:32:LEU:HD23	1.85	0.59
1:BK:89:ARG:HH21	1:BK:112:LEU:HD21	1.67	0.59
1:BX:205:VAL:HG12	1:BX:259:ILE:HG23	1.83	0.59
1:CR:165:ILE:HD13	1:CR:191:LEU:HD23	1.85	0.59
1:DA:89:ARG:HH21	1:DA:112:LEU:HD21	1.67	0.59
1:BV:109:ASN:O	4:FZ:24:ASN:ND2	2.36	0.59
1:CO:77:VAL:HG21	2:FA:32:LEU:HD23	1.85	0.59
4:GF:77:ILE:HG13	4:GF:91:PRO:HB3	1.84	0.59
1:AT:77:VAL:HG21	2:DP:32:LEU:HD23	1.84	0.59
1:AX:92:LYS:NZ	1:AX:94:THR:OG1	2.31	0.59
2:EC:165:LYS:HE3	2:EC:168:GLU:HA	1.84	0.59
1:AM:96:GLU:O	1:AM:100:THR:HG23	2.03	0.59
1:AQ:239:LYS:HA	1:AQ:242:ASN:OD1	2.03	0.59
1:BA:77:VAL:HG21	2:DT:32:LEU:HD23	1.85	0.59
1:BL:13:VAL:HG11	1:BL:281:PRO:HG2	1.85	0.59
1:BP:152:LEU:HD21	2:EJ:105:SER:HA	1.85	0.59
1:BR:13:VAL:HG11	1:BR:103:SER:HA	1.83	0.59
1:CP:135:LEU:HD21	1:CP:255:LEU:HG	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:65:ASN:ND2	4:FL:57:ASP:O	2.35	0.59
1:AG:165:ILE:HD13	1:AG:191:LEU:HD23	1.83	0.59
1:AU:286:ASP:HB2	1:AU:294:HIS:HB2	1.84	0.59
1:BC:77:VAL:HG21	2:EB:32:LEU:HD23	1.85	0.59
1:BP:261:ILE:HD12	1:BP:312:LEU:HD23	1.85	0.59
1:CJ:205:VAL:HG12	1:CJ:259:ILE:HG23	1.84	0.59
2:DT:75:LEU:HB3	2:DT:84:LEU:HD11	1.85	0.59
2:EX:123:LEU:HD21	2:EX:131:VAL:HG21	1.85	0.59
1:AN:241:ILE:HG22	1:AR:211:LEU:HD21	1.85	0.59
1:BN:261:ILE:HD12	1:BN:312:LEU:HD23	1.85	0.59
1:BZ:286:ASP:HB2	1:BZ:294:HIS:HB2	1.84	0.58
1:CW:164:GLN:HE22	1:CW:308:ARG:HA	1.66	0.58
2:DM:69:TYR:HB2	2:DM:101:ILE:HD12	1.85	0.58
2:EF:69:TYR:HB2	2:EF:101:ILE:HD12	1.85	0.58
2:EQ:165:LYS:HE3	2:EQ:168:GLU:HA	1.85	0.58
4:FK:149:LEU:HD13	4:FK:181:VAL:HG21	1.86	0.58
4:FV:77:ILE:HG13	4:FV:91:PRO:HB3	1.84	0.58
1:AL:13:VAL:HG11	1:AL:281:PRO:HG2	1.85	0.58
1:BC:162:PRO:HG2	2:EB:31:LEU:HD11	1.85	0.58
1:BL:77:VAL:HG21	2:EN:32:LEU:HD23	1.84	0.58
1:BS:62:ASN:OD1	1:CP:110:ASN:ND2	2.36	0.58
2:EL:65:LYS:HB2	2:EL:85:GLU:HG3	1.86	0.58
4:GC:26:GLN:NE2	4:GC:28:ASP:OD1	2.36	0.58
1:AS:164:GLN:HE22	1:AS:308:ARG:HA	1.68	0.58
1:BO:54:ASN:HB3	2:EL:51:VAL:HG12	1.85	0.58
1:CY:205:VAL:HG12	1:CY:259:ILE:HG23	1.85	0.58
2:EL:116:ASN:HD21	2:EM:58:LYS:HE2	1.67	0.58
1:BM:92:LYS:NZ	1:BM:94:THR:OG1	2.37	0.58
1:CS:205:VAL:HG12	1:CS:259:ILE:HG23	1.84	0.58
1:DA:110:ASN:OD1	1:DD:62:ASN:ND2	2.35	0.58
1:DD:16:ILE:HD12	1:DD:116:ALA:HB1	1.85	0.58
2:DS:100:ASP:HB3	2:DS:109:THR:HB	1.86	0.58
2:FA:63:PRO:HB2	2:FA:85:GLU:HG2	1.86	0.58
1:CB:16:ILE:HD12	1:CB:116:ALA:HB1	1.86	0.58
1:CL:79:LEU:HD11	1:CL:305:LEU:HB2	1.86	0.58
1:AS:66:THR:OG1	4:FS:58:LYS:NZ	2.37	0.58
1:AY:87:LYS:NZ	4:FR:53:THR:O	2.34	0.58
1:BK:22:ASP:OD1	5:HU:213:ARG:NE	2.37	0.58
1:BV:77:VAL:HG21	2:EF:32:LEU:HD23	1.84	0.58
1:CD:205:VAL:HG12	1:CD:259:ILE:HG23	1.86	0.58
1:CH:164:GLN:HE22	1:CH:308:ARG:HA	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:DX:165:LYS:HE3	2:DX:168:GLU:HA	1.85	0.58
2:FH:23:LYS:NZ	2:FH:100:ASP:OD1	2.35	0.58
1:AW:239:LYS:HA	1:AW:242:ASN:OD1	2.04	0.58
1:DA:79:LEU:HD11	1:DA:305:LEU:HB2	1.85	0.58
1:AK:261:ILE:HD12	1:AK:312:LEU:HD23	1.86	0.58
1:BH:286:ASP:HB2	1:BH:294:HIS:HB2	1.86	0.58
2:EZ:123:LEU:HD21	2:EZ:131:VAL:HG21	1.86	0.58
4:GB:77:ILE:HG13	4:GB:91:PRO:HB3	1.86	0.58
4:GE:69:TYR:HB2	4:GE:108:ILE:HD12	1.85	0.58
1:AF:165:ILE:HD13	1:AF:191:LEU:HD23	1.84	0.58
1:CA:84:LEU:HB3	1:CJ:57:PRO:HB2	1.85	0.58
2:EZ:167:THR:HG22	2:EZ:168:GLU:H	1.69	0.58
1:AK:240:ALA:HB2	1:AO:214:VAL:HG11	1.86	0.57
1:CR:59:THR:O	2:FD:61:ASN:ND2	2.36	0.57
1:CU:110:ASN:OD1	1:CW:62:ASN:ND2	2.33	0.57
4:GC:142:ILE:HD11	4:GC:152:VAL:HG23	1.86	0.57
1:AA:20:VAL:O	5:GK:213:ARG:NH2	2.36	0.57
1:AS:152:LEU:HD21	2:DT:105:SER:HA	1.85	0.57
1:AU:87:LYS:NZ	2:DT:53:THR:O	2.31	0.57
1:AV:77:VAL:HG21	2:DN:32:LEU:HD23	1.85	0.57
1:BX:212:LYS:HA	1:BX:215:LYS:HE3	1.85	0.57
1:CO:16:ILE:HD12	1:CO:116:ALA:HB1	1.86	0.57
2:FH:148:VAL:HG21	2:FH:155:VAL:HG12	1.86	0.57
4:FM:149:LEU:HD13	4:FM:181:VAL:HG21	1.85	0.57
1:CN:165:ILE:HD13	1:CN:191:LEU:HD23	1.85	0.57
2:DM:137:LEU:HD11	2:DM:159:ALA:HB2	1.86	0.57
2:DV:56:LYS:HD2	4:FQ:56:PHE:HD1	1.69	0.57
1:AX:239:LYS:HB3	1:AX:244:ARG:HG2	1.85	0.57
1:BF:150:ARG:HE	2:EB:63:PRO:HB3	1.68	0.57
1:BY:85:GLN:HE22	1:CO:289:SER:HB2	1.70	0.57
1:DA:77:VAL:HG21	2:FB:32:LEU:HD23	1.86	0.57
2:EK:148:VAL:HG11	2:EK:153:LYS:HD3	1.86	0.57
2:ER:75:LEU:HD22	2:ER:84:LEU:HD13	1.87	0.57
1:AB:239:LYS:HA	1:AB:242:ASN:OD1	2.04	0.57
1:AF:261:ILE:HD12	1:AF:312:LEU:HD23	1.86	0.57
1:BN:152:LEU:HD21	2:EG:105:SER:HA	1.86	0.57
1:DB:13:VAL:HG11	1:DB:281:PRO:HG3	1.86	0.57
2:EM:137:LEU:HD11	2:EM:159:ALA:HB2	1.85	0.57
4:GJ:77:ILE:HG13	4:GJ:91:PRO:HB3	1.85	0.57
1:BV:317:LYS:NZ	1:BV:319:SER:OXT	2.36	0.57
1:CE:164:GLN:HE22	1:CE:308:ARG:HA	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CW:13:VAL:HG11	1:CW:281:PRO:HG2	1.87	0.57
2:EZ:77:PHE:HB2	4:GF:138:LYS:HE2	1.86	0.57
1:BB:80:ASN:ND2	1:BB:153:PRO:O	2.38	0.57
1:CA:77:VAL:HG21	2:EM:32:LEU:HD23	1.85	0.57
2:DL:137:LEU:HD11	2:DL:159:ALA:HB2	1.85	0.57
2:DT:63:PRO:HB2	2:DT:85:GLU:HG2	1.86	0.57
4:GH:107:ASP:HB3	4:GH:116:THR:HB	1.85	0.57
1:AF:13:VAL:HG11	1:AF:281:PRO:HG2	1.87	0.57
1:AK:244:ARG:NH1	1:AO:210:SER:OG	2.35	0.57
1:AZ:80:ASN:ND2	1:AZ:153:PRO:O	2.36	0.57
1:BE:158:LEU:HB3	1:BE:260:LEU:HD21	1.86	0.57
1:CP:286:ASP:HB2	1:CP:294:HIS:HB2	1.85	0.57
1:CU:77:VAL:HG21	2:EV:32:LEU:HD23	1.86	0.57
1:DA:286:ASP:HB2	1:DA:294:HIS:HB2	1.86	0.57
2:EB:165:LYS:HE3	2:EB:168:GLU:HA	1.87	0.57
2:EX:77:PHE:HB2	4:GE:138:LYS:HE2	1.87	0.57
1:AW:196:GLU:OE1	1:AW:265:ASN:ND2	2.36	0.57
1:BJ:77:VAL:HG11	1:BJ:305:LEU:HD13	1.87	0.57
1:CE:59:THR:O	4:GE:61:ASN:ND2	2.38	0.57
2:DX:76:SER:HB3	2:DX:87:GLU:HG2	1.87	0.57
1:CG:65:ASN:ND2	2:ET:57:ASP:O	2.38	0.56
2:DK:165:LYS:HE3	2:DK:168:GLU:HA	1.87	0.56
2:DV:23:LYS:N	2:DV:67:TYR:OH	2.37	0.56
2:DY:123:LEU:HD21	2:DY:131:VAL:HG21	1.87	0.56
2:EV:75:LEU:HD22	2:EV:84:LEU:HD13	1.87	0.56
2:EY:165:LYS:HE3	2:EY:168:GLU:HA	1.86	0.56
2:FG:76:SER:HB3	2:FG:87:GLU:HG2	1.86	0.56
2:FI:165:LYS:HE3	2:FI:168:GLU:HA	1.87	0.56
1:AL:143:LYS:HE3	4:FM:40:ASP:HB2	1.87	0.56
1:BL:152:LEU:HD21	2:EF:105:SER:HA	1.88	0.56
1:CY:174:LYS:O	1:CY:212:LYS:NZ	2.38	0.56
4:FN:149:LEU:HD13	4:FN:181:VAL:HG21	1.87	0.56
4:GA:69:TYR:HB2	4:GA:108:ILE:HD12	1.87	0.56
1:AH:59:THR:O	2:DN:61:ASN:ND2	2.37	0.56
1:AY:286:ASP:HB2	1:AY:294:HIS:HB2	1.86	0.56
1:AZ:110:ASN:ND2	1:CY:62:ASN:OD1	2.38	0.56
1:BR:261:ILE:HD12	1:BR:312:LEU:HD23	1.87	0.56
1:CG:152:LEU:HD21	4:GD:112:SER:HA	1.87	0.56
1:CK:13:VAL:HG11	1:CK:281:PRO:HG2	1.88	0.56
1:CM:152:LEU:HD21	4:GF:112:SER:HA	1.87	0.56
1:DD:91:LEU:HD21	1:DD:112:LEU:HD13	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:DS:166:LEU:HB2	2:DS:170:LEU:HD23	1.86	0.56
2:ED:137:LEU:HD11	2:ED:159:ALA:HB2	1.86	0.56
2:EW:63:PRO:HB2	2:EW:85:GLU:HG2	1.87	0.56
3:FJ:94:TYR:CE2	3:FJ:96:PHE:HB2	2.41	0.56
4:FL:161:ILE:HA	4:FL:186:ASN:HA	1.87	0.56
4:FZ:149:LEU:HD13	4:FZ:181:VAL:HG21	1.87	0.56
4:GG:69:TYR:HB2	4:GG:108:ILE:HD12	1.87	0.56
4:GI:69:TYR:HB2	4:GI:108:ILE:HD12	1.87	0.56
1:BA:152:LEU:HD21	2:DZ:105:SER:HA	1.87	0.56
1:CJ:152:LEU:HD21	2:EX:105:SER:HA	1.87	0.56
1:CQ:16:ILE:HD12	1:CQ:116:ALA:HB1	1.88	0.56
1:DB:210:SER:O	1:DB:214:VAL:HG13	2.05	0.56
2:DN:165:LYS:HE3	2:DN:168:GLU:HA	1.87	0.56
2:DS:58:LYS:HE2	2:DT:116:ASN:HD21	1.70	0.56
2:EF:165:LYS:HE3	2:EF:168:GLU:HA	1.87	0.56
2:ER:180:ASN:O	2:ES:180:ASN:ND2	2.36	0.56
2:FC:165:LYS:HE3	2:FC:168:GLU:HA	1.86	0.56
1:BK:158:LEU:HB3	1:BK:260:LEU:HD21	1.86	0.56
1:CB:79:LEU:HD11	1:CB:305:LEU:HB2	1.88	0.56
2:EO:156:ASN:ND2	2:EO:180:ASN:O	2.39	0.56
4:GB:107:ASP:HB3	4:GB:116:THR:HB	1.86	0.56
1:AB:152:LEU:HD21	2:DF:105:SER:HA	1.88	0.56
1:AK:158:LEU:HB3	1:AK:260:LEU:HD21	1.86	0.56
1:AL:92:LYS:NZ	1:AL:95:SER:OG	2.38	0.56
1:AN:13:VAL:HG11	1:AN:281:PRO:HG2	1.88	0.56
1:BO:59:THR:O	2:EM:61:ASN:ND2	2.39	0.56
1:BP:43:TYR:HE1	1:BP:45:LYS:HG3	1.71	0.56
1:BQ:13:VAL:HG11	1:BQ:281:PRO:HG2	1.87	0.56
2:EB:69:TYR:HB2	2:EB:101:ILE:HD12	1.87	0.56
2:EL:69:TYR:HB2	2:EL:101:ILE:HD12	1.86	0.56
1:AX:205:VAL:HG12	1:AX:259:ILE:HG23	1.87	0.56
1:BS:240:ALA:HB2	1:BZ:214:VAL:HG11	1.87	0.56
1:BZ:65:ASN:ND2	2:EP:57:ASP:O	2.38	0.56
1:CD:152:LEU:HD21	2:ET:105:SER:HA	1.87	0.56
1:CM:80:ASN:ND2	1:CM:153:PRO:O	2.34	0.56
1:CZ:13:VAL:HG11	1:CZ:281:PRO:HG2	1.87	0.56
2:DW:56:LYS:HD2	2:DX:56:LYS:HA	1.87	0.56
1:AH:13:VAL:HG11	1:AH:281:PRO:HG2	1.86	0.56
1:AS:59:THR:O	4:FS:61:ASN:ND2	2.38	0.56
1:AZ:132:HIS:HA	1:AZ:254:LEU:HD13	1.88	0.56
3:FJ:181:LEU:HD11	3:FJ:204:ALA:HB2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:13:VAL:HG11	1:AE:281:PRO:HG2	1.86	0.56
1:BD:178:ASP:OD1	1:BD:179:LYS:N	2.38	0.56
1:BO:13:VAL:HG11	1:BO:281:PRO:HG2	1.87	0.56
1:BV:107:ASP:OD2	1:BV:110:ASN:ND2	2.35	0.56
1:BX:57:PRO:HG2	1:CO:84:LEU:HD13	1.88	0.56
1:CV:13:VAL:HG11	1:CV:281:PRO:HG3	1.88	0.56
2:EM:181:ARG:NH1	2:EM:182:ALA:O	2.39	0.56
1:AS:196:GLU:HB3	1:AS:265:ASN:HD22	1.69	0.56
1:AS:239:LYS:HA	1:AS:242:ASN:OD1	2.06	0.56
1:DB:152:LEU:HD21	4:GJ:112:SER:HA	1.88	0.56
2:DM:180:ASN:ND2	2:DN:180:ASN:O	2.39	0.56
2:DT:180:ASN:ND2	4:FP:186:ASN:O	2.39	0.56
2:EG:9:GLN:O	2:EG:13:LYS:HG2	2.06	0.56
1:AR:13:VAL:HG11	1:AR:281:PRO:HG2	1.87	0.55
1:AX:239:LYS:HA	1:AX:242:ASN:OD1	2.07	0.55
1:BJ:178:ASP:OD1	1:BJ:179:LYS:N	2.39	0.55
1:BY:87:LYS:NZ	4:GA:53:THR:O	2.35	0.55
1:CL:89:ARG:HH21	1:CL:112:LEU:HD21	1.70	0.55
2:EH:137:LEU:HD11	2:EH:159:ALA:HB2	1.86	0.55
2:EV:77:PHE:HB2	4:GD:138:LYS:HE2	1.87	0.55
4:FO:77:ILE:HG12	4:FO:91:PRO:HB3	1.87	0.55
4:GD:141:LEU:HD11	4:GD:165:ALA:HB2	1.87	0.55
2:EV:123:LEU:HD21	2:EV:131:VAL:HG21	1.87	0.55
2:FE:63:PRO:HB2	2:FE:85:GLU:HG2	1.87	0.55
1:AB:203:VAL:HG22	1:AB:261:ILE:HG23	1.87	0.55
1:AF:89:ARG:HH21	1:AF:112:LEU:HD21	1.71	0.55
1:AH:240:ALA:HB2	1:AL:214:VAL:HG11	1.88	0.55
1:AK:57:PRO:HB2	1:AO:84:LEU:HD13	1.88	0.55
1:CO:13:VAL:HG11	1:CO:281:PRO:HG2	1.88	0.55
2:EX:22:MET:HG3	2:EX:26:GLN:HE22	1.70	0.55
2:FI:69:TYR:HB2	2:FI:101:ILE:HD12	1.89	0.55
1:AN:80:ASN:ND2	1:AN:153:PRO:O	2.36	0.55
1:AX:13:VAL:HG11	1:AX:281:PRO:HG2	1.86	0.55
1:BC:239:LYS:HA	1:BC:242:ASN:OD1	2.06	0.55
1:CG:286:ASP:HB2	1:CG:294:HIS:HB2	1.89	0.55
1:CK:47:VAL:HG22	1:CK:76:VAL:HG22	1.87	0.55
1:CM:210:SER:O	1:CM:214:VAL:HG13	2.06	0.55
2:DU:23:LYS:N	2:DU:67:TYR:OH	2.40	0.55
2:EA:136:LYS:HD3	2:EA:181:ARG:HH12	1.72	0.55
2:EB:153:LYS:HG3	2:EB:154:SER:H	1.71	0.55
4:FQ:161:ILE:HA	4:FQ:186:ASN:HA	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:152:LEU:HD21	2:DI:105:SER:HA	1.88	0.55
1:AO:188:LEU:HA	1:AO:191:LEU:HD12	1.88	0.55
1:CB:214:VAL:HG11	1:CL:240:ALA:HB2	1.88	0.55
4:FS:107:ASP:HB3	4:FS:116:THR:HB	1.87	0.55
1:BG:152:LEU:HD21	2:EC:105:SER:HA	1.88	0.55
1:BS:158:LEU:HB3	1:BS:260:LEU:HD21	1.89	0.55
1:CG:21:LYS:NZ	1:CH:195:ASP:OD2	2.37	0.55
1:CI:165:ILE:HD13	1:CI:191:LEU:HD23	1.87	0.55
1:CL:16:ILE:HD12	1:CL:116:ALA:HB1	1.88	0.55
1:AX:152:LEU:HD21	2:DU:105:SER:HA	1.88	0.55
1:AY:188:LEU:HA	1:AY:191:LEU:HD12	1.88	0.55
1:BK:240:ALA:HB2	1:BO:214:VAL:HG11	1.88	0.55
1:BU:164:GLN:HE22	1:BU:308:ARG:HA	1.71	0.55
1:CK:140:SER:HB2	1:CK:148:GLN:HG2	1.88	0.55
1:CP:16:ILE:HD12	1:CP:116:ALA:HB1	1.88	0.55
1:DA:135:LEU:HD21	1:DA:255:LEU:HG	1.89	0.55
2:FG:165:LYS:HE3	2:FG:168:GLU:HA	1.89	0.55
1:AC:239:LYS:HA	1:AC:242:ASN:OD1	2.06	0.55
1:AY:162:PRO:HG2	2:DU:31:LEU:HD11	1.89	0.55
1:CQ:13:VAL:HG11	1:CQ:281:PRO:HG2	1.89	0.55
1:CQ:239:LYS:HA	1:CQ:242:ASN:OD1	2.07	0.55
1:CS:240:ALA:HB2	1:CZ:214:VAL:HG11	1.89	0.55
1:DB:239:LYS:HA	1:DB:242:ASN:OD1	2.07	0.55
2:EN:23:LYS:N	2:EN:67:TYR:OH	2.40	0.55
2:ES:165:LYS:HE3	2:ES:168:GLU:HA	1.89	0.55
2:FA:165:LYS:HE3	2:FA:168:GLU:HA	1.89	0.55
4:FL:77:ILE:HG12	4:FL:91:PRO:HB3	1.88	0.55
4:GB:161:ILE:HA	4:GB:186:ASN:HA	1.88	0.55
1:AO:152:LEU:HD21	2:DP:105:SER:HA	1.89	0.55
1:AQ:152:LEU:HD21	4:FO:112:SER:HA	1.89	0.55
1:AT:239:LYS:HA	1:AT:242:ASN:OD1	2.07	0.55
1:AX:201:MET:HG2	1:AX:242:ASN:HD22	1.72	0.55
1:AZ:286:ASP:HB2	1:AZ:294:HIS:HB2	1.88	0.55
1:BB:284:GLN:NE2	1:BB:286:ASP:OD1	2.38	0.55
1:BH:152:LEU:HD21	4:FV:112:SER:HA	1.89	0.55
1:BR:239:LYS:NZ	1:BR:245:GLU:O	2.40	0.55
1:BY:286:ASP:HB2	1:BY:294:HIS:HB2	1.90	0.55
1:CL:135:LEU:HD21	1:CL:255:LEU:HG	1.89	0.55
2:EG:124:LYS:HE2	2:EG:126:ASP:HB2	1.88	0.55
1:AH:77:VAL:HG11	1:AH:305:LEU:HD13	1.89	0.54
1:AT:169:VAL:HG22	1:AT:183:LYS:HG3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CK:152:LEU:HD21	2:FA:105:SER:HA	1.89	0.54
2:DY:148:VAL:HG21	2:DY:155:VAL:HG12	1.88	0.54
2:FI:63:PRO:HB2	2:FI:85:GLU:HG2	1.89	0.54
1:AA:152:LEU:HD21	2:DG:105:SER:HA	1.89	0.54
1:AV:239:LYS:HA	1:AV:242:ASN:OD1	2.07	0.54
1:BB:13:VAL:HG11	1:BB:281:PRO:HG2	1.88	0.54
1:CG:13:VAL:HG11	1:CG:281:PRO:HG3	1.89	0.54
1:DA:308:ARG:O	2:FB:34:ASN:ND2	2.36	0.54
1:DD:239:LYS:HA	1:DD:242:ASN:OD1	2.07	0.54
2:EO:137:LEU:HD11	2:EO:159:ALA:HB2	1.89	0.54
2:EP:123:LEU:HD21	2:EP:131:VAL:HG21	1.89	0.54
4:FY:77:ILE:HG13	4:FY:91:PRO:HB3	1.88	0.54
1:AL:49:TRP:CZ3	1:AL:74:SER:HB3	2.43	0.54
1:AW:13:VAL:HG11	1:AW:281:PRO:HG2	1.88	0.54
1:CB:13:VAL:HG11	1:CB:281:PRO:HG2	1.89	0.54
1:CC:143:LYS:HA	2:EU:39:ARG:HE	1.73	0.54
1:CD:48:LYS:NZ	2:EZ:33:SER:O	2.40	0.54
1:CH:13:VAL:HG11	1:CH:281:PRO:HG2	1.90	0.54
1:CJ:174:LYS:O	1:CJ:212:LYS:NZ	2.39	0.54
1:CT:80:ASN:ND2	1:CT:153:PRO:O	2.41	0.54
2:EG:167:THR:HB	2:EG:170:LEU:HB3	1.89	0.54
2:FD:23:LYS:NZ	2:FD:100:ASP:OD1	2.39	0.54
4:FQ:69:TYR:HB2	4:FQ:108:ILE:HD12	1.89	0.54
4:FT:165:ALA:HA	4:FT:181:VAL:HG22	1.88	0.54
4:FW:93:VAL:HG21	4:FW:117:ILE:HD11	1.89	0.54
1:AK:152:LEU:HD21	2:DM:105:SER:HA	1.89	0.54
1:AQ:13:VAL:HG11	1:AQ:281:PRO:HG2	1.89	0.54
1:BT:174:LYS:O	1:BT:212:LYS:NZ	2.39	0.54
1:BU:165:ILE:HD13	1:BU:191:LEU:HD23	1.89	0.54
1:DE:152:LEU:HD21	2:DY:105:SER:HA	1.90	0.54
2:DH:23:LYS:N	2:DH:67:TYR:OH	2.40	0.54
2:EC:69:TYR:HB2	2:EC:101:ILE:HD12	1.88	0.54
2:EZ:75:LEU:HD22	2:EZ:84:LEU:HD13	1.89	0.54
4:FO:23:LYS:N	4:FO:67:TYR:OH	2.39	0.54
4:GF:69:TYR:HB2	4:GF:108:ILE:HD12	1.90	0.54
1:CL:110:ASN:OD1	1:CO:62:ASN:ND2	2.39	0.54
4:GC:69:TYR:HB2	4:GC:108:ILE:HD12	1.89	0.54
1:AJ:239:LYS:HA	1:AJ:242:ASN:OD1	2.08	0.54
1:AR:239:LYS:HA	1:AR:242:ASN:OD1	2.07	0.54
1:BM:239:LYS:HA	1:BM:242:ASN:OD1	2.08	0.54
1:CJ:161:MET:SD	2:ER:31:LEU:HD21	2.48	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CU:286:ASP:HB2	1:CU:294:HIS:HB2	1.88	0.54
1:CX:165:ILE:HD13	1:CX:191:LEU:HD23	1.89	0.54
1:DA:16:ILE:HD12	1:DA:116:ALA:HB1	1.89	0.54
2:DS:137:LEU:HD11	2:DS:159:ALA:HB2	1.90	0.54
2:FF:22:MET:HG3	2:FF:26:GLN:HE22	1.72	0.54
1:AA:239:LYS:HA	1:AA:242:ASN:OD1	2.08	0.54
1:BC:85:GLN:NE2	1:BC:298:ASP:OD1	2.40	0.54
1:BG:286:ASP:HB2	1:BG:294:HIS:HB2	1.89	0.54
1:BR:96:GLU:O	1:BR:100:THR:HB	2.08	0.54
1:CB:239:LYS:HA	1:CB:242:ASN:OD1	2.08	0.54
1:CP:308:ARG:O	2:EX:34:ASN:ND2	2.36	0.54
2:FA:69:TYR:HB2	2:FA:101:ILE:HD12	1.88	0.54
1:AZ:203:VAL:HG22	1:AZ:261:ILE:HG23	1.90	0.54
1:BP:239:LYS:HA	1:BP:242:ASN:OD1	2.07	0.54
1:BX:240:ALA:HB2	1:CO:214:VAL:HG11	1.90	0.54
2:EV:148:VAL:HG21	2:EV:155:VAL:HG12	1.89	0.54
1:BI:13:VAL:HG11	1:BI:281:PRO:HG2	1.90	0.54
1:CF:164:GLN:HE22	1:CF:308:ARG:HA	1.73	0.54
1:CV:239:LYS:HA	1:CV:242:ASN:OD1	2.08	0.54
1:DB:317:LYS:NZ	1:DB:319:SER:OXT	2.41	0.54
2:DZ:69:TYR:HB2	2:DZ:101:ILE:HD12	1.88	0.54
1:AB:13:VAL:HG11	1:AB:281:PRO:HG2	1.89	0.54
1:CK:308:ARG:HH21	2:EQ:31:LEU:HB2	1.73	0.54
1:CZ:270:LYS:HG2	1:CZ:272:LYS:HE3	1.90	0.54
1:DD:13:VAL:HG11	1:DD:281:PRO:HG2	1.90	0.54
2:EA:123:LEU:HD21	2:EA:131:VAL:HG21	1.89	0.54
1:AU:143:LYS:HA	2:DT:39:ARG:HE	1.73	0.53
1:BS:239:LYS:HA	1:BS:242:ASN:OD1	2.08	0.53
1:BT:165:ILE:HD13	1:BT:191:LEU:HD23	1.90	0.53
1:DE:16:ILE:HD12	1:DE:116:ALA:HB1	1.90	0.53
2:EW:69:TYR:HB2	2:EW:101:ILE:HD12	1.90	0.53
2:FD:180:ASN:O	2:FE:180:ASN:ND2	2.37	0.53
1:AE:239:LYS:HA	1:AE:242:ASN:OD1	2.08	0.53
1:BU:8:TYR:CD2	1:BU:93:GLN:HG3	2.43	0.53
1:CG:210:SER:O	1:CG:214:VAL:HG13	2.08	0.53
1:CT:140:SER:HB2	1:CT:148:GLN:HG2	1.90	0.53
1:CW:194:GLY:HA3	2:FE:36:ILE:HG21	1.90	0.53
2:FB:181:ARG:HH12	2:FC:94:LEU:HB3	1.72	0.53
4:GD:23:LYS:N	4:GD:67:TYR:OH	2.41	0.53
1:AG:80:ASN:ND2	1:AG:153:PRO:O	2.41	0.53
1:AG:239:LYS:HA	1:AG:242:ASN:OD1	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AI:239:LYS:HA	1:AI:242:ASN:OD1	2.08	0.53
1:AX:20:VAL:O	5:HH:213:ARG:NH2	2.41	0.53
1:BM:49:TRP:CZ3	1:BM:74:SER:HB3	2.44	0.53
1:BW:152:LEU:HD21	2:EO:105:SER:HA	1.90	0.53
1:CM:239:LYS:HA	1:CM:242:ASN:OD1	2.08	0.53
1:CM:317:LYS:NZ	1:CM:319:SER:OXT	2.42	0.53
1:CO:239:LYS:HA	1:CO:242:ASN:OD1	2.08	0.53
4:GH:161:ILE:HA	4:GH:186:ASN:HA	1.90	0.53
1:AI:13:VAL:HG11	1:AI:281:PRO:HG2	1.91	0.53
1:AI:159:LEU:HD12	1:AI:260:LEU:HD21	1.89	0.53
1:AK:239:LYS:HA	1:AK:242:ASN:OD1	2.09	0.53
1:AO:13:VAL:HG11	1:AO:281:PRO:HG2	1.90	0.53
1:AZ:181:PHE:HD1	1:AZ:184:ILE:HD12	1.74	0.53
1:BL:307:THR:HG22	2:EN:32:LEU:HB2	1.90	0.53
1:CE:13:VAL:HG11	1:CE:281:PRO:HG2	1.90	0.53
1:CF:110:ASN:OD1	1:CH:62:ASN:ND2	2.40	0.53
1:CU:152:LEU:HD21	2:FD:105:SER:HA	1.91	0.53
4:GB:141:LEU:HD11	4:GB:165:ALA:HB2	1.90	0.53
4:GH:77:ILE:HG13	4:GH:91:PRO:HB3	1.89	0.53
5:HF:200:THR:O	5:HF:204:GLN:HG2	2.08	0.53
1:AL:239:LYS:HA	1:AL:242:ASN:OD1	2.08	0.53
1:BE:80:ASN:ND2	1:BE:153:PRO:O	2.42	0.53
1:BS:13:VAL:HG11	1:BS:281:PRO:HG2	1.91	0.53
1:CG:80:ASN:ND2	1:CG:153:PRO:O	2.35	0.53
1:CI:89:ARG:HH21	1:CI:112:LEU:HD21	1.74	0.53
1:CL:196:GLU:HB3	1:CL:265:ASN:HD22	1.72	0.53
2:FE:69:TYR:HB2	2:FE:101:ILE:HD12	1.89	0.53
4:FS:161:ILE:HA	4:FS:186:ASN:HA	1.89	0.53
1:AB:143:LYS:HA	2:DH:39:ARG:HE	1.74	0.53
1:AQ:257:HIS:CE1	1:AQ:318:GLN:HG3	2.44	0.53
1:BD:286:ASP:HB2	1:BD:294:HIS:HB2	1.90	0.53
1:BF:13:VAL:HG11	1:BF:281:PRO:HG2	1.91	0.53
1:CE:140:SER:HB2	1:CE:148:GLN:HG2	1.91	0.53
1:CN:210:SER:O	1:CN:214:VAL:HG13	2.09	0.53
2:DH:137:LEU:HD11	2:DH:159:ALA:HB2	1.91	0.53
2:ES:75:LEU:HD22	2:ES:84:LEU:HD13	1.91	0.53
2:FC:76:SER:HB3	2:FC:87:GLU:HG2	1.91	0.53
4:FO:93:VAL:HG21	4:FO:117:ILE:HD11	1.89	0.53
1:AF:77:VAL:HG21	2:DH:32:LEU:HD23	1.91	0.53
1:AI:169:VAL:HG22	1:AI:183:LYS:HG3	1.91	0.53
1:AY:169:VAL:HG22	1:AY:183:LYS:HG3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:164:GLN:HE22	1:BA:308:ARG:HA	1.73	0.53
1:BN:239:LYS:HA	1:BN:242:ASN:OD1	2.08	0.53
1:BR:239:LYS:HA	1:BR:242:ASN:OD1	2.09	0.53
1:BU:143:LYS:HA	2:EM:39:ARG:HE	1.73	0.53
1:BU:152:LEU:HD21	2:EK:105:SER:HA	1.91	0.53
1:CK:158:LEU:HB3	1:CK:260:LEU:HD21	1.91	0.53
1:CV:210:SER:O	1:CV:214:VAL:HG13	2.07	0.53
2:ES:69:TYR:HB2	2:ES:101:ILE:HD12	1.90	0.53
2:FD:123:LEU:HD21	2:FD:131:VAL:HG21	1.90	0.53
1:AU:13:VAL:HG11	1:AU:281:PRO:HG2	1.90	0.53
1:BF:214:VAL:HG11	1:BQ:240:ALA:HB2	1.91	0.53
1:BI:143:LYS:HA	2:EC:39:ARG:HE	1.74	0.53
1:CE:307:THR:HG22	2:EY:32:LEU:HB2	1.91	0.53
1:CH:239:LYS:HA	1:CH:242:ASN:OD1	2.08	0.53
1:CS:239:LYS:HA	1:CS:242:ASN:OD1	2.09	0.53
2:EL:56:LYS:NZ	2:EM:55:SER:O	2.41	0.53
1:AN:43:TYR:HE2	1:AN:45:LYS:HE3	1.73	0.53
1:AX:57:PRO:HB2	1:DD:84:LEU:HB3	1.91	0.53
1:AX:57:PRO:HG2	1:DD:84:LEU:HD13	1.90	0.53
1:BV:13:VAL:HG11	1:BV:281:PRO:HG2	1.90	0.53
1:BY:13:VAL:HG11	1:BY:281:PRO:HG2	1.91	0.53
1:CD:174:LYS:O	1:CD:212:LYS:NZ	2.41	0.53
2:DH:74:LYS:HE2	2:DH:89:GLY:HA3	1.91	0.53
2:DW:77:PHE:HD2	4:FR:138:LYS:HG3	1.74	0.53
2:DW:181:ARG:HH12	2:DX:94:LEU:HB3	1.74	0.53
1:AD:49:TRP:CZ3	1:AD:74:SER:HB3	2.44	0.53
1:BK:13:VAL:HG11	1:BK:281:PRO:HG2	1.91	0.53
1:BT:66:THR:HG22	4:FX:52:ARG:HB3	1.90	0.53
1:CN:39:LEU:O	1:CN:274:SER:OG	2.20	0.53
1:DC:210:SER:O	1:DC:214:VAL:HG13	2.09	0.53
2:FD:148:VAL:HG21	2:FD:155:VAL:HG12	1.91	0.53
5:JO:189:LEU:HD11	5:JO:206:ILE:HG12	1.91	0.53
1:AE:240:ALA:HB2	1:AI:214:VAL:HG11	1.91	0.52
1:AO:239:LYS:HA	1:AO:242:ASN:OD1	2.08	0.52
1:BM:80:ASN:ND2	1:BM:153:PRO:O	2.42	0.52
1:BQ:257:HIS:CE1	1:BQ:318:GLN:HG3	2.44	0.52
1:CG:14:ALA:HB2	5:IQ:202:PHE:HE1	1.75	0.52
1:CG:239:LYS:HA	1:CG:242:ASN:OD1	2.09	0.52
1:DA:196:GLU:HB3	1:DA:265:ASN:HD22	1.74	0.52
1:DD:152:LEU:HD21	2:DX:105:SER:HA	1.91	0.52
1:DE:89:ARG:HH21	1:DE:112:LEU:HD21	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:DO:153:LYS:HA	2:DO:181:ARG:HH21	1.75	0.52
2:DT:181:ARG:NH1	2:DT:182:ALA:O	2.42	0.52
1:AH:239:LYS:HA	1:AH:242:ASN:OD1	2.08	0.52
1:BF:107:ASP:OD2	1:BF:110:ASN:ND2	2.37	0.52
1:BR:174:LYS:O	1:BR:212:LYS:NZ	2.40	0.52
1:CA:158:LEU:HB3	1:CA:260:LEU:HD21	1.90	0.52
1:CS:77:VAL:HG21	2:FH:32:LEU:HD23	1.92	0.52
1:CW:79:LEU:HD11	1:CW:305:LEU:HB2	1.90	0.52
1:DE:257:HIS:CE1	1:DE:318:GLN:HG3	2.45	0.52
1:AX:87:LYS:NZ	4:FQ:53:THR:O	2.37	0.52
1:AX:92:LYS:HZ2	1:AX:94:THR:HG1	1.51	0.52
1:BK:55:ALA:HB2	2:EH:51:VAL:HB	1.91	0.52
1:BP:77:VAL:HG11	1:BP:305:LEU:HD13	1.91	0.52
1:BQ:261:ILE:HD12	1:BQ:312:LEU:HD23	1.91	0.52
1:BV:158:LEU:HB3	1:BV:260:LEU:HD21	1.91	0.52
1:CK:257:HIS:CE1	1:CK:318:GLN:HG3	2.44	0.52
1:CQ:214:VAL:HG11	1:DA:240:ALA:HB2	1.91	0.52
1:CR:239:LYS:HA	1:CR:242:ASN:OD1	2.09	0.52
1:CT:196:GLU:OE1	1:CT:265:ASN:ND2	2.42	0.52
1:CT:257:HIS:CE1	1:CT:318:GLN:HG3	2.44	0.52
1:CT:308:ARG:HH21	2:FG:31:LEU:HB2	1.73	0.52
1:CX:210:SER:O	1:CX:214:VAL:HG13	2.09	0.52
2:DL:63:PRO:HB2	2:DL:85:GLU:HG2	1.92	0.52
4:GJ:69:TYR:HB2	4:GJ:108:ILE:HD12	1.89	0.52
1:AN:239:LYS:HA	1:AN:242:ASN:OD1	2.09	0.52
1:AY:13:VAL:HG11	1:AY:281:PRO:HG2	1.91	0.52
1:AZ:59:THR:O	2:DW:61:ASN:ND2	2.43	0.52
1:BA:16:ILE:HD11	1:BA:120:LYS:HE3	1.92	0.52
1:BF:49:TRP:CZ3	1:BF:74:SER:HB3	2.44	0.52
1:BK:16:ILE:HD11	1:BK:120:LYS:HE3	1.92	0.52
1:BL:49:TRP:CZ3	1:BL:74:SER:HB3	2.44	0.52
1:CF:16:ILE:HD12	1:CF:116:ALA:HB1	1.92	0.52
1:CL:49:TRP:CZ3	1:CL:74:SER:HB3	2.45	0.52
1:CQ:79:LEU:HD11	1:CQ:305:LEU:HB2	1.92	0.52
1:CR:210:SER:O	1:CR:214:VAL:HG13	2.09	0.52
1:CT:239:LYS:HA	1:CT:242:ASN:OD1	2.10	0.52
1:CY:308:ARG:O	2:DY:34:ASN:ND2	2.40	0.52
2:DP:165:LYS:HE3	2:DP:168:GLU:HA	1.90	0.52
2:DV:137:LEU:HD11	2:DV:159:ALA:HB2	1.92	0.52
4:GH:141:LEU:HD11	4:GH:165:ALA:HB2	1.91	0.52
5:HA:200:THR:O	5:HA:204:GLN:HG2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AP:239:LYS:HA	1:AP:242:ASN:OD1	2.10	0.52
1:BB:286:ASP:HB2	1:BB:294:HIS:HB2	1.90	0.52
1:BE:13:VAL:HG11	1:BE:281:PRO:HG2	1.92	0.52
1:BH:239:LYS:HA	1:BH:242:ASN:OD1	2.09	0.52
1:BL:165:ILE:HG13	1:BL:191:LEU:HD23	1.92	0.52
1:BM:13:VAL:HG21	1:BM:103:SER:HB2	1.91	0.52
1:BN:165:ILE:HD13	1:BN:191:LEU:HD23	1.91	0.52
1:CC:210:SER:O	1:CC:214:VAL:HG13	2.10	0.52
1:CI:210:SER:O	1:CI:214:VAL:HG13	2.09	0.52
1:CL:59:THR:O	2:EU:61:ASN:ND2	2.43	0.52
1:CL:169:VAL:HG22	1:CL:183:LYS:HG3	1.91	0.52
1:CP:49:TRP:CZ3	1:CP:74:SER:HB3	2.44	0.52
1:CU:257:HIS:CE1	1:CU:318:GLN:HG3	2.45	0.52
1:CZ:239:LYS:HA	1:CZ:242:ASN:OD1	2.09	0.52
2:EF:180:ASN:O	4:FW:186:ASN:ND2	2.42	0.52
2:EK:123:LEU:HD13	2:EK:173:VAL:HG11	1.92	0.52
4:FX:137:VAL:HG12	4:FX:138:LYS:HG3	1.91	0.52
4:GF:73:VAL:HG21	4:GF:117:ILE:HD13	1.92	0.52
1:AF:35:GLU:O	1:AF:272:LYS:HA	2.10	0.52
1:AH:158:LEU:HB3	1:AH:260:LEU:HD21	1.92	0.52
1:AL:307:THR:HG22	2:DV:32:LEU:HB2	1.91	0.52
1:AS:140:SER:HB2	1:AS:148:GLN:HG2	1.91	0.52
1:AX:161:MET:SD	2:DW:31:LEU:HD21	2.49	0.52
1:AY:84:LEU:HD13	1:AZ:57:PRO:HB2	1.90	0.52
1:BC:54:ASN:HA	2:EB:42:ASN:HD22	1.75	0.52
1:BE:286:ASP:HB2	1:BE:294:HIS:HB2	1.92	0.52
1:BM:11:LYS:HB2	1:BP:39:LEU:HD13	1.92	0.52
1:BO:49:TRP:CZ3	1:BO:74:SER:HB3	2.45	0.52
1:CK:164:GLN:HE22	1:CK:308:ARG:HA	1.75	0.52
1:CV:59:THR:O	2:FB:61:ASN:ND2	2.42	0.52
1:DB:14:ALA:HB2	5:JL:202:PHE:HE1	1.75	0.52
2:EK:140:ASN:OD1	2:EK:144:GLU:N	2.39	0.52
2:EX:181:ARG:HH12	2:EY:94:LEU:HB3	1.74	0.52
2:FE:165:LYS:HE3	2:FE:168:GLU:HA	1.91	0.52
4:FK:77:ILE:HG13	4:FK:91:PRO:HB3	1.91	0.52
4:FW:149:LEU:HD13	4:FW:181:VAL:HG21	1.91	0.52
4:GF:141:LEU:HD11	4:GF:165:ALA:HB2	1.90	0.52
1:AC:13:VAL:HG11	1:AC:281:PRO:HG2	1.91	0.52
1:AL:169:VAL:HG22	1:AL:183:LYS:HG3	1.89	0.52
1:BF:261:ILE:HD12	1:BF:312:LEU:HD23	1.91	0.52
1:BO:169:VAL:HG22	1:BO:183:LYS:HG3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BX:22:ASP:OD1	5:IH:213:ARG:NE	2.32	0.52
1:CN:239:LYS:HA	1:CN:242:ASN:OD1	2.09	0.52
1:CQ:91:LEU:HD21	1:CQ:112:LEU:HD13	1.90	0.52
1:CZ:257:HIS:CE1	1:CZ:318:GLN:HG3	2.45	0.52
1:DB:158:LEU:HB3	1:DB:260:LEU:HD21	1.90	0.52
4:FO:149:LEU:HD13	4:FO:181:VAL:HG21	1.92	0.52
4:FT:69:TYR:HB2	4:FT:108:ILE:HD12	1.92	0.52
1:AU:143:LYS:HG3	2:DT:39:ARG:HH21	1.74	0.52
1:AZ:25:MET:HE1	1:AZ:130:ILE:HG22	1.92	0.52
1:BE:65:ASN:ND2	2:ED:57:ASP:O	2.43	0.52
1:BG:239:LYS:HA	1:BG:242:ASN:OD1	2.09	0.52
1:BJ:49:TRP:CZ3	1:BJ:74:SER:HB3	2.45	0.52
1:BL:239:LYS:HA	1:BL:242:ASN:OD1	2.09	0.52
1:BW:184:ILE:HG12	1:BW:314:VAL:HG21	1.92	0.52
1:CD:239:LYS:HA	1:CD:242:ASN:OD1	2.10	0.52
2:DK:69:TYR:HB2	2:DK:101:ILE:HD12	1.92	0.52
2:EE:167:THR:HG22	2:EE:168:GLU:H	1.75	0.52
2:EJ:137:LEU:HD11	2:EJ:159:ALA:HB2	1.90	0.52
2:FH:136:LYS:HD3	2:FH:155:VAL:HG11	1.92	0.52
4:FM:93:VAL:HG21	4:FM:117:ILE:HD11	1.91	0.52
1:AA:165:ILE:HG13	1:AA:191:LEU:HD23	1.92	0.52
1:AP:109:ASN:O	4:FO:24:ASN:ND2	2.43	0.52
1:BM:48:LYS:HD2	4:FW:32:LEU:HD23	1.91	0.52
1:CT:13:VAL:HG11	1:CT:281:PRO:HG2	1.91	0.52
1:CY:77:VAL:HG21	2:DY:32:LEU:HD23	1.92	0.52
1:CY:152:LEU:HD21	2:FF:105:SER:HA	1.90	0.52
4:GD:161:ILE:HA	4:GD:186:ASN:HA	1.91	0.52
1:AD:13:VAL:HG11	1:AD:281:PRO:HG2	1.93	0.52
1:AQ:231:GLU:O	1:AQ:235:ILE:HG13	2.10	0.52
1:AV:164:GLN:HE22	1:AV:308:ARG:HA	1.75	0.52
1:AX:240:ALA:HB2	1:DD:214:VAL:HG11	1.92	0.52
1:AZ:152:LEU:HD21	4:FS:112:SER:HA	1.92	0.52
1:BK:256:LYS:HG2	1:BK:257:HIS:CD2	2.44	0.52
1:BX:57:PRO:HB2	1:CO:84:LEU:HB3	1.92	0.52
1:CE:239:LYS:HA	1:CE:242:ASN:OD1	2.10	0.52
1:CU:196:GLU:HB3	1:CU:265:ASN:HD22	1.75	0.52
1:CV:317:LYS:HZ3	1:CV:319:SER:HB2	1.75	0.52
2:DS:23:LYS:HG3	2:DS:24:ASN:H	1.75	0.52
2:EH:56:LYS:HD2	4:FX:56:PHE:HA	1.92	0.52
4:FT:149:LEU:HD13	4:FT:181:VAL:HG21	1.91	0.52
4:GD:10:GLU:O	4:GD:14:LYS:HG2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AF:84:LEU:HD13	1:AQ:57:PRO:HB2	1.92	0.51
1:AK:165:ILE:HD12	1:AK:191:LEU:HD23	1.91	0.51
1:AT:54:ASN:HB3	2:DP:51:VAL:HG12	1.93	0.51
1:BD:239:LYS:HA	1:BD:242:ASN:OD1	2.09	0.51
1:BV:239:LYS:HA	1:BV:242:ASN:OD1	2.10	0.51
1:BX:100:THR:HG22	1:BX:105:ILE:HG23	1.92	0.51
1:CH:158:LEU:HB3	1:CH:260:LEU:HD21	1.92	0.51
1:CJ:169:VAL:HG22	1:CJ:183:LYS:HG3	1.92	0.51
1:CL:239:LYS:HA	1:CL:242:ASN:OD1	2.09	0.51
1:CN:47:VAL:HG22	1:CN:76:VAL:HG22	1.92	0.51
4:FY:149:LEU:HD13	4:FY:181:VAL:HG21	1.91	0.51
4:GH:78:GLN:HE22	4:GH:89:TYR:HB2	1.75	0.51
1:AD:208:ALA:O	1:AD:212:LYS:HG3	2.11	0.51
1:AN:240:ALA:HB2	1:AR:214:VAL:HG11	1.92	0.51
1:AU:239:LYS:HA	1:AU:242:ASN:OD1	2.10	0.51
1:BE:59:THR:O	2:ED:61:ASN:ND2	2.43	0.51
1:BE:239:LYS:HA	1:BE:242:ASN:OD1	2.10	0.51
1:BL:143:LYS:HE3	2:EE:40:ASP:HB2	1.90	0.51
1:CD:161:MET:SD	2:EZ:31:LEU:HD21	2.51	0.51
1:CN:240:ALA:HB2	1:CP:214:VAL:HG11	1.91	0.51
1:CZ:81:TYR:OH	1:CZ:272:LYS:O	2.22	0.51
2:FI:75:LEU:HD22	2:FI:84:LEU:HD13	1.93	0.51
1:AA:39:LEU:O	1:AA:274:SER:OG	2.25	0.51
1:AB:231:GLU:O	1:AB:235:ILE:HG13	2.11	0.51
1:AR:96:GLU:O	1:AR:100:THR:HG23	2.10	0.51
1:BC:107:ASP:OD2	1:BC:110:ASN:ND2	2.36	0.51
1:BD:13:VAL:HG11	1:BD:281:PRO:HG2	1.92	0.51
1:BS:80:ASN:ND2	1:BS:153:PRO:O	2.42	0.51
1:BT:286:ASP:HB2	1:BT:294:HIS:HB2	1.91	0.51
1:CU:66:THR:OG1	2:EW:58:LYS:NZ	2.44	0.51
1:CV:80:ASN:ND2	1:CV:153:PRO:O	2.35	0.51
2:DG:69:TYR:HB2	2:DG:101:ILE:HD12	1.91	0.51
2:DQ:153:LYS:O	2:DQ:181:ARG:NE	2.39	0.51
4:GJ:10:GLU:O	4:GJ:14:LYS:HG2	2.10	0.51
1:AQ:169:VAL:HG22	1:AQ:183:LYS:HG3	1.93	0.51
1:AV:126:ILE:O	1:AV:130:ILE:HG13	2.11	0.51
1:BG:132:HIS:HA	1:BG:254:LEU:HD13	1.93	0.51
1:BW:239:LYS:HA	1:BW:242:ASN:OD1	2.11	0.51
1:CE:257:HIS:CE1	1:CE:318:GLN:HG3	2.46	0.51
1:CI:239:LYS:HA	1:CI:242:ASN:OD1	2.09	0.51
1:DC:239:LYS:HA	1:DC:242:ASN:OD1	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:DU:165:LYS:HE3	2:DU:168:GLU:HA	1.92	0.51
4:FK:137:VAL:HG12	4:FK:138:LYS:HG3	1.91	0.51
4:FR:142:ILE:HD11	4:FR:152:VAL:HG23	1.92	0.51
4:FS:10:GLU:O	4:FS:14:LYS:HG2	2.10	0.51
5:HC:202:PHE:O	5:HC:206:ILE:HG13	2.11	0.51
1:AM:239:LYS:HA	1:AM:242:ASN:OD1	2.09	0.51
1:AS:8:TYR:CD2	1:AS:93:GLN:HG3	2.45	0.51
1:AS:16:ILE:HD12	1:AS:116:ALA:HB1	1.93	0.51
1:AS:194:GLY:HA3	2:DZ:36:ILE:HG21	1.92	0.51
1:AV:152:LEU:HD21	2:DV:105:SER:HA	1.91	0.51
1:AY:239:LYS:HA	1:AY:242:ASN:OD1	2.11	0.51
1:AZ:239:LYS:HA	1:AZ:242:ASN:OD1	2.10	0.51
1:BB:167:GLU:HB2	1:BB:314:VAL:HG22	1.91	0.51
1:BQ:165:ILE:HG13	1:BQ:191:LEU:HD23	1.91	0.51
1:CC:239:LYS:HA	1:CC:242:ASN:OD1	2.10	0.51
1:CG:49:TRP:CZ3	1:CG:74:SER:HB3	2.45	0.51
1:CK:239:LYS:HA	1:CK:242:ASN:OD1	2.10	0.51
1:CO:203:VAL:HG22	1:CO:261:ILE:HG23	1.92	0.51
2:DP:69:TYR:HB2	2:DP:101:ILE:HD12	1.92	0.51
2:EB:137:LEU:HD11	2:EB:159:ALA:HB2	1.93	0.51
2:EI:158:ILE:HG13	2:EI:178:PHE:HE2	1.74	0.51
4:GA:161:ILE:HA	4:GA:186:ASN:HA	1.92	0.51
4:GF:23:LYS:N	4:GF:67:TYR:OH	2.42	0.51
4:GI:141:LEU:HD11	4:GI:165:ALA:HB2	1.91	0.51
1:AJ:152:LEU:HD21	4:FM:112:SER:HA	1.92	0.51
1:AM:152:LEU:HD11	2:DO:105:SER:HA	1.92	0.51
1:AP:132:HIS:HA	1:AP:254:LEU:HD13	1.92	0.51
1:AU:8:TYR:CD2	1:AU:93:GLN:HG3	2.45	0.51
1:AV:13:VAL:HG11	1:AV:281:PRO:HG2	1.92	0.51
1:BF:169:VAL:HG22	1:BF:183:LYS:HG3	1.93	0.51
1:BJ:239:LYS:HA	1:BJ:242:ASN:OD1	2.10	0.51
1:BQ:158:LEU:HB3	1:BQ:260:LEU:HD21	1.93	0.51
1:CT:286:ASP:HB2	1:CT:294:HIS:HB2	1.92	0.51
1:CW:214:VAL:HG11	1:DE:240:ALA:HB2	1.93	0.51
1:CX:239:LYS:HA	1:CX:242:ASN:OD1	2.10	0.51
1:CZ:174:LYS:O	1:CZ:212:LYS:NZ	2.42	0.51
1:DA:239:LYS:HA	1:DA:242:ASN:OD1	2.09	0.51
1:DD:158:LEU:HB3	1:DD:260:LEU:HD21	1.93	0.51
2:DT:181:ARG:HG2	2:DT:182:ALA:H	1.76	0.51
2:EN:181:ARG:NH1	2:EN:182:ALA:O	2.44	0.51
3:FJ:102:THR:HG21	4:FU:56:PHE:HA	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:FW:73:VAL:HG21	4:FW:117:ILE:HD13	1.91	0.51
1:AM:49:TRP:CZ3	1:AM:74:SER:HB3	2.46	0.51
1:BC:13:VAL:HG11	1:BC:281:PRO:HG2	1.91	0.51
1:BD:240:ALA:HB2	1:BP:214:VAL:HG11	1.93	0.51
1:BF:286:ASP:HB2	1:BF:294:HIS:HB2	1.93	0.51
1:BJ:152:LEU:HD21	2:EE:105:SER:HA	1.91	0.51
1:BX:20:VAL:O	5:IH:213:ARG:NH2	2.44	0.51
1:CP:164:GLN:HE22	1:CP:308:ARG:HA	1.76	0.51
1:CS:135:LEU:HD21	1:CS:255:LEU:HG	1.93	0.51
1:DA:158:LEU:HB3	1:DA:260:LEU:HD21	1.93	0.51
2:EE:22:MET:HB2	2:EE:25:PRO:HG3	1.93	0.51
2:ET:59:ILE:HG22	2:ET:111:ILE:HG12	1.92	0.51
2:EU:76:SER:HB3	2:EU:87:GLU:HG2	1.92	0.51
2:EW:75:LEU:HD22	2:EW:84:LEU:HD13	1.92	0.51
2:FE:75:LEU:HD22	2:FE:84:LEU:HD13	1.93	0.51
4:GA:142:ILE:HD11	4:GA:152:VAL:HG23	1.93	0.51
1:AC:41:MET:HE2	1:AC:83:LYS:H	1.74	0.51
1:AH:66:THR:HG22	4:FM:52:ARG:HB3	1.92	0.51
1:AJ:214:VAL:HG11	1:AM:240:ALA:HB2	1.92	0.51
1:AO:49:TRP:CZ3	1:AO:74:SER:HB3	2.46	0.51
1:BA:8:TYR:CD2	1:BA:93:GLN:HG3	2.46	0.51
1:BI:48:LYS:HE2	1:BI:75:GLU:HB2	1.93	0.51
1:BV:66:THR:HG22	2:EF:52:CYS:HB3	1.92	0.51
1:BW:181:PHE:HD1	1:BW:184:ILE:HD12	1.74	0.51
1:CE:196:GLU:OE1	1:CE:265:ASN:ND2	2.43	0.51
1:CF:257:HIS:CE1	1:CF:318:GLN:HG3	2.45	0.51
1:CM:158:LEU:HB3	1:CM:260:LEU:HD21	1.92	0.51
1:CP:239:LYS:HA	1:CP:242:ASN:OD1	2.09	0.51
1:CV:49:TRP:CZ3	1:CV:74:SER:HB3	2.46	0.51
2:DJ:137:LEU:HD11	2:DJ:159:ALA:HB2	1.92	0.51
4:FL:149:LEU:HD13	4:FL:181:VAL:HG21	1.92	0.51
5:HC:200:THR:O	5:HC:204:GLN:HG2	2.11	0.51
1:AE:158:LEU:HB3	1:AE:260:LEU:HD21	1.93	0.51
1:AF:239:LYS:NZ	1:AF:245:GLU:O	2.42	0.51
1:AR:196:GLU:HB3	1:AR:265:ASN:HD22	1.76	0.51
1:BY:29:PHE:O	5:II:223:ARG:NH2	2.43	0.51
1:CN:143:LYS:HA	2:EQ:39:ARG:HE	1.76	0.51
1:CQ:196:GLU:HB3	1:CQ:265:ASN:HD22	1.76	0.51
1:CW:239:LYS:HA	1:CW:242:ASN:OD1	2.11	0.51
2:EB:180:ASN:O	3:FJ:242:ASN:ND2	2.44	0.51
4:GB:10:GLU:O	4:GB:14:LYS:HG2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:GD:149:LEU:HD13	4:GD:181:VAL:HG21	1.93	0.51
4:GG:161:ILE:HA	4:GG:186:ASN:HA	1.93	0.51
1:AF:239:LYS:HA	1:AF:242:ASN:OD1	2.10	0.51
1:AP:16:ILE:HD12	1:AP:116:ALA:HB1	1.92	0.51
1:BF:205:VAL:HG12	1:BF:259:ILE:HG23	1.93	0.51
1:BF:239:LYS:HA	1:BF:242:ASN:OD1	2.10	0.51
1:BL:169:VAL:HG22	1:BL:183:LYS:HG3	1.92	0.51
1:BS:203:VAL:HG22	1:BS:261:ILE:HG23	1.92	0.51
1:CH:214:VAL:HG11	1:CP:240:ALA:HB2	1.92	0.51
1:DC:194:GLY:HA3	4:FS:36:ASN:OD1	2.10	0.51
1:DE:135:LEU:HD21	1:DE:255:LEU:HG	1.91	0.51
2:DX:75:LEU:HD22	2:DX:84:LEU:HD13	1.93	0.51
2:EH:69:TYR:HB2	2:EH:101:ILE:HD12	1.92	0.51
4:FS:141:LEU:HD11	4:FS:165:ALA:HB2	1.93	0.51
1:AU:203:VAL:HG22	1:AU:261:ILE:HG23	1.93	0.50
1:AY:152:LEU:HD21	2:DW:105:SER:HA	1.93	0.50
1:BB:81:TYR:OH	1:BB:272:LYS:O	2.22	0.50
1:BD:163:GLU:HB2	2:EI:31:LEU:HD22	1.92	0.50
1:BG:214:VAL:HG11	1:BJ:240:ALA:HB2	1.94	0.50
1:BI:152:LEU:HD21	2:ED:105:SER:HA	1.93	0.50
1:BJ:84:LEU:HB3	1:BM:57:PRO:HB2	1.93	0.50
1:CA:286:ASP:HB2	1:CA:294:HIS:HB2	1.93	0.50
1:CH:196:GLU:HB3	1:CH:265:ASN:HD22	1.76	0.50
1:CY:169:VAL:HG22	1:CY:183:LYS:HG3	1.92	0.50
2:EI:69:TYR:HB2	2:EI:101:ILE:HD12	1.92	0.50
2:EO:75:LEU:HD22	2:EO:84:LEU:HD13	1.92	0.50
4:FX:140:LYS:HD3	4:FX:161:ILE:HD13	1.93	0.50
1:AC:50:ASP:OD1	1:AC:51:ALA:N	2.44	0.50
1:AI:180:ILE:O	1:AI:184:ILE:HG13	2.11	0.50
1:AJ:80:ASN:ND2	1:AJ:153:PRO:O	2.44	0.50
1:AL:133:PHE:CD2	1:AL:301:LEU:HD22	2.47	0.50
1:AM:286:ASP:HB2	1:AM:294:HIS:HB2	1.92	0.50
1:AO:135:LEU:HD21	1:AO:255:LEU:HG	1.93	0.50
1:CC:52:PHE:HB3	4:GD:41:LYS:HE2	1.94	0.50
1:CG:16:ILE:HD12	1:CG:116:ALA:HB1	1.93	0.50
1:CG:84:LEU:HD13	1:CH:57:PRO:HB2	1.93	0.50
1:DE:239:LYS:HA	1:DE:242:ASN:OD1	2.10	0.50
2:DM:167:THR:HG22	2:DM:168:GLU:H	1.76	0.50
2:EP:23:LYS:N	2:EP:67:TYR:OH	2.44	0.50
4:FQ:43:VAL:HG22	4:FQ:172:ILE:HD11	1.93	0.50
1:AO:194:GLY:HA3	4:FP:36:ASN:ND2	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AV:87:LYS:NZ	2:DU:53:THR:O	2.38	0.50
1:AW:181:PHE:HD1	1:AW:184:ILE:HD12	1.75	0.50
1:BA:239:LYS:HA	1:BA:242:ASN:OD1	2.11	0.50
1:BC:49:TRP:CZ3	1:BC:74:SER:HB3	2.46	0.50
1:BI:239:LYS:HA	1:BI:242:ASN:OD1	2.10	0.50
1:BM:85:GLN:HE22	1:BO:289:SER:HB2	1.76	0.50
1:BR:152:LEU:HD11	4:FY:112:SER:HA	1.93	0.50
1:BS:196:GLU:HB3	1:BS:265:ASN:HD22	1.76	0.50
1:BV:205:VAL:HG12	1:BV:259:ILE:HG23	1.91	0.50
1:BY:79:LEU:HD11	1:BY:305:LEU:HB2	1.92	0.50
1:BZ:80:ASN:ND2	1:BZ:153:PRO:O	2.33	0.50
1:CA:239:LYS:HA	1:CA:242:ASN:OD1	2.11	0.50
1:CD:240:ALA:HB2	1:CK:214:VAL:HG11	1.93	0.50
1:CO:79:LEU:HD11	1:CO:305:LEU:HB2	1.93	0.50
1:CO:194:GLY:HA3	2:FA:36:ILE:HG21	1.92	0.50
1:CR:52:PHE:HB3	4:GH:41:LYS:HE2	1.93	0.50
1:CS:92:LYS:NZ	1:CS:94:THR:OG1	2.36	0.50
1:CU:164:GLN:HE22	1:CU:308:ARG:HA	1.77	0.50
1:CW:158:LEU:HB3	1:CW:260:LEU:HD21	1.91	0.50
1:CX:286:ASP:HB2	1:CX:294:HIS:HB2	1.93	0.50
1:CZ:286:ASP:HB2	1:CZ:294:HIS:HB2	1.94	0.50
2:DG:165:LYS:HE3	2:DG:168:GLU:HA	1.92	0.50
2:DT:75:LEU:HD22	2:DT:84:LEU:HD21	1.93	0.50
4:FP:165:ALA:HA	4:FP:181:VAL:HG12	1.94	0.50
1:AP:305:LEU:HD11	4:FN:32:LEU:HG	1.92	0.50
1:BX:169:VAL:HG22	1:BX:183:LYS:HG3	1.94	0.50
1:BZ:13:VAL:HG11	1:BZ:281:PRO:HG2	1.93	0.50
1:CA:174:LYS:O	1:CA:212:LYS:NZ	2.45	0.50
1:CO:161:MET:SD	2:FA:31:LEU:HD21	2.51	0.50
1:CU:161:MET:SD	2:EV:31:LEU:HD21	2.51	0.50
1:AD:240:ALA:HB2	1:AP:214:VAL:HG11	1.93	0.50
1:AM:54:ASN:HA	2:DM:42:ASN:HD22	1.75	0.50
1:AZ:210:SER:O	1:AZ:214:VAL:HG13	2.11	0.50
1:BQ:239:LYS:HA	1:BQ:242:ASN:OD1	2.11	0.50
1:BS:165:ILE:HD13	1:BS:191:LEU:HD23	1.94	0.50
1:BZ:174:LYS:O	1:BZ:212:LYS:NZ	2.45	0.50
1:CE:152:LEU:HD21	2:EW:105:SER:HA	1.94	0.50
1:CP:257:HIS:CE1	1:CP:318:GLN:HG3	2.46	0.50
1:CT:66:THR:HG22	2:FG:52:CYS:HB3	1.92	0.50
1:CT:174:LYS:O	1:CT:212:LYS:NZ	2.44	0.50
1:CU:239:LYS:HA	1:CU:242:ASN:OD1	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CY:135:LEU:HD21	1:CY:255:LEU:HG	1.93	0.50
2:EY:76:SER:HB3	2:EY:87:GLU:HG2	1.94	0.50
2:FB:56:LYS:HD2	2:FC:56:LYS:HA	1.93	0.50
1:AO:66:THR:HG22	4:FP:52:ARG:HD2	1.93	0.50
1:BB:165:ILE:HD13	1:BB:191:LEU:HD23	1.94	0.50
1:BE:240:ALA:HB2	1:BI:214:VAL:HG11	1.91	0.50
1:CJ:13:VAL:HG11	1:CJ:281:PRO:HG2	1.94	0.50
1:CV:14:ALA:HB2	5:JF:202:PHE:HE1	1.76	0.50
2:EM:167:THR:HG22	2:EM:168:GLU:H	1.76	0.50
2:EN:76:SER:HB3	2:EN:87:GLU:HG2	1.92	0.50
4:GI:25:PRO:HB2	4:GI:27:HIS:CD2	2.46	0.50
1:AG:66:THR:HG22	2:DI:52:CYS:SG	2.51	0.50
1:AJ:286:ASP:HB2	1:AJ:294:HIS:HB2	1.94	0.50
1:AO:35:GLU:O	1:AO:272:LYS:HA	2.12	0.50
1:BS:77:VAL:HG21	2:ES:32:LEU:HD23	1.94	0.50
1:BU:16:ILE:HD11	1:BU:120:LYS:HE3	1.93	0.50
1:BU:86:TYR:HE1	1:CA:57:PRO:HA	1.76	0.50
1:BU:96:GLU:O	1:BU:100:THR:HG23	2.12	0.50
1:CA:49:TRP:CZ3	1:CA:74:SER:HB3	2.47	0.50
1:CJ:135:LEU:HD21	1:CJ:255:LEU:HG	1.94	0.50
1:CK:307:THR:HG22	2:EQ:32:LEU:HB2	1.93	0.50
2:DN:75:LEU:HD22	2:DN:84:LEU:HD13	1.94	0.50
2:DZ:165:LYS:HE3	2:DZ:168:GLU:HA	1.93	0.50
2:EP:59:ILE:HG22	2:EP:111:ILE:HG12	1.93	0.50
2:FH:75:LEU:HD22	2:FH:84:LEU:HD13	1.93	0.50
4:FR:161:ILE:HA	4:FR:186:ASN:HA	1.93	0.50
5:GM:200:THR:O	5:GM:204:GLN:HG2	2.11	0.50
1:AD:181:PHE:O	1:AD:185:GLU:HG3	2.11	0.50
1:AF:150:ARG:HH12	4:FK:92:HIS:CD2	2.29	0.50
1:AF:211:LEU:HD21	1:AQ:241:ILE:HG22	1.94	0.50
1:AX:100:THR:HG22	1:AX:105:ILE:HG23	1.93	0.50
1:CB:196:GLU:HB3	1:CB:265:ASN:HD22	1.77	0.50
1:CC:80:ASN:ND2	1:CC:153:PRO:O	2.45	0.50
1:CC:165:ILE:HD13	1:CC:191:LEU:HD23	1.94	0.50
1:CD:317:LYS:HE2	1:CD:319:SER:HB2	1.94	0.50
1:CF:49:TRP:CZ3	1:CF:74:SER:HB3	2.46	0.50
1:CF:135:LEU:HD21	1:CF:255:LEU:HG	1.93	0.50
1:CJ:239:LYS:HA	1:CJ:242:ASN:OD1	2.12	0.50
1:CZ:164:GLN:HE22	1:CZ:308:ARG:HA	1.76	0.50
1:DA:161:MET:SD	2:FB:31:LEU:HD21	2.52	0.50
1:DA:169:VAL:HG22	1:DA:183:LYS:HG3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DE:49:TRP:CZ3	1:DE:74:SER:HB3	2.47	0.50
2:DP:180:ASN:O	4:FN:186:ASN:ND2	2.36	0.50
4:FR:51:THR:HG21	4:FR:180:LYS:HE3	1.93	0.50
5:GV:200:THR:O	5:GV:204:GLN:HG2	2.12	0.50
5:HH:211:LYS:O	5:HH:215:ILE:HG13	2.12	0.50
1:AK:226:SER:OG	1:AV:226:SER:O	2.27	0.50
1:AQ:180:ILE:O	1:AQ:184:ILE:HG13	2.11	0.50
1:AR:169:VAL:HG22	1:AR:183:LYS:HG3	1.94	0.50
1:AV:257:HIS:CE1	1:AV:318:GLN:HG3	2.47	0.50
1:BB:239:LYS:HA	1:BB:242:ASN:OD1	2.12	0.50
1:BC:174:LYS:O	1:BC:212:LYS:NZ	2.44	0.50
1:BF:35:GLU:O	1:BF:272:LYS:HA	2.12	0.50
1:BK:218:ALA:HA	1:BK:224:ALA:HA	1.92	0.50
1:BT:135:LEU:HD21	1:BT:255:LEU:HG	1.94	0.50
1:BV:257:HIS:CE1	1:BV:318:GLN:HG3	2.47	0.50
1:CF:196:GLU:HB3	1:CF:265:ASN:HD22	1.76	0.50
1:CH:79:LEU:HD11	1:CH:305:LEU:HB2	1.94	0.50
1:CO:107:ASP:OD2	1:CO:110:ASN:ND2	2.36	0.50
1:CS:152:LEU:HD21	2:FB:105:SER:HA	1.94	0.50
1:CU:89:ARG:HH21	1:CU:112:LEU:HD21	1.76	0.50
1:CV:152:LEU:HD21	4:GH:112:SER:HA	1.94	0.50
1:DD:196:GLU:HB3	1:DD:265:ASN:HD22	1.77	0.50
2:DO:165:LYS:HE3	2:DO:168:GLU:HA	1.93	0.50
2:EK:166:LEU:HB2	2:EK:170:LEU:HD23	1.94	0.50
2:FB:77:PHE:HD2	4:GG:138:LYS:HG3	1.77	0.50
2:FF:56:LYS:HD2	2:FG:56:LYS:HA	1.93	0.50
4:FU:166:LEU:HD12	4:FU:180:LYS:HG2	1.93	0.50
1:AM:214:VAL:HG11	1:AP:240:ALA:HB2	1.94	0.49
1:AS:197:PHE:HD2	1:AS:243:ASN:HB2	1.76	0.49
1:BW:169:VAL:HG22	1:BW:183:LYS:HG3	1.94	0.49
1:BX:239:LYS:HA	1:BX:242:ASN:OD1	2.11	0.49
1:CF:205:VAL:HG12	1:CF:259:ILE:HG23	1.94	0.49
1:CF:240:ALA:HB2	1:CT:214:VAL:HG11	1.94	0.49
1:CI:163:GLU:HB3	1:CI:308:ARG:HG3	1.93	0.49
1:CK:196:GLU:HB3	1:CK:265:ASN:HD22	1.76	0.49
1:CO:158:LEU:HB3	1:CO:260:LEU:HD21	1.93	0.49
1:CV:286:ASP:HB2	1:CV:294:HIS:HB2	1.93	0.49
1:CW:140:SER:HB2	1:CW:148:GLN:HG2	1.94	0.49
1:DA:49:TRP:CZ3	1:DA:74:SER:HB3	2.47	0.49
2:DW:59:ILE:HG22	2:DW:111:ILE:HG12	1.93	0.49
3:FJ:102:THR:HG22	4:FU:56:PHE:HD1	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:36:ASP:OD1	5:GY:214:ARG:NH1	2.42	0.49
1:AQ:66:THR:HG22	2:DJ:52:CYS:SG	2.53	0.49
1:BB:174:LYS:O	1:BB:212:LYS:NZ	2.45	0.49
1:BE:36:ASP:OD1	5:HO:214:ARG:NH2	2.37	0.49
1:BH:20:VAL:O	5:HR:213:ARG:NH2	2.29	0.49
1:BP:96:GLU:O	1:BP:100:THR:HG23	2.12	0.49
1:BS:8:TYR:CD2	1:BS:93:GLN:HG3	2.47	0.49
1:BV:152:LEU:HD21	2:EN:105:SER:HA	1.93	0.49
1:BW:13:VAL:HG11	1:BW:281:PRO:HG2	1.94	0.49
1:CK:59:THR:O	4:GA:61:ASN:ND2	2.44	0.49
1:CU:13:VAL:HG11	1:CU:281:PRO:HG2	1.94	0.49
1:DB:84:LEU:HD13	1:DD:57:PRO:HB2	1.95	0.49
1:DC:62:ASN:ND2	2:DY:102:ASP:HB2	2.27	0.49
1:DD:161:MET:SD	2:FI:31:LEU:HD21	2.52	0.49
3:FJ:101:TYR:CD2	3:FJ:102:THR:HG23	2.47	0.49
4:GH:149:LEU:HD13	4:GH:181:VAL:HG21	1.93	0.49
1:AT:13:VAL:HG11	1:AT:281:PRO:HG2	1.94	0.49
1:AY:126:ILE:O	1:AY:130:ILE:HG13	2.12	0.49
1:BD:84:LEU:HB3	1:BG:57:PRO:HB2	1.94	0.49
1:CT:158:LEU:HB3	1:CT:260:LEU:HD21	1.94	0.49
1:CW:196:GLU:HB3	1:CW:265:ASN:HD22	1.76	0.49
1:DE:161:MET:SD	2:FF:31:LEU:HD21	2.52	0.49
2:EH:165:LYS:HE3	2:EH:168:GLU:HA	1.94	0.49
2:EO:56:LYS:HD2	4:FZ:56:PHE:HD1	1.77	0.49
2:EY:23:LYS:N	2:EY:67:TYR:OH	2.44	0.49
1:AD:239:LYS:HA	1:AD:242:ASN:OD1	2.11	0.49
1:AH:126:ILE:O	1:AH:130:ILE:HG13	2.12	0.49
1:AJ:92:LYS:NZ	1:AJ:95:SER:OG	2.31	0.49
1:AP:150:ARG:HH22	2:DQ:64:ALA:H	1.60	0.49
1:BK:57:PRO:HB2	1:BO:84:LEU:HB3	1.95	0.49
1:BM:261:ILE:HD12	1:BM:312:LEU:HD23	1.94	0.49
1:BZ:126:ILE:O	1:BZ:130:ILE:HG13	2.12	0.49
1:CE:289:SER:HB2	1:CF:85:GLN:HE22	1.76	0.49
1:CG:203:VAL:HA	1:CG:260:LEU:O	2.13	0.49
1:CN:194:GLY:HA3	4:GB:36:ASN:OD1	2.11	0.49
1:CQ:203:VAL:HG22	1:CQ:261:ILE:HG23	1.94	0.49
2:ER:65:LYS:HD3	2:ER:87:GLU:HB3	1.94	0.49
2:FA:75:LEU:HD22	2:FA:84:LEU:HD13	1.94	0.49
4:FR:26:GLN:NE2	4:FR:28:ASP:OD1	2.45	0.49
4:FY:44:GLU:CD	4:FY:45:PHE:H	2.16	0.49
4:GF:10:GLU:O	4:GF:14:LYS:HG2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AK:59:THR:O	2:DP:61:ASN:ND2	2.46	0.49
1:AM:150:ARG:NH2	2:DO:106:GLY:O	2.45	0.49
1:AZ:13:VAL:HG11	1:AZ:281:PRO:HG2	1.94	0.49
1:BA:192:GLU:HB3	2:DT:36:ILE:HD11	1.93	0.49
1:BC:307:THR:HG22	2:EB:32:LEU:HB2	1.94	0.49
1:CK:162:PRO:HG2	2:EQ:31:LEU:HD11	1.94	0.49
1:CP:66:THR:HG22	2:EX:52:CYS:HB3	1.94	0.49
1:CS:13:VAL:HG11	1:CS:281:PRO:HG2	1.93	0.49
1:CU:49:TRP:CZ3	1:CU:74:SER:HB3	2.47	0.49
2:FD:65:LYS:HD3	2:FD:87:GLU:HB3	1.94	0.49
4:FV:93:VAL:HG21	4:FV:117:ILE:HD11	1.95	0.49
4:GG:142:ILE:HD11	4:GG:152:VAL:HG23	1.94	0.49
1:AF:203:VAL:HG22	1:AF:261:ILE:HG23	1.95	0.49
1:AJ:180:ILE:O	1:AJ:184:ILE:HG13	2.13	0.49
1:AQ:165:ILE:HG13	1:AQ:191:LEU:HD23	1.94	0.49
1:AT:49:TRP:CZ3	1:AT:74:SER:HB3	2.48	0.49
1:AW:126:ILE:O	1:AW:130:ILE:HG13	2.12	0.49
1:AZ:203:VAL:HA	1:AZ:260:LEU:O	2.13	0.49
1:BN:305:LEU:HD11	2:EJ:32:LEU:HG	1.94	0.49
1:CO:126:ILE:O	1:CO:130:ILE:HG13	2.13	0.49
1:CZ:96:GLU:O	1:CZ:100:THR:HG23	2.13	0.49
2:FF:77:PHE:HD2	4:GI:138:LYS:HG3	1.76	0.49
2:FG:63:PRO:HB2	2:FG:85:GLU:HG2	1.95	0.49
4:FW:28:ASP:N	4:FW:28:ASP:OD1	2.45	0.49
4:GH:10:GLU:O	4:GH:14:LYS:HG2	2.12	0.49
1:AD:132:HIS:HA	1:AD:254:LEU:HD13	1.95	0.49
1:AT:66:THR:HG22	2:DP:52:CYS:HB3	1.93	0.49
1:BL:257:HIS:CE1	1:BL:318:GLN:HG3	2.48	0.49
1:BY:214:VAL:HG11	1:BZ:240:ALA:HB2	1.94	0.49
1:BY:239:LYS:HA	1:BY:242:ASN:OD1	2.12	0.49
1:BZ:132:HIS:HA	1:BZ:254:LEU:HD13	1.94	0.49
1:CE:79:LEU:HD11	1:CE:305:LEU:HB2	1.94	0.49
1:CE:214:VAL:HG11	1:CU:240:ALA:HB2	1.95	0.49
1:CH:66:THR:HG22	2:EW:52:CYS:HB3	1.94	0.49
1:CL:66:THR:HG22	2:ET:52:CYS:HB3	1.95	0.49
2:DM:23:LYS:N	2:DM:67:TYR:OH	2.45	0.49
2:DR:167:THR:HB	2:DR:170:LEU:HB3	1.95	0.49
4:FO:142:ILE:HG13	4:FO:152:VAL:HG22	1.95	0.49
1:AA:132:HIS:HA	1:AA:254:LEU:HD13	1.95	0.49
1:AD:152:LEU:HD11	2:DJ:105:SER:HA	1.94	0.49
1:AS:137:GLY:HA3	1:AS:160:ASN:OD1	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AT:16:ILE:HD12	1:AT:116:ALA:HB1	1.93	0.49
1:BO:239:LYS:HA	1:BO:242:ASN:OD1	2.11	0.49
1:BV:133:PHE:CD2	1:BV:301:LEU:HD22	2.48	0.49
1:BX:92:LYS:NZ	1:BX:94:THR:OG1	2.41	0.49
1:BY:152:LEU:HD21	2:EP:105:SER:HA	1.95	0.49
1:CF:239:LYS:HA	1:CF:242:ASN:OD1	2.11	0.49
2:EF:75:LEU:HD22	2:EF:84:LEU:HD13	1.95	0.49
4:GF:149:LEU:HD13	4:GF:181:VAL:HG21	1.94	0.49
1:AE:87:LYS:NZ	4:FK:53:THR:O	2.36	0.49
1:AN:57:PRO:HA	1:AR:86:TYR:HE1	1.78	0.49
1:BA:84:LEU:HB3	1:CY:57:PRO:HB2	1.94	0.49
1:BA:188:LEU:HD23	1:BA:191:LEU:HD12	1.95	0.49
1:BC:57:PRO:HB2	1:BE:84:LEU:HB3	1.93	0.49
1:BH:307:THR:O	1:BH:310:THR:OG1	2.26	0.49
1:BK:196:GLU:HB3	1:BK:265:ASN:HD22	1.77	0.49
1:BZ:152:LEU:HD21	4:GB:112:SER:HA	1.93	0.49
1:CB:158:LEU:HB3	1:CB:260:LEU:HD21	1.95	0.49
1:CE:49:TRP:CZ3	1:CE:74:SER:HB3	2.48	0.49
1:CF:66:THR:HG22	2:FD:52:CYS:HB3	1.94	0.49
1:CH:194:GLY:HA3	2:EW:36:ILE:HG21	1.95	0.49
1:CY:59:THR:O	2:DZ:61:ASN:ND2	2.46	0.49
1:DD:16:ILE:HD11	1:DD:120:LYS:HE3	1.95	0.49
2:DT:58:LYS:HE2	4:FP:123:ASN:OD1	2.13	0.49
2:DW:125:LYS:HD2	2:DW:169:ASP:HA	1.94	0.49
2:EG:76:SER:HB3	2:EG:87:GLU:HG2	1.95	0.49
2:EH:140:ASN:OD1	2:EH:144:GLU:N	2.44	0.49
2:EM:75:LEU:HD22	2:EM:84:LEU:HD21	1.93	0.49
2:EP:167:THR:HG22	2:EP:168:GLU:H	1.78	0.49
1:AM:132:HIS:HA	1:AM:254:LEU:HD13	1.95	0.49
1:BJ:214:VAL:HG11	1:BM:240:ALA:HB2	1.94	0.49
1:BK:239:LYS:HA	1:BK:242:ASN:OD1	2.12	0.49
1:BX:59:THR:O	2:EQ:61:ASN:ND2	2.46	0.49
1:CS:66:THR:OG1	2:FI:58:LYS:NZ	2.46	0.49
1:CS:317:LYS:HE2	1:CS:319:SER:HB2	1.94	0.49
1:CT:307:THR:HG22	2:FG:32:LEU:HB2	1.95	0.49
1:CY:239:LYS:HA	1:CY:242:ASN:OD1	2.13	0.49
1:DB:80:ASN:ND2	1:DB:153:PRO:O	2.36	0.49
1:DD:126:ILE:O	1:DD:130:ILE:HG13	2.12	0.49
2:DQ:137:LEU:HD11	2:DQ:159:ALA:HB2	1.95	0.49
2:DY:23:LYS:NZ	2:DY:100:ASP:OD1	2.44	0.49
2:FB:75:LEU:HD22	2:FB:84:LEU:HD13	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:FL:69:TYR:HB2	4:FL:108:ILE:HD12	1.93	0.49
4:FZ:51:THR:HG21	4:FZ:180:LYS:HE3	1.94	0.49
4:GF:161:ILE:HA	4:GF:186:ASN:HA	1.94	0.49
1:AH:241:ILE:HG22	1:AL:211:LEU:HD21	1.94	0.48
1:BA:66:THR:HG22	2:DT:52:CYS:HB3	1.95	0.48
1:BH:101:SER:OG	1:BH:102:ASP:N	2.46	0.48
1:BS:16:ILE:HD12	1:BS:116:ALA:HB1	1.94	0.48
1:BZ:210:SER:O	1:BZ:214:VAL:HG13	2.13	0.48
1:CA:80:ASN:ND2	1:CA:153:PRO:O	2.33	0.48
1:CA:96:GLU:O	1:CA:100:THR:HG23	2.13	0.48
1:CD:107:ASP:OD2	1:CD:110:ASN:ND2	2.39	0.48
1:CH:161:MET:SD	2:EW:31:LEU:HD21	2.53	0.48
1:CK:96:GLU:O	1:CK:100:THR:HG23	2.13	0.48
1:CK:286:ASP:HB2	1:CK:294:HIS:HB2	1.94	0.48
1:CV:203:VAL:HA	1:CV:260:LEU:O	2.13	0.48
1:CY:13:VAL:HG11	1:CY:281:PRO:HG2	1.95	0.48
1:DD:79:LEU:HD11	1:DD:305:LEU:HB2	1.95	0.48
4:FL:43:VAL:HG11	4:FL:170:LYS:HD3	1.95	0.48
1:AL:257:HIS:CD2	1:AL:318:GLN:HG3	2.47	0.48
1:AO:57:PRO:HG2	1:AS:84:LEU:HD13	1.95	0.48
1:BF:96:GLU:O	1:BF:100:THR:HG23	2.12	0.48
1:BJ:132:HIS:HA	1:BJ:254:LEU:HD13	1.95	0.48
1:CF:13:VAL:HG11	1:CF:281:PRO:HG2	1.95	0.48
1:CQ:169:VAL:HG22	1:CQ:183:LYS:HG3	1.95	0.48
1:DA:205:VAL:HG12	1:DA:259:ILE:HG23	1.95	0.48
2:DL:165:LYS:HE3	2:DL:168:GLU:HA	1.95	0.48
2:DP:75:LEU:HD22	2:DP:84:LEU:HD13	1.95	0.48
2:DQ:153:LYS:HB2	2:DQ:181:ARG:HH21	1.79	0.48
2:EB:76:SER:HB3	2:EB:87:GLU:HG2	1.95	0.48
2:EQ:75:LEU:HD22	2:EQ:84:LEU:HD13	1.94	0.48
2:EV:23:LYS:NZ	2:EV:100:ASP:OD1	2.42	0.48
1:AG:169:VAL:HG22	1:AG:183:LYS:HG3	1.96	0.48
1:AL:152:LEU:HD21	2:DN:105:SER:HA	1.94	0.48
1:AY:259:ILE:HB	1:AY:314:VAL:HB	1.96	0.48
1:AZ:80:ASN:HD22	1:AZ:154:ASN:HB2	1.78	0.48
1:BA:49:TRP:CZ3	1:BA:74:SER:HB3	2.48	0.48
1:BF:158:LEU:HB3	1:BF:260:LEU:HD21	1.95	0.48
1:BM:39:LEU:O	1:BM:274:SER:OG	2.19	0.48
1:BO:57:PRO:HB2	1:BS:84:LEU:HB3	1.94	0.48
1:CD:77:VAL:HG21	2:EZ:32:LEU:HD23	1.95	0.48
1:CF:39:LEU:O	1:CF:274:SER:OG	2.22	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CF:59:THR:O	2:FE:61:ASN:ND2	2.45	0.48
1:CS:59:THR:O	2:FI:61:ASN:ND2	2.46	0.48
1:CS:84:LEU:HD13	1:CV:57:PRO:HB2	1.95	0.48
1:CU:79:LEU:HD11	1:CU:305:LEU:HB2	1.94	0.48
1:DC:52:PHE:HB3	4:FS:41:LYS:HE2	1.95	0.48
1:DC:240:ALA:HB2	1:DE:214:VAL:HG11	1.94	0.48
2:DT:167:THR:HG22	2:DT:168:GLU:H	1.77	0.48
2:EP:133:PRO:HG3	2:EP:161:SER:HA	1.95	0.48
4:GE:149:LEU:HD13	4:GE:181:VAL:HG21	1.95	0.48
1:AF:214:VAL:HG11	1:AQ:240:ALA:HB2	1.94	0.48
1:AG:49:TRP:CZ3	1:AG:74:SER:HB3	2.48	0.48
1:AN:77:VAL:HG11	1:AN:305:LEU:HD13	1.94	0.48
1:AS:143:LYS:HA	4:FP:39:ARG:HE	1.78	0.48
1:AW:49:TRP:CE3	1:AW:74:SER:HB3	2.48	0.48
1:AW:80:ASN:ND2	1:AW:153:PRO:O	2.46	0.48
1:BU:39:LEU:O	1:BU:274:SER:OG	2.22	0.48
1:BV:214:VAL:HG11	1:BY:240:ALA:HB2	1.94	0.48
1:CC:39:LEU:O	1:CC:274:SER:OG	2.21	0.48
1:CH:257:HIS:CE1	1:CH:318:GLN:HG3	2.49	0.48
1:CK:137:GLY:HA3	1:CK:160:ASN:OD1	2.13	0.48
1:CV:16:ILE:HD12	1:CV:116:ALA:HB1	1.96	0.48
1:CW:174:LYS:O	1:CW:212:LYS:NZ	2.46	0.48
1:DB:30:SER:HB3	1:DB:33:GLN:HG3	1.95	0.48
2:FF:59:ILE:HG22	2:FF:111:ILE:HG12	1.95	0.48
4:GG:14:LYS:HG3	4:GH:14:LYS:HG3	1.94	0.48
5:GQ:200:THR:O	5:GQ:204:GLN:HG2	2.14	0.48
1:AB:96:GLU:O	1:AB:100:THR:HG23	2.13	0.48
1:AG:174:LYS:O	1:AG:212:LYS:NZ	2.47	0.48
1:AJ:49:TRP:CZ3	1:AJ:74:SER:HB3	2.49	0.48
1:AR:85:GLN:NE2	1:AR:298:ASP:OD1	2.44	0.48
1:AY:54:ASN:HB3	2:DU:51:VAL:HG12	1.96	0.48
1:BC:240:ALA:HB2	1:BE:214:VAL:HG11	1.95	0.48
1:BT:239:LYS:HA	1:BT:242:ASN:OD1	2.13	0.48
1:CH:91:LEU:HD21	1:CH:112:LEU:HD13	1.94	0.48
1:CH:203:VAL:HG22	1:CH:261:ILE:HG23	1.94	0.48
1:CQ:158:LEU:HB3	1:CQ:260:LEU:HD21	1.96	0.48
1:DC:62:ASN:HD21	2:DY:102:ASP:HB2	1.78	0.48
5:GZ:200:THR:O	5:GZ:204:GLN:HG2	2.14	0.48
5:IZ:189:LEU:HD11	5:IZ:206:ILE:HG12	1.95	0.48
1:AA:36:ASP:OD1	5:GK:214:ARG:NH1	2.43	0.48
1:AF:169:VAL:HG22	1:AF:183:LYS:HG3	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AI:216:PRO:HB2	1:AI:224:ALA:HB1	1.96	0.48
1:AV:121:LEU:O	1:AV:125:GLU:HG2	2.14	0.48
1:BN:13:VAL:HG11	1:BN:281:PRO:HG2	1.94	0.48
1:BZ:164:GLN:HE22	1:BZ:308:ARG:HA	1.79	0.48
1:CC:87:LYS:NZ	2:EU:53:THR:O	2.39	0.48
1:CM:84:LEU:HD13	1:CO:57:PRO:HB2	1.95	0.48
1:CP:59:THR:O	2:EY:61:ASN:ND2	2.46	0.48
1:CS:55:ALA:HA	1:CZ:141:ILE:HD13	1.96	0.48
1:CU:16:ILE:HD12	1:CU:116:ALA:HB1	1.96	0.48
1:DD:49:TRP:CZ3	1:DD:74:SER:HB3	2.48	0.48
1:DD:203:VAL:HG22	1:DD:261:ILE:HG23	1.95	0.48
2:DK:167:THR:HG22	2:DK:168:GLU:H	1.79	0.48
4:GB:149:LEU:HD13	4:GB:181:VAL:HG21	1.96	0.48
4:GG:51:THR:HG21	4:GG:180:LYS:HE3	1.95	0.48
4:GI:142:ILE:HD11	4:GI:152:VAL:HG23	1.95	0.48
5:HD:200:THR:O	5:HD:204:GLN:HG2	2.13	0.48
1:AA:85:GLN:NE2	1:AA:298:ASP:OD1	2.41	0.48
1:AG:96:GLU:O	1:AG:100:THR:HG23	2.14	0.48
1:AJ:181:PHE:O	1:AJ:185:GLU:HG3	2.14	0.48
1:AW:181:PHE:CD1	1:AW:184:ILE:HD12	2.49	0.48
1:BB:261:ILE:HD12	1:BB:312:LEU:HD23	1.96	0.48
1:BZ:239:LYS:HA	1:BZ:242:ASN:OD1	2.14	0.48
1:CS:66:THR:HG22	2:FH:52:CYS:HB3	1.95	0.48
1:CX:89:ARG:HH21	1:CX:112:LEU:HD21	1.79	0.48
2:DT:137:LEU:HD11	2:DT:159:ALA:HB2	1.95	0.48
2:EK:23:LYS:HG3	2:EK:24:ASN:H	1.78	0.48
2:EX:133:PRO:HG3	2:EX:161:SER:HA	1.96	0.48
2:FB:59:ILE:HG22	2:FB:111:ILE:HG12	1.94	0.48
4:GC:14:LYS:HG3	4:GD:14:LYS:HG3	1.95	0.48
5:GX:202:PHE:O	5:GX:206:ILE:HG13	2.13	0.48
1:AG:181:PHE:O	1:AG:185:GLU:HG3	2.14	0.48
1:BG:305:LEU:HD21	3:FJ:77:PHE:CE2	2.48	0.48
1:BH:158:LEU:HB3	1:BH:260:LEU:HD21	1.95	0.48
1:BU:80:ASN:ND2	1:BU:153:PRO:O	2.35	0.48
1:BV:80:ASN:ND2	1:BV:153:PRO:O	2.35	0.48
1:CC:240:ALA:HB2	1:CF:214:VAL:HG11	1.95	0.48
1:CH:49:TRP:CZ3	1:CH:74:SER:HB3	2.49	0.48
1:CU:39:LEU:O	1:CU:274:SER:OG	2.22	0.48
1:CW:169:VAL:HG22	1:CW:183:LYS:HG3	1.96	0.48
1:CZ:152:LEU:HD21	2:FI:105:SER:HA	1.96	0.48
1:DA:212:LYS:HA	1:DA:215:LYS:HE3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:EE:140:ASN:OD1	2:EE:144:GLU:N	2.46	0.48
1:AY:35:GLU:O	1:AY:272:LYS:HA	2.14	0.48
1:AZ:158:LEU:HB3	1:AZ:260:LEU:HD21	1.96	0.48
1:BM:50:ASP:OD1	1:BM:51:ALA:N	2.47	0.48
1:BO:165:ILE:HD13	1:BO:191:LEU:HD23	1.94	0.48
1:CA:196:GLU:HB3	1:CA:265:ASN:HD22	1.78	0.48
1:CM:16:ILE:HD12	1:CM:116:ALA:HB1	1.95	0.48
1:CW:203:VAL:HG22	1:CW:261:ILE:HG23	1.95	0.48
1:DD:194:GLY:HA3	2:FI:36:ILE:HG21	1.96	0.48
2:EQ:23:LYS:N	2:EQ:67:TYR:OH	2.46	0.48
2:ET:69:TYR:HE1	2:ET:100:ASP:HA	1.79	0.48
4:GE:141:LEU:HD11	4:GE:165:ALA:HB2	1.96	0.48
5:JN:211:LYS:O	5:JN:214:ARG:HG2	2.14	0.48
1:AB:186:ALA:O	1:AB:190:LYS:HG3	2.14	0.48
1:AC:205:VAL:HG12	1:AC:259:ILE:HG23	1.96	0.48
1:AO:59:THR:O	2:DT:61:ASN:ND2	2.47	0.48
1:AO:203:VAL:HG13	1:AO:261:ILE:HG12	1.96	0.48
1:AO:203:VAL:HG22	1:AO:261:ILE:HG23	1.96	0.48
1:AV:123:SER:O	1:AV:127:ILE:HG13	2.14	0.48
1:BK:256:LYS:O	1:BK:258:LYS:HG2	2.14	0.48
1:BP:13:VAL:HG11	1:BP:281:PRO:HG2	1.96	0.48
1:BT:49:TRP:CZ3	1:BT:74:SER:HB3	2.49	0.48
1:BZ:35:GLU:O	1:BZ:272:LYS:HA	2.14	0.48
1:CT:57:PRO:HB2	1:CX:84:LEU:HD13	1.96	0.48
1:DB:16:ILE:HD12	1:DB:116:ALA:HB1	1.96	0.48
2:DL:153:LYS:HG3	2:DL:154:SER:H	1.79	0.48
2:EH:23:LYS:N	2:EH:67:TYR:OH	2.46	0.48
2:EK:156:ASN:ND2	2:EK:180:ASN:O	2.47	0.48
4:FQ:171:GLN:HB2	4:FQ:177:TYR:CE1	2.49	0.48
1:AE:96:GLU:O	1:AE:100:THR:HG23	2.14	0.47
1:AN:152:LEU:HD21	4:FN:112:SER:HA	1.95	0.47
1:AR:180:ILE:O	1:AR:184:ILE:HG13	2.14	0.47
1:BG:77:VAL:HG11	1:BG:305:LEU:HD13	1.96	0.47
1:BH:77:VAL:HG11	1:BH:305:LEU:HD13	1.96	0.47
1:BU:203:VAL:HA	1:BU:260:LEU:O	2.14	0.47
1:BW:35:GLU:O	1:BW:272:LYS:HA	2.14	0.47
1:BY:150:ARG:HE	2:EP:82:THR:HB	1.79	0.47
1:CJ:196:GLU:HB3	1:CJ:265:ASN:HD22	1.79	0.47
1:CM:30:SER:HB3	1:CM:33:GLN:HG3	1.95	0.47
1:CS:174:LYS:O	1:CS:212:LYS:NZ	2.47	0.47
1:CZ:158:LEU:HB3	1:CZ:260:LEU:HD21	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:EF:183:ILE:H	4:FW:189:MET:HA	1.79	0.47
2:EI:137:LEU:HD11	2:EI:159:ALA:HB2	1.96	0.47
2:EL:137:LEU:HD11	2:EL:159:ALA:HB2	1.95	0.47
4:GB:78:GLN:HE22	4:GB:89:TYR:HB2	1.78	0.47
4:GG:149:LEU:HD13	4:GG:181:VAL:HG21	1.96	0.47
1:AI:96:GLU:O	1:AI:100:THR:HG23	2.14	0.47
1:AY:231:GLU:O	1:AY:235:ILE:HG13	2.14	0.47
1:BK:66:THR:HG22	2:EH:52:CYS:HB3	1.96	0.47
1:BL:57:PRO:HB2	1:BW:84:LEU:HB3	1.96	0.47
1:BM:135:LEU:HD23	1:BM:254:LEU:HB2	1.96	0.47
1:BO:277:MET:HA	1:BO:300:VAL:HB	1.96	0.47
1:BU:13:VAL:HG11	1:BU:281:PRO:HG2	1.96	0.47
1:BU:239:LYS:HA	1:BU:242:ASN:OD1	2.14	0.47
1:CA:35:GLU:O	1:CA:272:LYS:HA	2.13	0.47
1:CM:49:TRP:CZ3	1:CM:74:SER:HB3	2.49	0.47
1:CU:66:THR:HG22	2:EV:52:CYS:HB3	1.96	0.47
1:CV:214:VAL:HG11	1:CW:240:ALA:HB2	1.95	0.47
1:DE:286:ASP:HB2	1:DE:294:HIS:HB2	1.95	0.47
2:DF:137:LEU:HD11	2:DF:159:ALA:HB2	1.95	0.47
2:DF:167:THR:HB	2:DF:170:LEU:HB3	1.96	0.47
2:DR:137:LEU:HD11	2:DR:159:ALA:HB2	1.96	0.47
2:DS:140:ASN:OD1	2:DS:144:GLU:N	2.46	0.47
2:EE:69:TYR:HB2	2:EE:101:ILE:HD12	1.95	0.47
2:EW:165:LYS:HE3	2:EW:168:GLU:HA	1.96	0.47
2:FH:116:ASN:HB3	2:FI:114:THR:HG21	1.96	0.47
4:GE:142:ILE:HD11	4:GE:152:VAL:HG23	1.97	0.47
4:GG:26:GLN:NE2	4:GG:28:ASP:OD1	2.47	0.47
1:AB:80:ASN:ND2	1:AB:153:PRO:O	2.47	0.47
1:AG:214:VAL:HG11	1:AJ:240:ALA:HB2	1.97	0.47
1:AJ:54:ASN:OD1	2:DK:47:ASN:ND2	2.35	0.47
1:AL:205:VAL:HG12	1:AL:259:ILE:HG23	1.96	0.47
1:AV:80:ASN:ND2	1:AV:153:PRO:O	2.42	0.47
1:BG:135:LEU:HD23	1:BG:254:LEU:HB2	1.96	0.47
1:BU:86:TYR:HD2	1:CA:70:ILE:HD11	1.79	0.47
1:CA:78:ARG:O	1:CA:154:ASN:ND2	2.35	0.47
1:CE:84:LEU:HD13	1:CU:57:PRO:HB2	1.96	0.47
1:CL:158:LEU:HB3	1:CL:260:LEU:HD21	1.96	0.47
1:CO:257:HIS:CE1	1:CO:318:GLN:HG3	2.50	0.47
1:CP:196:GLU:HB3	1:CP:265:ASN:HD22	1.79	0.47
1:CY:161:MET:SD	2:DY:31:LEU:HD21	2.54	0.47
2:DL:167:THR:HG22	2:DL:168:GLU:H	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:DM:74:LYS:HE2	2:DM:89:GLY:HA3	1.95	0.47
2:FF:165:LYS:HE3	2:FF:168:GLU:HA	1.95	0.47
1:AJ:132:HIS:HA	1:AJ:254:LEU:HD13	1.96	0.47
1:AX:169:VAL:HG22	1:AX:183:LYS:HG3	1.95	0.47
1:AY:92:LYS:O	1:AY:96:GLU:HG3	2.14	0.47
1:BK:241:ILE:HG22	1:BO:211:LEU:HD21	1.96	0.47
1:BL:240:ALA:HB2	1:BW:214:VAL:HG11	1.96	0.47
1:BT:158:LEU:HB3	1:BT:260:LEU:HD21	1.96	0.47
1:BV:89:ARG:HH21	1:BV:112:LEU:HD21	1.78	0.47
1:CE:96:GLU:O	1:CE:100:THR:HG23	2.14	0.47
1:CF:79:LEU:HD11	1:CF:305:LEU:HB2	1.96	0.47
1:CV:86:TYR:OH	1:CW:55:ALA:O	2.29	0.47
1:CZ:140:SER:HB2	1:CZ:148:GLN:HG2	1.94	0.47
2:ED:165:LYS:HE3	2:ED:168:GLU:HA	1.97	0.47
1:AB:126:ILE:O	1:AB:130:ILE:HG13	2.14	0.47
1:AR:174:LYS:O	1:AR:212:LYS:NZ	2.47	0.47
1:AY:214:VAL:HG11	1:AZ:240:ALA:HB2	1.96	0.47
1:AZ:181:PHE:CE2	1:AZ:230:TRP:HE3	2.33	0.47
1:BD:241:ILE:HG22	1:BP:211:LEU:HD21	1.95	0.47
1:BP:80:ASN:ND2	1:BP:153:PRO:O	2.47	0.47
1:BR:19:GLU:HA	1:BR:120:LYS:HD3	1.97	0.47
1:BV:16:ILE:HD12	1:BV:116:ALA:HB1	1.97	0.47
1:BY:96:GLU:O	1:BY:100:THR:HG23	2.14	0.47
1:CG:214:VAL:HG11	1:CH:240:ALA:HB2	1.96	0.47
1:CL:39:LEU:O	1:CL:274:SER:OG	2.22	0.47
1:CU:35:GLU:O	1:CU:272:LYS:HA	2.15	0.47
1:CV:147:ASN:H	4:GH:88:HIS:HD2	1.62	0.47
1:CZ:169:VAL:HG22	1:CZ:183:LYS:HG3	1.96	0.47
2:DY:180:ASN:O	2:DZ:180:ASN:ND2	2.42	0.47
4:FN:93:VAL:HG21	4:FN:117:ILE:HD11	1.95	0.47
1:AE:164:GLN:HE22	1:AE:308:ARG:HA	1.79	0.47
1:AP:80:ASN:ND2	1:AP:153:PRO:O	2.47	0.47
1:AW:184:ILE:HG12	1:AW:314:VAL:HG21	1.97	0.47
1:AZ:174:LYS:O	1:AZ:212:LYS:NZ	2.47	0.47
1:BD:49:TRP:CZ3	1:BD:74:SER:HB3	2.49	0.47
1:BD:210:SER:HB3	1:BG:244:ARG:HH12	1.80	0.47
1:BN:35:GLU:O	1:BN:272:LYS:HA	2.13	0.47
1:BN:240:ALA:HB2	1:BR:214:VAL:HG11	1.97	0.47
1:BR:169:VAL:HG22	1:BR:183:LYS:HG3	1.97	0.47
1:BZ:96:GLU:O	1:BZ:100:THR:HG23	2.15	0.47
1:CA:65:ASN:ND2	2:EK:57:ASP:O	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CE:8:TYR:CD2	1:CE:93:GLN:HG3	2.48	0.47
1:CH:126:ILE:O	1:CH:130:ILE:HG13	2.15	0.47
1:CK:8:TYR:CD2	1:CK:93:GLN:HG3	2.49	0.47
1:CK:174:LYS:O	1:CK:212:LYS:NZ	2.48	0.47
1:CN:132:HIS:HA	1:CN:254:LEU:HD13	1.96	0.47
1:CS:57:PRO:HA	1:CZ:86:TYR:HE1	1.80	0.47
1:CS:92:LYS:HZ2	1:CS:94:THR:HG1	1.60	0.47
1:CW:161:MET:SD	2:FE:31:LEU:HD21	2.54	0.47
1:CY:66:THR:HG22	2:DY:52:CYS:HB3	1.97	0.47
2:DK:137:LEU:HD11	2:DK:159:ALA:HB2	1.97	0.47
2:DM:45:PHE:HD1	2:DM:172:ILE:HD11	1.79	0.47
2:EF:63:PRO:HB2	2:EF:85:GLU:HG2	1.96	0.47
2:EG:13:LYS:O	2:EG:17:GLU:HG3	2.14	0.47
2:EJ:140:ASN:OD1	2:EJ:144:GLU:N	2.46	0.47
2:ET:181:ARG:HH12	2:EU:94:LEU:HB3	1.80	0.47
4:FQ:19:GLU:OE1	4:FQ:27:HIS:NE2	2.47	0.47
5:HK:211:LYS:O	5:HK:215:ILE:HG13	2.14	0.47
5:JK:189:LEU:HD11	5:JK:206:ILE:HG12	1.97	0.47
1:AA:181:PHE:O	1:AA:185:GLU:HG3	2.14	0.47
1:AC:96:GLU:O	1:AC:100:THR:HG23	2.15	0.47
1:AC:231:GLU:O	1:AC:235:ILE:HG13	2.15	0.47
1:AG:152:LEU:HD21	2:DL:105:SER:HA	1.96	0.47
1:AN:180:ILE:O	1:AN:184:ILE:HG13	2.15	0.47
1:AR:152:LEU:HD21	2:DR:105:SER:HA	1.96	0.47
1:BA:65:ASN:HB2	2:DS:59:ILE:H	1.79	0.47
1:BB:35:GLU:O	1:BB:272:LYS:HA	2.15	0.47
1:BC:205:VAL:HG12	1:BC:259:ILE:HG23	1.96	0.47
1:BD:165:ILE:HD13	1:BD:191:LEU:HD23	1.95	0.47
1:BI:188:LEU:HD23	1:BI:191:LEU:HD12	1.96	0.47
1:BJ:305:LEU:HD11	4:FV:32:LEU:HG	1.95	0.47
1:BK:35:GLU:O	1:BK:272:LYS:HA	2.15	0.47
1:BS:35:GLU:O	1:BS:272:LYS:HA	2.15	0.47
1:BT:161:MET:HG3	4:FX:31:LEU:HD21	1.96	0.47
1:BT:164:GLN:HE22	1:BT:308:ARG:HA	1.80	0.47
1:BV:169:VAL:HG22	1:BV:183:LYS:HG3	1.97	0.47
1:BW:196:GLU:OE1	1:BW:265:ASN:ND2	2.45	0.47
1:CB:135:LEU:HD21	1:CB:255:LEU:HG	1.96	0.47
1:CH:288:ASP:OD1	1:CH:289:SER:N	2.43	0.47
1:CN:203:VAL:HA	1:CN:260:LEU:O	2.15	0.47
1:CV:84:LEU:HD13	1:CW:57:PRO:HB2	1.97	0.47
1:CX:203:VAL:HA	1:CX:260:LEU:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DA:164:GLN:HE22	1:DA:308:ARG:HA	1.79	0.47
1:DB:77:VAL:HG11	1:DB:305:LEU:HD13	1.97	0.47
1:DC:96:GLU:O	1:DC:100:THR:HG23	2.14	0.47
1:DC:132:HIS:HA	1:DC:254:LEU:HD13	1.96	0.47
2:DR:166:LEU:HD11	2:DR:172:ILE:HD13	1.97	0.47
2:EK:165:LYS:HE3	2:EK:168:GLU:HA	1.97	0.47
2:EM:123:LEU:HD21	2:EM:131:VAL:HG21	1.97	0.47
2:EO:180:ASN:O	4:FZ:186:ASN:ND2	2.40	0.47
2:FD:77:PHE:HD2	4:GH:138:LYS:HE2	1.80	0.47
4:GD:107:ASP:HB3	4:GD:116:THR:HB	1.95	0.47
1:AN:96:GLU:O	1:AN:100:THR:HG23	2.15	0.47
1:AU:84:LEU:HD13	1:BA:57:PRO:HB2	1.96	0.47
1:AU:123:SER:O	1:AU:127:ILE:HG13	2.14	0.47
1:AY:85:GLN:HE22	1:DD:289:SER:HB2	1.80	0.47
1:AY:180:ILE:O	1:AY:184:ILE:HG13	2.15	0.47
1:BE:77:VAL:HG11	1:BE:305:LEU:HD13	1.97	0.47
1:BP:307:THR:HB	1:BP:310:THR:HG21	1.96	0.47
1:CD:135:LEU:HD21	1:CD:255:LEU:HG	1.96	0.47
1:CP:161:MET:SD	2:EX:31:LEU:HD21	2.55	0.47
1:CR:60:ILE:HG23	1:CT:290:THR:HG22	1.96	0.47
1:CS:161:MET:SD	2:FH:31:LEU:HD21	2.55	0.47
1:DA:257:HIS:ND1	1:DA:318:GLN:HG3	2.30	0.47
1:DE:164:GLN:HE22	1:DE:308:ARG:HA	1.80	0.47
2:DU:63:PRO:HB2	2:DU:85:GLU:HB3	1.97	0.47
2:DV:156:ASN:OD1	2:DV:181:ARG:HB3	2.15	0.47
4:FW:137:VAL:HG12	4:FW:138:LYS:HG3	1.96	0.47
5:GU:202:PHE:O	5:GU:206:ILE:HG13	2.14	0.47
1:AL:207:PRO:O	1:AL:211:LEU:HG	2.15	0.47
1:AZ:306:ALA:O	4:FR:31:LEU:HB2	2.15	0.47
1:BA:16:ILE:HD12	1:BA:116:ALA:HB1	1.97	0.47
1:BA:289:SER:HB2	1:DE:85:GLN:HE22	1.79	0.47
1:BC:107:ASP:HB3	1:BC:112:LEU:HB2	1.97	0.47
1:BO:77:VAL:HG21	2:EL:32:LEU:HD23	1.97	0.47
1:CA:8:TYR:CD2	1:CA:93:GLN:HG3	2.50	0.47
1:CE:57:PRO:HB2	1:CI:84:LEU:HD13	1.97	0.47
1:CN:80:ASN:ND2	1:CN:153:PRO:O	2.47	0.47
2:DS:63:PRO:HB2	2:DS:85:GLU:HG2	1.97	0.47
4:FU:93:VAL:HG21	4:FU:117:ILE:HD11	1.96	0.47
4:GD:78:GLN:HE22	4:GD:89:TYR:HB2	1.79	0.47
4:GF:6:GLN:HA	4:GF:9:LYS:HD2	1.97	0.47
5:IA:200:THR:O	5:IA:204:GLN:HG2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AM:100:THR:HA	1:AM:105:ILE:HG23	1.96	0.47
1:AU:164:GLN:HE22	1:AU:308:ARG:HA	1.80	0.47
1:AZ:96:GLU:O	1:AZ:100:THR:HG23	2.15	0.47
1:BH:66:THR:HG22	2:EE:52:CYS:SG	2.54	0.47
1:BO:286:ASP:HB2	1:BO:294:HIS:HB2	1.97	0.47
1:BP:163:GLU:HB3	1:BP:308:ARG:HG3	1.96	0.47
1:BU:35:GLU:O	1:BU:272:LYS:HA	2.14	0.47
1:BW:80:ASN:ND2	1:BW:153:PRO:O	2.48	0.47
1:CI:96:GLU:O	1:CI:100:THR:HG23	2.14	0.47
1:CL:13:VAL:HG11	1:CL:281:PRO:HG2	1.97	0.47
1:CW:49:TRP:CZ3	1:CW:74:SER:HB3	2.49	0.47
4:FL:93:VAL:HG21	4:FL:117:ILE:HD11	1.96	0.47
4:FW:77:ILE:HG12	4:FW:91:PRO:HB3	1.97	0.47
4:FY:44:GLU:OE1	4:FY:45:PHE:N	2.47	0.47
5:IY:211:LYS:O	5:IY:214:ARG:HG2	2.15	0.47
1:AA:271:PHE:CD2	1:AA:273:PRO:HD3	2.50	0.46
1:AJ:66:THR:HG22	2:DK:52:CYS:SG	2.55	0.46
1:AS:158:LEU:HB3	1:AS:260:LEU:HD21	1.97	0.46
1:AU:209:THR:O	1:AU:213:LEU:HG	2.15	0.46
1:AY:59:THR:O	2:DV:61:ASN:ND2	2.48	0.46
1:BA:231:GLU:O	1:BA:235:ILE:HG13	2.15	0.46
1:BD:132:HIS:HA	1:BD:254:LEU:HD13	1.97	0.46
1:BT:35:GLU:O	1:BT:272:LYS:HA	2.14	0.46
1:CT:270:LYS:HG2	1:CT:272:LYS:HE3	1.97	0.46
1:CZ:308:ARG:HH21	2:DX:31:LEU:HB2	1.79	0.46
2:EE:23:LYS:N	2:EE:67:TYR:OH	2.49	0.46
2:EI:77:PHE:CD1	4:FY:138:LYS:HG2	2.50	0.46
2:EZ:136:LYS:HD3	2:EZ:155:VAL:HG11	1.96	0.46
4:FQ:149:LEU:HD13	4:FQ:181:VAL:HG21	1.96	0.46
4:FS:149:LEU:HD13	4:FS:181:VAL:HG21	1.95	0.46
4:FU:144:ASN:OD1	4:FU:148:ALA:N	2.46	0.46
5:GX:200:THR:O	5:GX:204:GLN:HG2	2.15	0.46
1:AB:286:ASP:HB2	1:AB:294:HIS:HB2	1.97	0.46
1:AI:188:LEU:HD23	1:AI:191:LEU:HD12	1.97	0.46
1:AJ:126:ILE:O	1:AJ:130:ILE:HG13	2.16	0.46
1:AT:123:SER:O	1:AT:127:ILE:HG13	2.15	0.46
1:AY:196:GLU:HB3	1:AY:265:ASN:HD22	1.81	0.46
1:AZ:35:GLU:O	1:AZ:272:LYS:HA	2.15	0.46
1:BK:165:ILE:HD12	1:BK:191:LEU:HD23	1.97	0.46
1:BQ:66:THR:HG22	4:FU:52:ARG:HB3	1.96	0.46
1:CP:85:GLN:NE2	1:CP:298:ASP:OD1	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CQ:49:TRP:CZ3	1:CQ:74:SER:HB3	2.50	0.46
1:CU:169:VAL:HG22	1:CU:183:LYS:HG3	1.96	0.46
1:DE:35:GLU:O	1:DE:272:LYS:HA	2.15	0.46
2:FF:75:LEU:HD22	2:FF:84:LEU:HD13	1.97	0.46
5:GL:200:THR:O	5:GL:204:GLN:HG2	2.15	0.46
1:AD:86:TYR:OH	1:AG:55:ALA:O	2.31	0.46
1:AE:35:GLU:O	1:AE:272:LYS:HA	2.15	0.46
1:AJ:169:VAL:HG22	1:AJ:183:LYS:HG3	1.97	0.46
1:AS:126:ILE:O	1:AS:130:ILE:HG13	2.15	0.46
1:BK:49:TRP:CE3	1:BK:74:SER:HB3	2.51	0.46
1:BL:217:TYR:O	1:BL:225:SER:N	2.40	0.46
1:BS:43:TYR:HE2	1:BS:45:LYS:HE2	1.80	0.46
1:CM:257:HIS:CE1	1:CM:318:GLN:HG3	2.50	0.46
1:DE:78:ARG:O	1:DE:154:ASN:ND2	2.38	0.46
2:DG:23:LYS:HE2	2:DG:48:SER:HB3	1.97	0.46
2:DW:167:THR:HG22	2:DW:168:GLU:H	1.80	0.46
2:EC:137:LEU:HD11	2:EC:159:ALA:HB2	1.98	0.46
4:FO:141:LEU:HD11	4:FO:165:ALA:HB2	1.97	0.46
4:FR:25:PRO:HB2	4:FR:27:HIS:CD2	2.50	0.46
4:FW:35:SER:HB2	4:FW:41:LYS:HE3	1.97	0.46
4:FX:47:ALA:O	4:FX:70:LYS:NZ	2.33	0.46
4:GI:161:ILE:HA	4:GI:186:ASN:HA	1.96	0.46
1:AE:16:ILE:HD12	1:AE:116:ALA:HB1	1.97	0.46
1:AF:126:ILE:O	1:AF:130:ILE:HG13	2.16	0.46
1:AG:13:VAL:HG11	1:AG:281:PRO:HG2	1.97	0.46
1:AQ:158:LEU:HB3	1:AQ:260:LEU:HD21	1.98	0.46
1:AX:209:THR:O	1:AX:213:LEU:HG	2.16	0.46
1:BE:96:GLU:O	1:BE:100:THR:HG23	2.15	0.46
1:BF:308:ARG:HG3	4:FT:33:SER:HA	1.96	0.46
1:BM:253:ASN:ND2	1:BP:195:ASP:OD1	2.39	0.46
1:BP:169:VAL:HG22	1:BP:183:LYS:HG3	1.96	0.46
1:BS:41:MET:HG2	2:EM:104:PHE:HE2	1.79	0.46
1:BS:67:ILE:HG13	1:BZ:296:TYR:HE2	1.81	0.46
1:CD:57:PRO:HA	1:CK:86:TYR:HE1	1.81	0.46
1:CO:196:GLU:HB3	1:CO:265:ASN:HD22	1.81	0.46
1:CT:49:TRP:CZ3	1:CT:74:SER:HB3	2.50	0.46
1:CT:96:GLU:O	1:CT:100:THR:HG23	2.15	0.46
1:DB:49:TRP:CZ3	1:DB:74:SER:HB3	2.50	0.46
1:DB:169:VAL:HG22	1:DB:183:LYS:HG3	1.98	0.46
1:DD:109:ASN:O	2:DW:24:ASN:ND2	2.48	0.46
2:DU:167:THR:HG22	2:DU:168:GLU:H	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:IL:211:LYS:O	5:IL:214:ARG:HG2	2.16	0.46
1:AG:35:GLU:O	1:AG:272:LYS:HA	2.16	0.46
1:AM:186:ALA:O	1:AM:190:LYS:HG3	2.15	0.46
1:AN:209:THR:O	1:AN:213:LEU:HG	2.15	0.46
1:AU:152:LEU:HD21	2:DS:105:SER:HA	1.96	0.46
1:BG:169:VAL:HG22	1:BG:183:LYS:HG3	1.98	0.46
1:BK:159:LEU:HD12	1:BK:260:LEU:HD13	1.97	0.46
1:BT:150:ARG:HH21	2:EL:63:PRO:HB3	1.80	0.46
1:BY:84:LEU:HD13	1:BZ:57:PRO:HB2	1.97	0.46
1:CM:178:ASP:OD1	1:CM:178:ASP:N	2.48	0.46
1:CN:96:GLU:O	1:CN:100:THR:HG23	2.15	0.46
1:CV:77:VAL:HG11	1:CV:305:LEU:HD13	1.96	0.46
1:CW:96:GLU:O	1:CW:100:THR:HG23	2.16	0.46
1:CZ:49:TRP:CZ3	1:CZ:74:SER:HB3	2.51	0.46
2:DU:37:ASP:O	2:DU:41:GLN:NE2	2.49	0.46
2:DU:181:ARG:NH1	2:DV:94:LEU:O	2.43	0.46
2:EJ:23:LYS:HA	2:EJ:45:PHE:HD2	1.79	0.46
2:EN:75:LEU:HD22	2:EN:84:LEU:HD13	1.98	0.46
3:FJ:171:ARG:HG2	3:FJ:190:ILE:HG22	1.96	0.46
4:FV:69:TYR:HB2	4:FV:108:ILE:HD12	1.98	0.46
1:AB:36:ASP:CG	5:GL:214:ARG:HH22	2.17	0.46
1:AC:35:GLU:O	1:AC:272:LYS:HA	2.16	0.46
1:AG:20:VAL:O	5:GQ:213:ARG:NH2	2.25	0.46
1:AH:164:GLN:HE22	1:AH:308:ARG:HA	1.80	0.46
1:AM:35:GLU:O	1:AM:272:LYS:HA	2.15	0.46
1:AY:209:THR:O	1:AY:213:LEU:HG	2.15	0.46
1:BR:41:MET:HE2	1:BR:83:LYS:H	1.80	0.46
1:CK:81:TYR:OH	1:CK:272:LYS:O	2.26	0.46
1:CO:288:ASP:OD1	1:CO:289:SER:N	2.43	0.46
2:DR:183:ILE:N	4:FO:188:ALA:O	2.41	0.46
2:DZ:75:LEU:HD22	2:DZ:84:LEU:HD13	1.98	0.46
2:FB:167:THR:HG22	2:FB:168:GLU:H	1.80	0.46
2:FD:75:LEU:HD22	2:FD:84:LEU:HD13	1.97	0.46
1:AH:35:GLU:O	1:AH:272:LYS:HA	2.16	0.46
1:AO:60:ILE:HG23	1:AU:290:THR:HG22	1.97	0.46
1:AS:169:VAL:HG22	1:AS:183:LYS:HG3	1.98	0.46
1:AV:169:VAL:HG22	1:AV:183:LYS:HG3	1.96	0.46
1:BI:169:VAL:HG22	1:BI:183:LYS:HG3	1.98	0.46
1:BJ:16:ILE:HD11	1:BJ:120:LYS:HE3	1.97	0.46
1:BM:35:GLU:O	1:BM:272:LYS:HA	2.16	0.46
1:BS:57:PRO:HB2	1:BZ:84:LEU:HD13	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BX:203:VAL:HG13	1:BX:261:ILE:HG12	1.97	0.46
1:BY:158:LEU:HB3	1:BY:260:LEU:HD21	1.96	0.46
1:CD:13:VAL:HG11	1:CD:281:PRO:HG2	1.96	0.46
1:CH:140:SER:HB2	1:CH:148:GLN:HG2	1.97	0.46
1:CS:96:GLU:O	1:CS:100:THR:HG23	2.15	0.46
1:CU:65:ASN:ND2	2:EW:57:ASP:O	2.49	0.46
1:CZ:80:ASN:ND2	1:CZ:153:PRO:O	2.49	0.46
1:DB:257:HIS:CE1	1:DB:318:GLN:HG3	2.51	0.46
1:DC:174:LYS:O	1:DC:212:LYS:NZ	2.48	0.46
2:DY:75:LEU:HD22	2:DY:84:LEU:HD13	1.97	0.46
2:ET:56:LYS:HD2	2:EU:56:LYS:HA	1.98	0.46
2:EW:134:GLY:HA2	4:GD:77:ILE:HD13	1.96	0.46
5:GL:202:PHE:O	5:GL:206:ILE:HG13	2.15	0.46
5:GY:211:LYS:O	5:GY:214:ARG:HG2	2.15	0.46
5:HQ:200:THR:O	5:HQ:204:GLN:HG2	2.16	0.46
1:AF:286:ASP:HB2	1:AF:294:HIS:HB2	1.98	0.46
1:AN:35:GLU:O	1:AN:272:LYS:HA	2.16	0.46
1:AT:79:LEU:HD11	1:AT:305:LEU:HB2	1.98	0.46
1:AV:137:GLY:HA3	1:AV:160:ASN:OD1	2.16	0.46
1:BA:96:GLU:O	1:BA:100:THR:HG23	2.16	0.46
1:BC:188:LEU:HD23	1:BC:191:LEU:HD12	1.97	0.46
1:BL:174:LYS:O	1:BL:212:LYS:NZ	2.49	0.46
1:BW:181:PHE:CD1	1:BW:184:ILE:HD12	2.50	0.46
1:BZ:158:LEU:HB3	1:BZ:260:LEU:HD21	1.98	0.46
1:CL:205:VAL:HG12	1:CL:259:ILE:HG23	1.97	0.46
1:CN:52:PHE:HB3	4:GB:41:LYS:HE2	1.98	0.46
1:CR:240:ALA:HB2	1:CU:214:VAL:HG11	1.97	0.46
1:CT:152:LEU:HD21	2:FE:105:SER:HA	1.98	0.46
1:CV:80:ASN:ND2	1:CV:154:ASN:HB2	2.30	0.46
2:DJ:140:ASN:OD1	2:DJ:144:GLU:N	2.47	0.46
2:DM:166:LEU:HB2	2:DM:170:LEU:HD23	1.98	0.46
2:ER:181:ARG:NH2	2:ES:92:ASP:O	2.49	0.46
4:FK:73:VAL:HG21	4:FK:117:ILE:HD13	1.97	0.46
4:FT:58:LYS:HD3	4:FT:119:PRO:HG2	1.98	0.46
4:FT:73:VAL:HG21	4:FT:117:ILE:HD13	1.97	0.46
5:HJ:211:LYS:O	5:HJ:215:ILE:HG13	2.16	0.46
5:HK:200:THR:O	5:HK:204:GLN:HG2	2.16	0.46
1:AO:306:ALA:O	4:FP:31:LEU:HB2	2.16	0.46
1:AV:231:GLU:O	1:AV:235:ILE:HG13	2.16	0.46
1:BA:180:ILE:O	1:BA:184:ILE:HG13	2.15	0.46
1:BM:214:VAL:HG11	1:BP:240:ALA:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CB:203:VAL:HG22	1:CB:261:ILE:HG23	1.97	0.46
1:CD:91:LEU:HD21	1:CD:112:LEU:HD13	1.98	0.46
1:CF:169:VAL:HG22	1:CF:183:LYS:HG3	1.97	0.46
1:CI:203:VAL:HA	1:CI:260:LEU:O	2.16	0.46
1:CO:49:TRP:CZ3	1:CO:74:SER:HB3	2.50	0.46
1:CV:21:LYS:NZ	1:CW:195:ASP:OD2	2.45	0.46
1:CX:87:LYS:NZ	2:FG:53:THR:O	2.40	0.46
2:DJ:23:LYS:N	2:DJ:67:TYR:OH	2.49	0.46
2:DL:69:TYR:HB2	2:DL:101:ILE:HD12	1.98	0.46
2:ET:125:LYS:HD2	2:ET:169:ASP:HA	1.98	0.46
2:EV:54:SER:HB2	2:EW:58:LYS:HZ3	1.80	0.46
2:EX:75:LEU:HD22	2:EX:84:LEU:HD13	1.98	0.46
5:IF:200:THR:O	5:IF:204:GLN:HG2	2.16	0.46
1:AA:135:LEU:HD23	1:AA:254:LEU:HB2	1.98	0.46
1:AE:77:VAL:HG11	1:AE:305:LEU:HD13	1.98	0.46
1:AH:259:ILE:HB	1:AH:314:VAL:HB	1.98	0.46
1:AL:165:ILE:HG13	1:AL:191:LEU:HD23	1.98	0.46
1:AO:169:VAL:HG22	1:AO:183:LYS:HG3	1.97	0.46
1:AS:80:ASN:ND2	1:AS:153:PRO:O	2.48	0.46
1:AT:8:TYR:CD2	1:AT:93:GLN:HG3	2.50	0.46
1:AT:59:THR:O	4:FN:61:ASN:ND2	2.48	0.46
1:AU:203:VAL:HA	1:AU:260:LEU:O	2.16	0.46
1:BE:203:VAL:HG22	1:BE:261:ILE:HG12	1.98	0.46
1:BG:39:LEU:O	1:BG:274:SER:OG	2.25	0.46
1:BS:197:PHE:HD2	1:BS:243:ASN:HB2	1.81	0.46
1:BX:308:ARG:O	2:EP:34:ASN:ND2	2.44	0.46
1:CC:96:GLU:O	1:CC:100:THR:HG23	2.15	0.46
1:CJ:96:GLU:O	1:CJ:100:THR:HG23	2.16	0.46
1:CM:140:SER:HB2	1:CM:148:GLN:HG2	1.98	0.46
1:CY:277:MET:HA	1:CY:300:VAL:HB	1.98	0.46
1:DB:203:VAL:HA	1:DB:260:LEU:O	2.16	0.46
2:DO:23:LYS:N	2:DO:67:TYR:OH	2.46	0.46
2:ED:123:LEU:HD21	2:ED:131:VAL:HG21	1.98	0.46
2:EI:136:LYS:HD3	2:EI:155:VAL:HG21	1.98	0.46
2:ET:167:THR:HG22	2:ET:168:GLU:H	1.81	0.46
5:GZ:202:PHE:O	5:GZ:206:ILE:HG13	2.15	0.46
1:AA:180:ILE:O	1:AA:184:ILE:HG13	2.16	0.45
1:AC:49:TRP:CZ3	1:AC:74:SER:HB3	2.52	0.45
1:AC:92:LYS:O	1:AC:96:GLU:HG3	2.16	0.45
1:AU:180:ILE:O	1:AU:184:ILE:HG13	2.16	0.45
1:BA:35:GLU:O	1:BA:272:LYS:HA	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BB:77:VAL:HG11	1:BB:305:LEU:HD13	1.97	0.45
1:BF:119:TYR:CE1	1:BF:281:PRO:HG3	2.51	0.45
1:BG:41:MET:HE2	1:BG:83:LYS:H	1.81	0.45
1:BK:80:ASN:ND2	1:BK:153:PRO:O	2.49	0.45
1:BK:203:VAL:HG13	1:BK:261:ILE:HG12	1.99	0.45
1:BV:289:SER:HB2	1:BX:85:GLN:HE22	1.81	0.45
1:BX:96:GLU:O	1:BX:100:THR:HG23	2.16	0.45
1:CG:96:GLU:O	1:CG:100:THR:HG23	2.16	0.45
1:CI:14:ALA:HB2	5:IS:202:PHE:HE1	1.81	0.45
1:DB:35:GLU:O	1:DB:272:LYS:HA	2.16	0.45
1:DB:178:ASP:N	1:DB:178:ASP:OD1	2.48	0.45
1:DC:203:VAL:HA	1:DC:260:LEU:O	2.16	0.45
1:DD:169:VAL:HG22	1:DD:183:LYS:HG3	1.98	0.45
2:DQ:165:LYS:HE3	2:DQ:168:GLU:HA	1.98	0.45
2:DS:101:ILE:HD12	2:DS:107:MET:O	2.16	0.45
2:ER:23:LYS:NZ	2:ER:100:ASP:OD1	2.45	0.45
2:EY:56:LYS:HD2	4:GE:56:PHE:HD1	1.82	0.45
2:FG:23:LYS:N	2:FG:67:TYR:OH	2.49	0.45
2:FG:116:ASN:ND2	4:GI:60:GLU:OE2	2.49	0.45
3:FJ:171:ARG:HB3	3:FJ:188:VAL:HG11	1.98	0.45
4:FP:133:SER:HB3	4:FP:177:TYR:CE2	2.51	0.45
4:FQ:172:ILE:HD12	4:FQ:178:LEU:HD12	1.98	0.45
4:FV:35:SER:HB2	4:FV:41:LYS:HE3	1.97	0.45
4:GI:149:LEU:HD13	4:GI:181:VAL:HG21	1.97	0.45
5:HJ:200:THR:O	5:HJ:204:GLN:HG2	2.16	0.45
5:IR:211:LYS:O	5:IR:214:ARG:HG2	2.17	0.45
1:AF:231:GLU:O	1:AF:235:ILE:HG13	2.15	0.45
1:AG:126:ILE:O	1:AG:130:ILE:HG13	2.16	0.45
1:AH:20:VAL:O	5:GR:213:ARG:NH2	2.32	0.45
1:AM:229:LYS:O	1:AM:233:VAL:HG23	2.16	0.45
1:AN:231:GLU:O	1:AN:235:ILE:HG13	2.15	0.45
1:AS:57:PRO:HB2	1:AZ:84:LEU:HD13	1.98	0.45
1:AS:209:THR:O	1:AS:213:LEU:HG	2.17	0.45
1:AT:231:GLU:O	1:AT:235:ILE:HG13	2.16	0.45
1:BJ:80:ASN:ND2	1:BJ:153:PRO:O	2.49	0.45
1:BK:257:HIS:HB2	1:BK:316:ILE:HB	1.97	0.45
1:BL:70:ILE:HD11	1:BW:86:TYR:HD2	1.81	0.45
1:BO:41:MET:HE2	1:BO:83:LYS:H	1.80	0.45
1:BO:196:GLU:HB3	1:BO:265:ASN:ND2	2.32	0.45
1:CF:57:PRO:HB2	1:CT:84:LEU:HD13	1.98	0.45
2:DZ:167:THR:HG22	2:DZ:168:GLU:H	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:EG:127:GLY:O	2:EG:131:VAL:HG23	2.16	0.45
4:FS:78:GLN:HE22	4:FS:89:TYR:HB2	1.80	0.45
1:AC:78:ARG:HH21	2:DH:104:PHE:HE1	1.63	0.45
1:AC:123:SER:O	1:AC:127:ILE:HG13	2.16	0.45
1:AK:35:GLU:O	1:AK:272:LYS:HA	2.17	0.45
1:AP:36:ASP:CG	5:GZ:214:ARG:HH22	2.20	0.45
1:AU:126:ILE:O	1:AU:130:ILE:HG13	2.16	0.45
1:AZ:20:VAL:O	5:HJ:213:ARG:NH1	2.49	0.45
1:BK:164:GLN:HE22	1:BK:308:ARG:HA	1.81	0.45
1:BU:26:TYR:O	5:IE:218:TYR:OH	2.31	0.45
1:CD:80:ASN:ND2	1:CD:153:PRO:O	2.49	0.45
1:CP:13:VAL:HG11	1:CP:281:PRO:HG2	1.99	0.45
1:CV:30:SER:HB3	1:CV:33:GLN:HG3	1.97	0.45
1:DA:203:VAL:HG22	1:DA:261:ILE:HG23	1.99	0.45
2:DS:23:LYS:HG3	2:DS:24:ASN:N	2.31	0.45
2:DT:74:LYS:HE2	2:DT:89:GLY:HA3	1.98	0.45
2:ED:180:ASN:HB2	4:FV:186:ASN:HD21	1.80	0.45
4:FP:142:ILE:HD11	4:FP:152:VAL:HG22	1.98	0.45
4:FV:144:ASN:OD1	4:FV:148:ALA:N	2.47	0.45
4:GC:149:LEU:HD13	4:GC:181:VAL:HG21	1.98	0.45
1:AM:13:VAL:HG11	1:AM:281:PRO:HG2	1.98	0.45
1:AP:49:TRP:CZ3	1:AP:74:SER:HB3	2.51	0.45
1:AP:66:THR:HG22	4:FN:52:ARG:HB3	1.98	0.45
1:AX:28:TRP:HB3	1:AX:262:TYR:OH	2.16	0.45
1:BJ:286:ASP:HB2	1:BJ:294:HIS:HB2	1.98	0.45
1:BS:96:GLU:O	1:BS:100:THR:HG23	2.17	0.45
1:CS:196:GLU:HB3	1:CS:265:ASN:HD22	1.81	0.45
1:CZ:210:SER:O	1:CZ:214:VAL:HG13	2.17	0.45
1:DD:257:HIS:CE1	1:DD:318:GLN:HG3	2.52	0.45
1:DE:13:VAL:HG11	1:DE:281:PRO:HG2	1.98	0.45
2:DK:23:LYS:NZ	2:DK:100:ASP:OD1	2.39	0.45
2:DQ:23:LYS:HG3	2:DQ:24:ASN:N	2.32	0.45
4:FP:73:VAL:HG21	4:FP:117:ILE:HD13	1.98	0.45
4:GC:23:LYS:N	4:GC:67:TYR:OH	2.49	0.45
1:AK:66:THR:HG22	2:DO:52:CYS:HB3	1.97	0.45
1:AK:180:ILE:O	1:AK:184:ILE:HG13	2.17	0.45
1:AK:256:LYS:O	1:AK:258:LYS:HG2	2.16	0.45
1:AL:59:THR:O	4:FQ:61:ASN:ND2	2.50	0.45
1:AT:126:ILE:O	1:AT:130:ILE:HG13	2.16	0.45
1:AW:169:VAL:HG22	1:AW:183:LYS:HG3	1.99	0.45
1:BV:188:LEU:HD23	1:BV:191:LEU:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BW:203:VAL:HA	1:BW:260:LEU:O	2.17	0.45
1:CC:163:GLU:HB3	1:CC:308:ARG:HG3	1.98	0.45
1:CK:270:LYS:HG2	1:CK:272:LYS:HE3	1.99	0.45
1:CP:35:GLU:O	1:CP:272:LYS:HA	2.17	0.45
1:CV:317:LYS:NZ	1:CV:319:SER:OXT	2.49	0.45
1:CW:126:ILE:O	1:CW:130:ILE:HG13	2.16	0.45
1:CY:286:ASP:HB2	1:CY:294:HIS:HB2	1.98	0.45
2:EP:69:TYR:HE1	2:EP:100:ASP:HA	1.81	0.45
2:ET:75:LEU:HD22	2:ET:84:LEU:HD13	1.98	0.45
3:FJ:104:LYS:H	3:FJ:162:ASN:ND2	2.15	0.45
4:FQ:58:LYS:HD3	4:FQ:119:PRO:HG2	1.98	0.45
4:GJ:78:GLN:HE22	4:GJ:89:TYR:HB2	1.81	0.45
5:HK:202:PHE:O	5:HK:206:ILE:HG13	2.16	0.45
1:AD:180:ILE:O	1:AD:184:ILE:HG13	2.17	0.45
1:AK:218:ALA:HA	1:AK:224:ALA:HA	1.99	0.45
1:AX:49:TRP:CZ3	1:AX:74:SER:HB3	2.51	0.45
1:BG:85:GLN:HE22	1:BI:289:SER:HB2	1.82	0.45
1:CM:14:ALA:HB2	5:IW:202:PHE:HE1	1.80	0.45
1:CT:43:TYR:HE2	1:CT:45:LYS:HE2	1.81	0.45
1:DA:78:ARG:O	1:DA:154:ASN:ND2	2.38	0.45
2:DP:37:ASP:O	2:DP:41:GLN:NE2	2.50	0.45
2:EU:123:LEU:HD21	2:EU:131:VAL:HG21	1.99	0.45
5:HF:202:PHE:O	5:HF:206:ILE:HG13	2.17	0.45
1:AB:169:VAL:HG22	1:AB:183:LYS:HG3	1.99	0.45
1:AC:174:LYS:O	1:AC:212:LYS:NZ	2.50	0.45
1:AD:66:THR:HG22	4:FO:52:ARG:HB3	1.97	0.45
1:AJ:96:GLU:O	1:AJ:100:THR:HG23	2.17	0.45
1:AJ:211:LEU:HD21	1:AM:241:ILE:HG22	1.97	0.45
1:AN:36:ASP:OD1	5:GX:214:ARG:NH1	2.48	0.45
1:BB:119:TYR:CE1	1:BB:281:PRO:HG3	2.50	0.45
1:BG:305:LEU:HD21	3:FJ:77:PHE:HE2	1.81	0.45
1:BN:178:ASP:OD1	1:BN:178:ASP:N	2.48	0.45
1:CD:84:LEU:HD13	1:CG:57:PRO:HB2	1.99	0.45
1:CF:35:GLU:O	1:CF:272:LYS:HA	2.16	0.45
1:CM:35:GLU:O	1:CM:272:LYS:HA	2.16	0.45
1:CR:67:ILE:HG13	1:CU:296:TYR:HE2	1.82	0.45
1:CX:96:GLU:O	1:CX:100:THR:HG23	2.17	0.45
1:CY:80:ASN:ND2	1:CY:153:PRO:O	2.49	0.45
2:DU:136:LYS:HD3	2:DU:155:VAL:HG21	1.97	0.45
2:DV:69:TYR:CZ	2:DV:70:LYS:HE2	2.51	0.45
2:EE:137:LEU:HD11	2:EE:159:ALA:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:EV:180:ASN:O	2:EW:180:ASN:ND2	2.45	0.45
4:GF:51:THR:HG21	4:GF:180:LYS:HE3	1.98	0.45
4:GJ:149:LEU:HD13	4:GJ:181:VAL:HG21	1.97	0.45
1:AH:49:TRP:CE3	1:AH:74:SER:HB3	2.52	0.45
1:AL:96:GLU:O	1:AL:100:THR:HG23	2.17	0.45
1:AN:70:ILE:HD11	1:AR:86:TYR:HD2	1.80	0.45
1:AP:35:GLU:O	1:AP:272:LYS:HA	2.16	0.45
1:AZ:181:PHE:CD1	1:AZ:184:ILE:HD12	2.52	0.45
1:BB:169:VAL:HG22	1:BB:183:LYS:HG3	1.99	0.45
1:BD:20:VAL:O	5:HN:213:ARG:NH2	2.34	0.45
1:BF:143:LYS:HE3	4:FU:40:ASP:HB2	1.99	0.45
1:BL:133:PHE:CD2	1:BL:301:LEU:HD22	2.52	0.45
1:BP:135:LEU:HD23	1:BP:254:LEU:HB2	1.98	0.45
1:BS:16:ILE:HD11	1:BS:120:LYS:HE3	1.98	0.45
1:BZ:49:TRP:CZ3	1:BZ:74:SER:HB3	2.51	0.45
1:CG:77:VAL:HG11	1:CG:305:LEU:HD13	1.98	0.45
1:CN:89:ARG:HH21	1:CN:112:LEU:HD21	1.81	0.45
1:CP:152:LEU:HD21	2:ER:105:SER:HA	1.99	0.45
1:CR:49:TRP:CE3	1:CR:74:SER:HB3	2.52	0.45
2:DG:23:LYS:N	2:DG:67:TYR:OH	2.47	0.45
2:DH:167:THR:HB	2:DH:170:LEU:HB3	1.99	0.45
2:EX:77:PHE:HD2	4:GE:138:LYS:HG3	1.81	0.45
4:FP:140:LYS:HD3	4:FP:161:ILE:HD13	1.99	0.45
4:GD:51:THR:HG21	4:GD:180:LYS:HE3	1.97	0.45
1:AF:49:TRP:CZ3	1:AF:74:SER:HB3	2.51	0.45
1:AG:194:GLY:HA3	2:DI:36:ILE:HG23	1.97	0.45
1:AK:231:GLU:O	1:AK:235:ILE:HG13	2.17	0.45
1:AN:307:THR:HG21	2:DQ:34:ASN:HB2	1.98	0.45
1:AW:35:GLU:O	1:AW:272:LYS:HA	2.17	0.45
1:AY:79:LEU:HD11	1:AY:305:LEU:HB2	1.97	0.45
1:BF:152:LEU:HD21	2:EB:105:SER:HA	1.98	0.45
1:BJ:135:LEU:HD23	1:BJ:254:LEU:HB2	1.98	0.45
1:BN:49:TRP:CE3	1:BN:74:SER:HB3	2.52	0.45
1:BQ:96:GLU:O	1:BQ:100:THR:HG23	2.17	0.45
1:BS:194:GLY:HA3	2:ES:36:ILE:HG21	1.98	0.45
1:BY:133:PHE:CD2	1:BY:301:LEU:HD22	2.52	0.45
1:CB:96:GLU:O	1:CB:100:THR:HG23	2.17	0.45
1:CT:169:VAL:HG22	1:CT:183:LYS:HG3	1.98	0.45
2:EP:56:LYS:HD2	2:EQ:56:LYS:HA	1.98	0.45
2:EZ:23:LYS:NZ	2:EZ:100:ASP:OD1	2.46	0.45
4:FW:51:THR:HG23	4:FW:126:GLY:HA2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:GC:161:ILE:HA	4:GC:186:ASN:HA	1.98	0.45
5:IB:211:LYS:HG3	5:IB:214:ARG:HH21	1.82	0.45
5:IF:190:LEU:HG	5:IF:209:THR:HG23	1.99	0.45
1:AE:41:MET:HE2	1:AE:83:LYS:H	1.82	0.45
1:AH:101:SER:OG	1:AH:102:ASP:N	2.50	0.45
1:AH:231:GLU:O	1:AH:235:ILE:HG13	2.17	0.45
1:AX:67:ILE:HG13	1:DD:296:TYR:HE2	1.82	0.45
1:AX:126:ILE:O	1:AX:130:ILE:HG13	2.17	0.45
1:AX:212:LYS:HA	1:AX:215:LYS:HE3	1.99	0.45
1:BO:35:GLU:O	1:BO:272:LYS:HA	2.17	0.45
1:CM:28:TRP:O	1:CM:262:TYR:OH	2.30	0.45
1:CQ:257:HIS:CE1	1:CQ:318:GLN:HG3	2.52	0.45
1:CR:96:GLU:O	1:CR:100:THR:HG23	2.16	0.45
1:CV:96:GLU:O	1:CV:100:THR:HG23	2.17	0.45
1:CY:107:ASP:OD2	1:CY:110:ASN:ND2	2.40	0.45
2:DX:58:LYS:H	2:DX:115:ASN:ND2	2.15	0.45
2:EP:75:LEU:HD22	2:EP:84:LEU:HD13	1.98	0.45
2:FC:63:PRO:HB2	2:FC:85:GLU:HG2	1.99	0.45
2:FG:134:GLY:HA2	4:GI:77:ILE:HD13	1.99	0.45
4:FN:37:GLU:HG3	4:FN:38:PHE:H	1.82	0.45
4:FV:149:LEU:HD13	4:FV:181:VAL:HG21	1.99	0.45
4:GD:144:ASN:OD1	4:GD:148:ALA:N	2.42	0.45
5:IU:200:THR:O	5:IU:204:GLN:HG2	2.17	0.45
1:AC:180:ILE:O	1:AC:184:ILE:HG13	2.17	0.44
1:AK:49:TRP:CZ3	1:AK:74:SER:HB3	2.52	0.44
1:AN:70:ILE:HD11	1:AR:86:TYR:CD2	2.52	0.44
1:AW:124:SER:O	1:AW:128:LYS:HG3	2.17	0.44
1:AZ:207:PRO:O	1:AZ:211:LEU:HG	2.17	0.44
1:BI:49:TRP:CZ3	1:BI:74:SER:HB3	2.52	0.44
1:BJ:92:LYS:NZ	1:BJ:95:SER:OG	2.36	0.44
1:CB:49:TRP:CZ3	1:CB:74:SER:HB3	2.52	0.44
1:CC:47:VAL:HG22	1:CC:76:VAL:HG22	1.99	0.44
1:CH:169:VAL:HG22	1:CH:183:LYS:HG3	1.99	0.44
1:CS:169:VAL:HG22	1:CS:183:LYS:HG3	1.99	0.44
1:DE:196:GLU:HB3	1:DE:265:ASN:HD22	1.82	0.44
2:DT:133:PRO:HG3	2:DT:161:SER:HA	1.99	0.44
2:DY:77:PHE:HD2	4:FS:138:LYS:HE2	1.83	0.44
2:EN:138:ASN:HD22	2:EN:153:LYS:HG2	1.81	0.44
2:EO:123:LEU:HD13	2:EO:173:VAL:HG11	1.98	0.44
2:EY:75:LEU:HD22	2:EY:84:LEU:HD13	1.99	0.44
2:FC:75:LEU:HD22	2:FC:84:LEU:HD13	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:FF:133:PRO:HG3	2:FF:161:SER:HA	1.97	0.44
2:FG:137:LEU:HD11	2:FG:159:ALA:HB2	1.99	0.44
3:FJ:180:ILE:HG12	3:FJ:203:TYR:CE1	2.52	0.44
4:GC:43:VAL:O	4:GC:43:VAL:HG13	2.17	0.44
5:HV:200:THR:O	5:HV:204:GLN:HG2	2.17	0.44
1:AA:49:TRP:CZ3	1:AA:74:SER:HB3	2.52	0.44
1:AP:135:LEU:HD23	1:AP:254:LEU:HB2	2.00	0.44
1:AP:181:PHE:O	1:AP:185:GLU:HG3	2.18	0.44
1:AQ:211:LEU:O	1:AQ:214:VAL:HG22	2.18	0.44
1:AS:35:GLU:O	1:AS:272:LYS:HA	2.17	0.44
1:BA:137:GLY:HA3	1:BA:160:ASN:OD1	2.17	0.44
1:BJ:89:ARG:HH21	1:BJ:112:LEU:HD21	1.81	0.44
1:BP:89:ARG:HH21	1:BP:112:LEU:HD13	1.82	0.44
1:BU:169:VAL:HG22	1:BU:183:LYS:HG3	1.99	0.44
1:BV:49:TRP:CZ3	1:BV:74:SER:HB3	2.51	0.44
1:BY:197:PHE:HD1	1:BY:243:ASN:HB2	1.82	0.44
1:CB:210:SER:O	1:CB:214:VAL:HG13	2.17	0.44
1:CC:49:TRP:CE3	1:CC:74:SER:HB3	2.52	0.44
1:CH:49:TRP:CH2	1:CH:74:SER:HB3	2.52	0.44
1:CM:23:PRO:HB2	1:CM:25:MET:HG2	1.98	0.44
1:CN:87:LYS:NZ	2:EQ:53:THR:O	2.36	0.44
1:CO:49:TRP:CH2	1:CO:74:SER:HB3	2.52	0.44
1:CQ:96:GLU:O	1:CQ:100:THR:HG23	2.17	0.44
1:CV:20:VAL:HG23	5:JF:213:ARG:HH22	1.83	0.44
1:DD:288:ASP:OD1	1:DD:289:SER:N	2.42	0.44
2:DT:125:LYS:NZ	2:DT:169:ASP:OD1	2.46	0.44
2:ER:30:GLY:O	2:ER:31:LEU:HD23	2.18	0.44
2:EZ:23:LYS:N	2:EZ:67:TYR:OH	2.51	0.44
2:FH:77:PHE:HD2	4:GJ:138:LYS:HE2	1.83	0.44
5:JA:211:LYS:O	5:JA:214:ARG:HG2	2.16	0.44
1:AH:108:ILE:HG22	4:FL:27:HIS:HE1	1.83	0.44
1:AK:96:GLU:O	1:AK:100:THR:HG23	2.17	0.44
1:AM:181:PHE:O	1:AM:185:GLU:HG3	2.18	0.44
1:AP:194:GLY:HA3	4:FN:36:ASN:HB2	1.99	0.44
1:AV:196:GLU:HB3	1:AV:265:ASN:HD22	1.82	0.44
1:BC:66:THR:HG22	2:EB:52:CYS:SG	2.57	0.44
1:BM:84:LEU:HB3	1:BP:57:PRO:HB2	1.99	0.44
1:BP:80:ASN:HB2	1:BP:155:MET:HG3	1.99	0.44
1:BR:178:ASP:OD1	1:BR:179:LYS:N	2.50	0.44
1:BS:169:VAL:HG22	1:BS:183:LYS:HG3	1.99	0.44
1:CD:96:GLU:O	1:CD:100:THR:HG23	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CG:80:ASN:ND2	1:CG:154:ASN:HB2	2.31	0.44
1:CG:164:GLN:HE22	1:CG:308:ARG:HA	1.81	0.44
1:CM:169:VAL:HG22	1:CM:183:LYS:HG3	1.99	0.44
1:CQ:174:LYS:O	1:CQ:212:LYS:NZ	2.50	0.44
1:DB:20:VAL:HG23	5:JL:213:ARG:HH22	1.82	0.44
1:DD:25:MET:HE1	1:DD:130:ILE:HG22	1.98	0.44
2:DN:69:TYR:HB2	2:DN:101:ILE:HD12	1.99	0.44
4:GA:23:LYS:N	4:GA:67:TYR:OH	2.50	0.44
5:HM:200:THR:O	5:HM:204:GLN:HG2	2.17	0.44
5:JG:211:LYS:O	5:JG:214:ARG:HG2	2.16	0.44
1:AC:169:VAL:HG22	1:AC:183:LYS:HG3	1.99	0.44
1:AD:126:ILE:O	1:AD:130:ILE:HG13	2.17	0.44
1:AD:187:GLY:HA3	1:AD:312:LEU:HD13	1.99	0.44
1:AI:196:GLU:HB3	1:AI:265:ASN:HD22	1.82	0.44
1:AP:286:ASP:HB2	1:AP:294:HIS:HB2	1.98	0.44
1:AV:16:ILE:HD12	1:AV:116:ALA:HB1	1.99	0.44
1:BC:165:ILE:HD13	1:BC:191:LEU:HD23	1.99	0.44
1:BN:143:LYS:HE3	4:FX:37:GLU:HG2	2.00	0.44
1:BO:96:GLU:O	1:BO:100:THR:HG23	2.18	0.44
1:BS:188:LEU:HD23	1:BS:191:LEU:HD12	2.00	0.44
1:BU:107:ASP:OD2	1:BU:110:ASN:ND2	2.36	0.44
1:BY:205:VAL:HG12	1:BY:259:ILE:HG23	1.98	0.44
1:CG:66:THR:HG22	4:GC:52:ARG:HB3	1.99	0.44
1:CZ:8:TYR:CD2	1:CZ:93:GLN:HG3	2.52	0.44
1:CZ:289:SER:HB2	1:DA:85:GLN:HE22	1.82	0.44
1:DB:96:GLU:O	1:DB:100:THR:HG23	2.18	0.44
2:DG:69:TYR:CZ	2:DG:70:LYS:HE2	2.52	0.44
2:EJ:165:LYS:HE3	2:EJ:168:GLU:HA	2.00	0.44
2:EO:74:LYS:HE2	2:EO:89:GLY:HA3	1.99	0.44
2:EY:63:PRO:HB2	2:EY:85:GLU:HG2	1.99	0.44
4:FY:22:MET:HB3	4:FY:23:LYS:H	1.55	0.44
4:FZ:37:GLU:HG3	4:FZ:39:ARG:H	1.83	0.44
5:GZ:202:PHE:CE2	5:GZ:206:ILE:HD11	2.53	0.44
5:HB:200:THR:O	5:HB:204:GLN:HG2	2.18	0.44
1:AI:231:GLU:O	1:AI:235:ILE:HG13	2.16	0.44
1:AJ:121:LEU:HB3	1:AM:51:ALA:HB2	1.99	0.44
1:AM:84:LEU:HB3	1:AP:57:PRO:HB2	1.99	0.44
1:AT:317:LYS:HE2	1:AT:319:SER:HB2	1.98	0.44
1:BA:79:LEU:HD11	1:BA:305:LEU:HB2	1.99	0.44
1:BR:205:VAL:HG12	1:BR:259:ILE:HG23	2.00	0.44
1:BU:256:LYS:HG2	1:BU:257:HIS:CD2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BY:119:TYR:CE1	1:BY:281:PRO:HG3	2.52	0.44
1:CA:16:ILE:HD11	1:CA:120:LYS:HE3	2.00	0.44
1:CI:39:LEU:O	1:CI:274:SER:OG	2.26	0.44
1:CK:80:ASN:ND2	1:CK:153:PRO:O	2.51	0.44
1:CM:203:VAL:HA	1:CM:260:LEU:O	2.18	0.44
1:DC:277:MET:HA	1:DC:300:VAL:HB	1.98	0.44
2:DF:156:ASN:HB2	2:DF:178:PHE:O	2.17	0.44
2:DN:137:LEU:HD11	2:DN:159:ALA:HB2	1.99	0.44
2:DX:123:LEU:HD21	2:DX:131:VAL:HG21	1.99	0.44
2:FC:23:LYS:N	2:FC:67:TYR:OH	2.49	0.44
4:GI:26:GLN:NE2	4:GI:28:ASP:OD1	2.50	0.44
4:GJ:35:SER:O	4:GJ:41:LYS:HD2	2.18	0.44
1:AD:289:SER:HB2	1:AE:85:GLN:HE22	1.82	0.44
1:AI:123:SER:O	1:AI:127:ILE:HG13	2.17	0.44
1:AL:78:ARG:HB3	1:AL:154:ASN:HD22	1.83	0.44
1:AM:130:ILE:O	1:AM:134:VAL:HG23	2.18	0.44
1:AO:57:PRO:HB2	1:AS:84:LEU:HB3	2.00	0.44
1:AS:180:ILE:O	1:AS:184:ILE:HG13	2.17	0.44
1:AT:180:ILE:O	1:AT:184:ILE:HG13	2.18	0.44
1:AZ:63:GLU:HG2	2:DW:59:ILE:HD11	1.99	0.44
1:BA:13:VAL:HG11	1:BA:281:PRO:HG2	1.99	0.44
1:BC:62:ASN:HB2	3:FJ:156:TYR:CZ	2.52	0.44
1:BD:152:LEU:HD11	4:FU:112:SER:HA	2.00	0.44
1:BG:35:GLU:O	1:BG:272:LYS:HA	2.18	0.44
1:BJ:96:GLU:O	1:BJ:100:THR:HG23	2.17	0.44
1:BJ:165:ILE:HD13	1:BJ:191:LEU:HD23	1.99	0.44
1:BN:317:LYS:NZ	1:BN:319:SER:OXT	2.36	0.44
1:BO:203:VAL:HG13	1:BO:261:ILE:HG12	2.00	0.44
1:BX:161:MET:SD	2:EP:31:LEU:HD21	2.58	0.44
1:CC:203:VAL:HA	1:CC:260:LEU:O	2.18	0.44
1:CE:35:GLU:O	1:CE:272:LYS:HA	2.18	0.44
1:CE:240:ALA:HB2	1:CI:214:VAL:HG11	1.99	0.44
1:CI:77:VAL:HG11	1:CI:305:LEU:HD13	1.99	0.44
1:CJ:277:MET:HA	1:CJ:300:VAL:HB	2.00	0.44
1:CM:96:GLU:O	1:CM:100:THR:HG23	2.17	0.44
1:CN:157:GLY:N	1:CN:160:ASN:OD1	2.47	0.44
1:CT:8:TYR:CD2	1:CT:93:GLN:HG3	2.53	0.44
1:CU:205:VAL:HG12	1:CU:259:ILE:HG23	2.00	0.44
1:CW:257:HIS:CE1	1:CW:318:GLN:HG3	2.51	0.44
1:CX:277:MET:HA	1:CX:300:VAL:HB	1.99	0.44
1:DA:13:VAL:HG11	1:DA:281:PRO:HG2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DA:152:LEU:HD21	2:FH:105:SER:HA	1.99	0.44
1:DE:66:THR:HG22	2:FF:52:CYS:HB3	2.00	0.44
1:DE:205:VAL:HG12	1:DE:259:ILE:HG23	2.00	0.44
2:DV:156:ASN:HB3	2:DV:178:PHE:HD2	1.82	0.44
2:EI:23:LYS:NZ	2:EI:100:ASP:OD1	2.42	0.44
2:EU:75:LEU:HD22	2:EU:84:LEU:HD13	2.00	0.44
4:FZ:133:SER:HB3	4:FZ:177:TYR:CE1	2.53	0.44
1:AB:35:GLU:O	1:AB:272:LYS:HA	2.18	0.44
1:AH:16:ILE:HD12	1:AH:116:ALA:HB1	1.98	0.44
1:AI:35:GLU:O	1:AI:272:LYS:HA	2.18	0.44
1:AO:240:ALA:HB2	1:AS:214:VAL:HG11	1.99	0.44
1:AS:162:PRO:O	2:DZ:31:LEU:HD21	2.18	0.44
1:BA:196:GLU:HB3	1:BA:265:ASN:HD22	1.83	0.44
1:BD:96:GLU:O	1:BD:100:THR:HG23	2.18	0.44
1:BY:41:MET:HA	1:BY:81:TYR:O	2.18	0.44
1:CA:13:VAL:HG11	1:CA:281:PRO:HG2	2.00	0.44
1:CC:57:PRO:HB2	1:CF:84:LEU:HB3	1.99	0.44
1:CG:20:VAL:HG23	5:IQ:213:ARG:HH22	1.82	0.44
1:CJ:66:THR:HG22	2:ER:52:CYS:HB3	2.00	0.44
1:CQ:210:SER:O	1:CQ:214:VAL:HG13	2.17	0.44
2:DW:133:PRO:HG3	2:DW:161:SER:HA	1.99	0.44
4:FK:69:TYR:HB2	4:FK:108:ILE:HD12	1.99	0.44
5:IC:200:THR:O	5:IC:204:GLN:HG2	2.18	0.44
1:AE:231:GLU:O	1:AE:235:ILE:HG13	2.18	0.44
1:AL:209:THR:O	1:AL:213:LEU:HG	2.18	0.44
1:AL:240:ALA:HB2	1:AW:214:VAL:HG11	1.98	0.44
1:AO:194:GLY:HA3	4:FP:36:ASN:HD22	1.81	0.44
1:AX:180:ILE:O	1:AX:184:ILE:HG13	2.17	0.44
1:BD:135:LEU:HD23	1:BD:254:LEU:HB2	2.00	0.44
1:BO:119:TYR:CE1	1:BO:281:PRO:HG3	2.53	0.44
1:BQ:45:LYS:HG2	1:BQ:78:ARG:HB2	1.99	0.44
1:BZ:89:ARG:HH21	1:BZ:112:LEU:HD21	1.83	0.44
1:CB:91:LEU:HD21	1:CB:112:LEU:HD13	1.98	0.44
1:DA:66:THR:HG22	2:FB:52:CYS:HB3	1.99	0.44
1:DB:214:VAL:HG11	1:DD:240:ALA:HB2	2.00	0.44
2:DP:167:THR:HB	2:DP:170:LEU:HB3	2.00	0.44
2:DQ:123:LEU:HD13	2:DQ:173:VAL:HG11	1.99	0.44
2:FD:23:LYS:N	2:FD:67:TYR:OH	2.51	0.44
4:FW:173:SER:HB3	4:FW:176:VAL:HB	2.00	0.44
4:GD:43:VAL:HG13	4:GD:43:VAL:O	2.17	0.44
1:AO:205:VAL:HG12	1:AO:259:ILE:HG23	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AO:277:MET:HA	1:AO:300:VAL:HB	2.00	0.44
1:AQ:49:TRP:CE3	1:AQ:74:SER:HB3	2.53	0.44
1:BD:119:TYR:CE1	1:BD:281:PRO:HG3	2.53	0.44
1:BF:20:VAL:O	5:HP:213:ARG:NH2	2.43	0.44
1:BH:174:LYS:HE2	1:BH:318:GLN:HE21	1.82	0.44
1:BO:60:ILE:HG23	1:BU:290:THR:HG22	2.00	0.44
1:CA:205:VAL:HG12	1:CA:259:ILE:HG23	1.99	0.44
1:CB:169:VAL:HG22	1:CB:183:LYS:HG3	2.00	0.44
1:CO:169:VAL:HG22	1:CO:183:LYS:HG3	2.00	0.44
1:CR:57:PRO:HB2	1:CU:84:LEU:HB3	1.99	0.44
1:DD:96:GLU:O	1:DD:100:THR:HG23	2.17	0.44
2:DY:181:ARG:NH1	2:DZ:94:LEU:O	2.49	0.44
2:EC:133:PRO:HG3	2:EC:161:SER:HA	1.99	0.44
2:EQ:76:SER:HB3	2:EQ:87:GLU:HG2	1.99	0.44
4:FU:141:LEU:HD11	4:FU:165:ALA:HB2	2.00	0.44
4:FZ:127:TYR:HE1	4:FZ:170:LYS:HZ3	1.65	0.44
4:GD:166:LEU:HD12	4:GD:180:LYS:HE2	1.99	0.44
5:GS:202:PHE:O	5:GS:206:ILE:HG13	2.17	0.44
5:GX:211:LYS:O	5:GX:214:ARG:HG2	2.17	0.44
1:AC:130:ILE:O	1:AC:134:VAL:HG23	2.18	0.43
1:AF:96:GLU:O	1:AF:100:THR:HG23	2.18	0.43
1:AJ:35:GLU:O	1:AJ:272:LYS:HA	2.17	0.43
1:AN:164:GLN:HE22	1:AN:308:ARG:HA	1.82	0.43
1:AO:96:GLU:O	1:AO:100:THR:HG23	2.18	0.43
1:AS:197:PHE:CD2	1:AS:243:ASN:HB2	2.53	0.43
1:AX:79:LEU:HD11	1:AX:305:LEU:HB2	1.99	0.43
1:BO:135:LEU:HD21	1:BO:255:LEU:HG	2.00	0.43
1:BQ:135:LEU:HD23	1:BQ:254:LEU:HB2	1.99	0.43
1:BT:96:GLU:O	1:BT:100:THR:HG23	2.18	0.43
1:BW:87:LYS:NZ	2:EN:53:THR:O	2.35	0.43
1:BY:16:ILE:HD12	1:BY:116:ALA:HB1	2.00	0.43
1:CA:16:ILE:HD12	1:CA:116:ALA:HB1	2.00	0.43
1:CD:196:GLU:HB3	1:CD:265:ASN:HD22	1.82	0.43
1:CE:80:ASN:ND2	1:CE:153:PRO:O	2.51	0.43
1:CF:101:SER:OG	1:CF:102:ASP:N	2.51	0.43
1:CM:164:GLN:HE22	1:CM:308:ARG:HA	1.83	0.43
1:CR:87:LYS:NZ	2:FC:53:THR:O	2.35	0.43
1:CV:158:LEU:HB3	1:CV:260:LEU:HD21	2.00	0.43
1:CX:14:ALA:HB2	5:JH:202:PHE:HE1	1.82	0.43
1:CZ:203:VAL:HG22	1:CZ:261:ILE:HG23	2.00	0.43
2:FB:133:PRO:HG3	2:FB:161:SER:HA	1.98	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:FO:162:ASN:HB2	4:FO:184:PHE:O	2.17	0.43
4:GI:144:ASN:HD21	4:GI:148:ALA:HB3	1.83	0.43
5:GQ:202:PHE:O	5:GQ:206:ILE:HG13	2.17	0.43
5:IH:200:THR:O	5:IH:204:GLN:HG2	2.17	0.43
1:AL:231:GLU:O	1:AL:235:ILE:HG13	2.18	0.43
1:AP:13:VAL:HG11	1:AP:281:PRO:HG2	2.00	0.43
1:AR:35:GLU:O	1:AR:272:LYS:HA	2.18	0.43
1:AS:55:ALA:O	1:AZ:86:TYR:OH	2.27	0.43
1:AU:49:TRP:CE3	1:AU:74:SER:HB3	2.53	0.43
1:AV:229:LYS:O	1:AV:233:VAL:HG23	2.19	0.43
1:BA:89:ARG:HH21	1:BA:112:LEU:HD21	1.81	0.43
1:BG:13:VAL:HG11	1:BG:281:PRO:HG2	1.98	0.43
1:BH:14:ALA:HB2	5:HR:202:PHE:HE1	1.83	0.43
1:BQ:159:LEU:HD12	1:BQ:260:LEU:HD13	1.99	0.43
1:BS:49:TRP:CZ3	1:BS:74:SER:HB3	2.53	0.43
1:BT:169:VAL:HG22	1:BT:183:LYS:HG3	1.98	0.43
1:BU:43:TYR:HB2	1:BU:78:ARG:HG3	2.00	0.43
1:BX:79:LEU:HD11	1:BX:305:LEU:HB2	2.00	0.43
1:CR:34:ILE:HA	1:CR:271:PHE:O	2.18	0.43
1:CW:161:MET:HG3	2:FE:31:LEU:HD11	2.00	0.43
2:DJ:56:LYS:HD2	4:FK:56:PHE:HD1	1.83	0.43
2:EO:165:LYS:HE3	2:EO:168:GLU:HA	2.00	0.43
2:EZ:37:ASP:O	2:EZ:41:GLN:NE2	2.51	0.43
2:FD:181:ARG:NH1	2:FE:94:LEU:O	2.50	0.43
4:FL:73:VAL:HG21	4:FL:117:ILE:HD13	1.98	0.43
4:FM:140:LYS:HD3	4:FM:161:ILE:HG21	2.00	0.43
4:GG:43:VAL:HG13	4:GG:43:VAL:O	2.18	0.43
4:GH:43:VAL:O	4:GH:43:VAL:HG13	2.18	0.43
5:GU:189:LEU:HD11	5:GU:206:ILE:HG12	2.00	0.43
1:AF:180:ILE:O	1:AF:184:ILE:HG13	2.18	0.43
1:AF:203:VAL:HG13	1:AF:261:ILE:HG12	1.99	0.43
1:AH:169:VAL:HG22	1:AH:183:LYS:HG3	2.01	0.43
1:AN:59:THR:O	2:DR:61:ASN:ND2	2.52	0.43
1:AP:89:ARG:HH21	1:AP:112:LEU:HD13	1.83	0.43
1:AV:49:TRP:CZ3	1:AV:74:SER:HB3	2.53	0.43
1:AY:96:GLU:O	1:AY:100:THR:HG23	2.18	0.43
1:BR:3:LEU:HD23	2:EG:19:GLN:HG3	1.99	0.43
1:BR:78:ARG:O	1:BR:154:ASN:ND2	2.43	0.43
1:BW:49:TRP:CE3	1:BW:74:SER:HB3	2.52	0.43
1:CA:113:LEU:HD11	1:CJ:49:TRP:CZ3	2.53	0.43
1:CA:211:LEU:O	1:CA:214:VAL:HG22	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:307:THR:HG22	2:EM:32:LEU:HB2	2.01	0.43
1:CK:210:SER:O	1:CK:214:VAL:HG13	2.18	0.43
1:CO:16:ILE:HD11	1:CO:120:LYS:HE3	2.00	0.43
1:CT:240:ALA:HB2	1:CX:214:VAL:HG11	2.00	0.43
1:CU:203:VAL:HG22	1:CU:261:ILE:HG23	2.00	0.43
1:CY:96:GLU:O	1:CY:100:THR:HG23	2.17	0.43
1:CZ:43:TYR:HE2	1:CZ:45:LYS:HE2	1.83	0.43
2:DL:123:LEU:HD13	2:DL:173:VAL:HG11	1.99	0.43
2:DT:183:ILE:HD12	4:FP:188:ALA:HB3	1.99	0.43
2:EC:123:LEU:HD13	2:EC:173:VAL:HG11	1.99	0.43
4:FN:142:ILE:HG13	4:FN:152:VAL:HG22	2.00	0.43
5:IK:200:THR:O	5:IK:204:GLN:HG2	2.18	0.43
5:JE:189:LEU:HD11	5:JE:206:ILE:HG12	1.99	0.43
1:AA:126:ILE:O	1:AA:130:ILE:HG13	2.19	0.43
1:AB:210:SER:O	1:AB:214:VAL:HG13	2.18	0.43
1:AJ:209:THR:O	1:AJ:213:LEU:HG	2.18	0.43
1:AL:180:ILE:O	1:AL:184:ILE:HG13	2.18	0.43
1:AP:208:ALA:O	1:AP:212:LYS:HG3	2.18	0.43
1:AX:257:HIS:CE1	1:AX:318:GLN:HG3	2.54	0.43
1:AY:211:LEU:HD21	1:AZ:241:ILE:HG22	2.00	0.43
1:BA:161:MET:SD	2:DT:31:LEU:HD21	2.58	0.43
1:BG:49:TRP:CZ3	1:BG:74:SER:HB3	2.54	0.43
1:BJ:165:ILE:HD12	1:BJ:165:ILE:H	1.84	0.43
1:BJ:186:ALA:O	1:BJ:190:LYS:HG3	2.19	0.43
1:BU:159:LEU:HD12	1:BU:260:LEU:HD13	1.99	0.43
1:BY:48:LYS:HD2	4:FZ:32:LEU:HD22	2.00	0.43
1:CC:34:ILE:HA	1:CC:271:PHE:O	2.18	0.43
1:CC:317:LYS:HE2	1:CC:319:SER:HB2	2.00	0.43
1:CP:16:ILE:HD11	1:CP:120:LYS:HE3	2.00	0.43
1:CP:79:LEU:HD11	1:CP:305:LEU:HB2	1.99	0.43
1:CX:163:GLU:HB3	1:CX:308:ARG:HG3	1.99	0.43
1:DC:45:LYS:NZ	4:FS:28:ASP:OD2	2.46	0.43
2:DO:69:TYR:HB2	2:DO:101:ILE:HD12	2.01	0.43
2:EE:125:LYS:HD2	2:EE:169:ASP:HA	2.00	0.43
2:EG:137:LEU:HD11	2:EG:159:ALA:HB2	2.00	0.43
2:FH:123:LEU:HD21	2:FH:131:VAL:HG21	1.99	0.43
1:AE:124:SER:O	1:AE:128:LYS:HG3	2.18	0.43
1:AL:126:ILE:O	1:AL:130:ILE:HG13	2.18	0.43
1:AO:126:ILE:O	1:AO:130:ILE:HG13	2.19	0.43
1:AR:205:VAL:HG12	1:AR:259:ILE:HG23	2.01	0.43
1:AU:124:SER:O	1:AU:128:LYS:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AV:35:GLU:O	1:AV:272:LYS:HA	2.17	0.43
1:AV:180:ILE:O	1:AV:184:ILE:HG13	2.17	0.43
1:BH:49:TRP:CE3	1:BH:74:SER:HB3	2.53	0.43
1:BI:49:TRP:CH2	1:BI:74:SER:HB3	2.54	0.43
1:BJ:35:GLU:O	1:BJ:272:LYS:HA	2.18	0.43
1:BK:96:GLU:O	1:BK:100:THR:HG23	2.18	0.43
1:BY:49:TRP:CZ3	1:BY:74:SER:HB3	2.54	0.43
1:CG:257:HIS:CE1	1:CG:318:GLN:HG3	2.53	0.43
1:CJ:79:LEU:HD11	1:CJ:305:LEU:HB2	2.00	0.43
1:CM:80:ASN:ND2	1:CM:154:ASN:HB2	2.33	0.43
2:ED:31:LEU:HB3	2:ED:34:ASN:ND2	2.33	0.43
2:EO:153:LYS:HG3	2:EO:154:SER:H	1.84	0.43
4:FS:43:VAL:HG13	4:FS:43:VAL:O	2.18	0.43
4:FY:93:VAL:HG21	4:FY:117:ILE:HD11	2.01	0.43
4:FZ:64:PHE:CZ	4:FZ:108:ILE:HD11	2.52	0.43
4:FZ:71:ARG:NH1	4:FZ:146:ASP:O	2.47	0.43
5:JJ:200:THR:O	5:JJ:204:GLN:HG2	2.18	0.43
1:AD:35:GLU:O	1:AD:272:LYS:HA	2.19	0.43
1:AD:80:ASN:ND2	1:AD:153:PRO:O	2.52	0.43
1:AD:241:ILE:HG22	1:AP:211:LEU:HD21	2.00	0.43
1:AF:290:THR:HG22	1:AG:60:ILE:HG23	2.01	0.43
1:AS:43:TYR:HE2	1:AS:45:LYS:HE2	1.83	0.43
1:AX:96:GLU:O	1:AX:100:THR:HG23	2.18	0.43
1:BE:203:VAL:HG22	1:BE:261:ILE:HG23	2.01	0.43
1:BM:214:VAL:HG21	1:BP:240:ALA:HB2	2.00	0.43
1:BP:206:ASP:OD1	1:BP:209:THR:OG1	2.27	0.43
1:BU:158:LEU:HB3	1:BU:260:LEU:HD21	2.00	0.43
1:BY:35:GLU:O	1:BY:272:LYS:HA	2.18	0.43
1:CE:286:ASP:HB2	1:CE:294:HIS:HB2	2.01	0.43
1:CJ:77:VAL:HG21	2:ER:32:LEU:HD23	2.00	0.43
1:CR:157:GLY:N	1:CR:160:ASN:OD1	2.43	0.43
1:CS:113:LEU:HD11	1:CV:49:TRP:CE3	2.53	0.43
1:CU:34:ILE:HG12	1:CU:271:PHE:HB3	2.00	0.43
1:CZ:77:VAL:HG21	2:DX:32:LEU:HD23	2.00	0.43
2:EG:14:LYS:O	2:EG:18:ILE:HG13	2.18	0.43
4:FR:149:LEU:HD13	4:FR:181:VAL:HG21	2.00	0.43
4:FW:142:ILE:HG13	4:FW:152:VAL:HG22	2.01	0.43
4:GA:43:VAL:HG13	4:GA:43:VAL:O	2.19	0.43
4:GF:43:VAL:O	4:GF:43:VAL:HG13	2.19	0.43
4:GG:37:GLU:O	4:GG:41:LYS:HD2	2.19	0.43
5:GQ:211:LYS:O	5:GQ:215:ILE:HG13	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:GW:200:THR:O	5:GW:204:GLN:HG2	2.18	0.43
5:HE:200:THR:O	5:HE:204:GLN:HG2	2.18	0.43
5:HL:200:THR:O	5:HL:204:GLN:HG2	2.18	0.43
1:AG:66:THR:OG1	2:DI:54:SER:HB2	2.19	0.43
1:AT:16:ILE:HD11	1:AT:120:LYS:HE3	1.99	0.43
1:AY:28:TRP:HB3	1:AY:262:TYR:OH	2.18	0.43
1:BI:196:GLU:HB3	1:BI:265:ASN:HD22	1.84	0.43
1:BJ:13:VAL:HG11	1:BJ:281:PRO:HG2	1.99	0.43
1:BU:214:VAL:HG11	1:CA:240:ALA:HB2	2.00	0.43
1:BV:203:VAL:HG13	1:BV:261:ILE:HG12	2.00	0.43
1:CD:49:TRP:HH2	1:CK:111:ASN:HA	1.83	0.43
1:CE:203:VAL:HG22	1:CE:261:ILE:HG23	2.00	0.43
1:CE:226:SER:OG	1:CU:226:SER:O	2.29	0.43
1:CI:277:MET:HA	1:CI:300:VAL:HB	2.01	0.43
1:CL:164:GLN:HE22	1:CL:308:ARG:HA	1.84	0.43
2:DO:70:LYS:HA	2:DO:98:CYS:O	2.19	0.43
2:DV:74:LYS:HE2	2:DV:89:GLY:HA3	2.01	0.43
2:EN:167:THR:HG22	2:EN:168:GLU:N	2.33	0.43
4:FU:165:ALA:HA	4:FU:181:VAL:HG12	2.00	0.43
4:GA:149:LEU:HD13	4:GA:181:VAL:HG21	2.00	0.43
4:GE:43:VAL:HG13	4:GE:43:VAL:O	2.18	0.43
5:JD:200:THR:O	5:JD:204:GLN:HG2	2.19	0.43
1:AI:126:ILE:O	1:AI:130:ILE:HG13	2.18	0.43
1:AJ:165:ILE:HD13	1:AJ:191:LEU:HD23	2.01	0.43
1:AK:174:LYS:HE2	1:AK:318:GLN:HG2	2.01	0.43
1:AS:41:MET:HE2	1:AS:41:MET:HB2	1.90	0.43
1:AX:59:THR:O	2:DX:61:ASN:ND2	2.52	0.43
1:AZ:126:ILE:O	1:AZ:130:ILE:HG13	2.18	0.43
1:BA:169:VAL:HB	1:BA:316:ILE:HA	2.00	0.43
1:BH:16:ILE:HD12	1:BH:116:ALA:HB1	1.99	0.43
1:BL:70:ILE:HD11	1:BW:86:TYR:CD2	2.54	0.43
1:BQ:211:LEU:O	1:BQ:214:VAL:HG22	2.19	0.43
1:BX:55:ALA:HA	1:CO:141:ILE:HD13	1.99	0.43
1:BY:59:THR:O	2:EN:61:ASN:ND2	2.51	0.43
1:CE:158:LEU:HB3	1:CE:260:LEU:HD21	2.00	0.43
1:CF:70:ILE:HD11	1:CT:86:TYR:HD2	1.83	0.43
1:CF:161:MET:SD	2:FD:31:LEU:HD21	2.58	0.43
1:CI:35:GLU:O	1:CI:272:LYS:HA	2.19	0.43
1:CO:35:GLU:O	1:CO:272:LYS:HA	2.19	0.43
1:CO:66:THR:HG22	2:FA:52:CYS:HB3	2.00	0.43
1:CS:49:TRP:CZ3	1:CS:74:SER:HB3	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CU:158:LEU:HB3	1:CU:260:LEU:HD21	2.01	0.43
1:DC:89:ARG:HH21	1:DC:112:LEU:HD21	1.84	0.43
2:DP:137:LEU:HD11	2:DP:159:ALA:HB2	2.01	0.43
4:FS:166:LEU:HD12	4:FS:180:LYS:HE2	2.00	0.43
4:FX:93:VAL:HG21	4:FX:117:ILE:HD11	2.00	0.43
4:GB:43:VAL:HG13	4:GB:43:VAL:O	2.18	0.43
4:GE:144:ASN:HD21	4:GE:148:ALA:HB3	1.84	0.43
4:GI:43:VAL:O	4:GI:43:VAL:HG13	2.18	0.43
5:GM:211:LYS:O	5:GM:215:ILE:HG13	2.18	0.43
5:IB:215:ILE:O	5:IB:219:GLU:HG3	2.19	0.43
1:AF:78:ARG:HH21	4:FK:111:PHE:HE1	1.67	0.43
1:AH:96:GLU:O	1:AH:100:THR:HG23	2.19	0.43
1:AS:16:ILE:HD11	1:AS:120:LYS:HE3	2.01	0.43
1:AS:96:GLU:O	1:AS:100:THR:HG23	2.19	0.43
1:AT:317:LYS:HG2	1:AT:319:SER:H	1.84	0.43
1:BE:35:GLU:O	1:BE:272:LYS:HA	2.19	0.43
1:BK:226:SER:OG	1:BV:226:SER:O	2.29	0.43
1:BO:165:ILE:H	1:BO:165:ILE:HD12	1.83	0.43
1:BV:307:THR:HG22	2:EF:32:LEU:HB2	2.01	0.43
1:BX:54:ASN:ND2	2:EP:47:ASN:HD21	2.17	0.43
1:BY:290:THR:HG22	1:CK:60:ILE:HG23	2.00	0.43
1:BZ:289:SER:HB2	1:CA:85:GLN:HE22	1.84	0.43
1:CA:282:ASN:HB3	1:CA:296:TYR:HB2	2.00	0.43
1:CF:203:VAL:HG22	1:CF:261:ILE:HG23	2.00	0.43
1:CG:158:LEU:HB3	1:CG:260:LEU:HD21	2.00	0.43
1:CM:107:ASP:OD2	1:CM:110:ASN:ND2	2.39	0.43
2:DI:69:TYR:HB2	2:DI:101:ILE:HD12	2.01	0.43
5:GN:202:PHE:O	5:GN:206:ILE:HG13	2.19	0.43
1:AQ:121:LEU:O	1:AQ:125:GLU:HG2	2.19	0.43
1:AT:43:TYR:HB3	1:AT:80:ASN:ND2	2.33	0.43
1:AT:174:LYS:O	1:AT:212:LYS:NZ	2.52	0.43
1:AU:296:TYR:HE2	1:BA:67:ILE:HG13	1.83	0.43
1:AV:124:SER:O	1:AV:128:LYS:HG3	2.17	0.43
1:AV:307:THR:HG22	2:DN:32:LEU:HB2	2.00	0.43
1:BA:158:LEU:HB3	1:BA:260:LEU:HD21	2.01	0.43
1:BC:35:GLU:O	1:BC:272:LYS:HA	2.19	0.43
1:BL:260:LEU:HD23	1:BL:260:LEU:HA	1.91	0.43
1:BP:112:LEU:HD21	1:BP:292:VAL:HG22	2.00	0.43
1:BS:282:ASN:OD1	1:BS:283:GLU:N	2.52	0.43
1:BU:79:LEU:HD11	1:BU:305:LEU:HB2	1.99	0.43
1:BV:35:GLU:O	1:BV:272:LYS:HA	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BY:174:LYS:O	1:BY:212:LYS:NZ	2.52	0.43
1:CC:77:VAL:HG11	1:CC:305:LEU:HD13	2.01	0.43
1:CG:35:GLU:O	1:CG:272:LYS:HA	2.19	0.43
1:CL:35:GLU:O	1:CL:272:LYS:HA	2.19	0.43
1:CQ:286:ASP:HB2	1:CQ:294:HIS:HB2	2.01	0.43
1:CX:35:GLU:O	1:CX:272:LYS:HA	2.19	0.43
1:CX:157:GLY:N	1:CX:160:ASN:OD1	2.49	0.43
1:CY:49:TRP:CZ3	1:CY:74:SER:HB3	2.53	0.43
1:DA:96:GLU:O	1:DA:100:THR:HG23	2.19	0.43
1:DC:49:TRP:CE3	1:DC:74:SER:HB3	2.54	0.43
2:DJ:154:SER:HA	2:DJ:181:ARG:HB2	2.00	0.43
2:DT:125:LYS:HD2	2:DT:169:ASP:HA	2.01	0.43
2:DV:167:THR:HG22	2:DV:168:GLU:N	2.34	0.43
2:DY:30:GLY:O	2:DY:31:LEU:HD23	2.19	0.43
2:EH:167:THR:HB	2:EH:170:LEU:HB3	2.01	0.43
4:FS:133:SER:HB3	4:FS:177:TYR:CE1	2.54	0.43
1:AF:188:LEU:HD23	1:AF:191:LEU:HD12	2.01	0.42
1:AO:188:LEU:HD23	1:AO:191:LEU:HD12	2.00	0.42
1:AQ:54:ASN:OD1	2:DJ:47:ASN:ND2	2.37	0.42
1:AS:49:TRP:CZ3	1:AS:74:SER:HB3	2.54	0.42
1:AS:130:ILE:O	1:AS:134:VAL:HG23	2.19	0.42
1:AV:66:THR:HG22	2:DN:52:CYS:HB3	2.01	0.42
1:AW:203:VAL:HA	1:AW:260:LEU:O	2.19	0.42
1:AX:203:VAL:HG22	1:AX:261:ILE:HG23	2.01	0.42
1:BF:211:LEU:HD23	1:BF:211:LEU:HA	1.88	0.42
1:BS:97:LYS:HE2	1:BS:97:LYS:HB3	1.88	0.42
1:BT:282:ASN:OD1	1:BT:283:GLU:N	2.51	0.42
1:CD:87:LYS:NZ	4:GC:53:THR:O	2.38	0.42
1:CH:174:LYS:O	1:CH:212:LYS:NZ	2.52	0.42
1:CJ:59:THR:O	2:ES:61:ASN:ND2	2.51	0.42
1:CR:35:GLU:O	1:CR:272:LYS:HA	2.19	0.42
1:CU:101:SER:OG	1:CU:102:ASP:N	2.52	0.42
1:CV:35:GLU:O	1:CV:272:LYS:HA	2.18	0.42
1:DD:159:LEU:HD12	1:DD:260:LEU:HD13	2.01	0.42
2:EK:58:LYS:HE2	2:EM:116:ASN:HD21	1.83	0.42
2:EK:137:LEU:HD11	2:EK:159:ALA:HB2	2.01	0.42
2:EM:76:SER:O	2:EM:84:LEU:HD12	2.19	0.42
2:FI:56:LYS:HD2	4:GJ:56:PHE:HD1	1.84	0.42
4:FM:142:ILE:HG23	4:FM:152:VAL:HG22	2.01	0.42
4:FR:43:VAL:O	4:FR:43:VAL:HG13	2.19	0.42
4:FU:64:PHE:CZ	4:FU:108:ILE:HD11	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:FZ:137:VAL:HG12	4:FZ:138:LYS:HG3	2.00	0.42
5:HB:202:PHE:O	5:HB:206:ILE:HG13	2.19	0.42
5:HZ:200:THR:O	5:HZ:204:GLN:HG2	2.19	0.42
1:AK:241:ILE:HG22	1:AO:211:LEU:HD21	2.01	0.42
1:AM:169:VAL:HG22	1:AM:183:LYS:HG3	2.01	0.42
1:AO:79:LEU:HD11	1:AO:305:LEU:HB2	2.00	0.42
1:AT:35:GLU:O	1:AT:272:LYS:HA	2.19	0.42
1:AU:256:LYS:HG2	1:AU:257:HIS:CD2	2.54	0.42
1:AZ:65:ASN:ND2	2:DW:57:ASP:O	2.52	0.42
1:AZ:231:GLU:O	1:AZ:235:ILE:HG13	2.19	0.42
1:BN:169:VAL:HG22	1:BN:183:LYS:HG3	1.99	0.42
1:BO:126:ILE:O	1:BO:130:ILE:HG13	2.20	0.42
1:BP:35:GLU:O	1:BP:272:LYS:HA	2.19	0.42
1:BQ:35:GLU:O	1:BQ:272:LYS:HA	2.18	0.42
1:BQ:49:TRP:CZ3	1:BQ:74:SER:HB3	2.54	0.42
1:BS:55:ALA:O	1:BZ:86:TYR:OH	2.30	0.42
1:CL:96:GLU:O	1:CL:100:THR:HG23	2.19	0.42
1:CL:211:LEU:HD23	1:CL:211:LEU:HA	1.86	0.42
2:DY:114:THR:O	2:DZ:114:THR:HB	2.20	0.42
2:ET:133:PRO:HG3	2:ET:161:SER:HA	2.01	0.42
2:EW:167:THR:HG22	2:EW:168:GLU:H	1.84	0.42
4:GH:107:ASP:OD1	4:GH:108:ILE:N	2.52	0.42
5:HI:200:THR:O	5:HI:204:GLN:HG2	2.18	0.42
5:IS:198:ASN:OD1	5:IS:201:GLU:HG3	2.18	0.42
1:AI:203:VAL:HG22	1:AI:261:ILE:HG23	2.01	0.42
1:AI:205:VAL:HG12	1:AI:259:ILE:HG23	2.01	0.42
1:AK:126:ILE:O	1:AK:130:ILE:HG13	2.20	0.42
1:AU:231:GLU:O	1:AU:235:ILE:HG13	2.19	0.42
1:AX:231:GLU:O	1:AX:235:ILE:HG13	2.19	0.42
1:BH:35:GLU:O	1:BH:272:LYS:HA	2.18	0.42
1:BJ:101:SER:OG	1:BJ:102:ASP:N	2.52	0.42
1:BM:19:GLU:HA	1:BM:120:LYS:HD3	2.01	0.42
1:BQ:169:VAL:HG22	1:BQ:183:LYS:HG3	2.00	0.42
1:BR:188:LEU:O	1:BR:191:LEU:HB2	2.19	0.42
1:BW:231:GLU:O	1:BW:235:ILE:HG13	2.19	0.42
1:BY:174:LYS:HE2	1:BY:318:GLN:HE21	1.83	0.42
1:CB:41:MET:HE2	1:CB:41:MET:HB2	1.92	0.42
1:CD:49:TRP:CZ3	1:CD:74:SER:HB3	2.54	0.42
1:CH:48:LYS:HG3	2:EW:32:LEU:HD22	2.01	0.42
1:CK:258:LYS:HZ3	1:CK:315:ASN:HB2	1.84	0.42
1:CV:164:GLN:HE22	1:CV:308:ARG:HA	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CW:49:TRP:CH2	1:CW:74:SER:HB3	2.55	0.42
1:CW:91:LEU:HD21	1:CW:112:LEU:HD13	2.01	0.42
1:CZ:163:GLU:HB2	2:DX:31:LEU:HD13	2.01	0.42
1:DC:35:GLU:O	1:DC:272:LYS:HA	2.19	0.42
2:DF:123:LEU:HD13	2:DF:173:VAL:HG11	2.02	0.42
2:DP:160:LEU:HD11	4:FN:75:ARG:HH12	1.84	0.42
2:DR:23:LYS:N	2:DR:67:TYR:OH	2.51	0.42
2:EM:71:ARG:NH1	2:EM:142:HIS:O	2.53	0.42
5:IV:200:THR:O	5:IV:204:GLN:HG2	2.19	0.42
5:JM:189:LEU:HD11	5:JM:206:ILE:HG12	2.00	0.42
1:AA:231:GLU:O	1:AA:235:ILE:HG13	2.20	0.42
1:AD:96:GLU:O	1:AD:100:THR:HG23	2.19	0.42
1:AE:57:PRO:HB2	1:AI:84:LEU:HD13	2.01	0.42
1:AO:286:ASP:HB2	1:AO:294:HIS:HB2	2.02	0.42
1:AR:143:LYS:HA	2:DQ:39:ARG:HE	1.83	0.42
1:AS:211:LEU:O	1:AS:214:VAL:HG22	2.19	0.42
1:AT:124:SER:O	1:AT:128:LYS:HG3	2.19	0.42
1:BA:80:ASN:ND2	1:BA:153:PRO:O	2.40	0.42
1:BB:214:VAL:HG11	1:BF:240:ALA:HB2	2.01	0.42
1:BB:231:GLU:O	1:BB:235:ILE:HG13	2.20	0.42
1:BC:163:GLU:HB2	2:EB:31:LEU:HD13	2.01	0.42
1:BH:240:ALA:HB2	1:BL:214:VAL:HG11	2.01	0.42
1:BI:96:GLU:O	1:BI:100:THR:HG23	2.18	0.42
1:BN:133:PHE:CD2	1:BN:301:LEU:HD22	2.54	0.42
1:BY:80:ASN:ND2	1:BY:153:PRO:O	2.34	0.42
1:CE:210:SER:O	1:CE:214:VAL:HG13	2.20	0.42
1:CF:65:ASN:ND2	2:FE:57:ASP:O	2.53	0.42
1:CN:49:TRP:CE3	1:CN:74:SER:HB3	2.55	0.42
1:CP:122:ALA:O	1:CP:126:ILE:HG13	2.20	0.42
1:CS:277:MET:HA	1:CS:300:VAL:HB	2.02	0.42
2:DJ:167:THR:HG22	2:DJ:168:GLU:N	2.35	0.42
2:EA:166:LEU:HB2	2:EA:170:LEU:HD23	2.01	0.42
2:ER:114:THR:O	2:ES:114:THR:HB	2.19	0.42
2:FB:75:LEU:HD23	2:FB:75:LEU:HA	1.91	0.42
4:FP:64:PHE:CZ	4:FP:108:ILE:HD11	2.55	0.42
4:FV:73:VAL:HG21	4:FV:117:ILE:HD13	2.01	0.42
5:IO:200:THR:O	5:IO:204:GLN:HG2	2.19	0.42
1:AJ:77:VAL:HG11	1:AJ:305:LEU:HD13	1.99	0.42
1:AO:207:PRO:O	1:AO:211:LEU:HG	2.19	0.42
1:AR:78:ARG:HH21	2:DR:104:PHE:HE1	1.67	0.42
1:AU:96:GLU:O	1:AU:100:THR:HG23	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AV:209:THR:O	1:AV:213:LEU:HG	2.19	0.42
1:AZ:135:LEU:HD21	1:AZ:255:LEU:HG	2.01	0.42
1:BD:92:LYS:O	1:BD:96:GLU:HG3	2.20	0.42
1:BI:178:ASP:OD1	1:BI:179:LYS:N	2.53	0.42
1:BY:126:ILE:O	1:BY:130:ILE:HG13	2.18	0.42
1:CA:111:ASN:HA	1:CJ:49:TRP:HH2	1.85	0.42
1:CB:16:ILE:HD11	1:CB:120:LYS:HE3	2.02	0.42
1:CB:174:LYS:O	1:CB:212:LYS:NZ	2.51	0.42
1:CI:49:TRP:CE3	1:CI:74:SER:HB3	2.54	0.42
1:CO:135:LEU:HD21	1:CO:255:LEU:HG	2.01	0.42
1:CP:211:LEU:HD23	1:CP:211:LEU:HA	1.86	0.42
1:CR:178:ASP:OD1	1:CR:178:ASP:N	2.52	0.42
1:DD:66:THR:HG22	2:FI:52:CYS:HB3	2.01	0.42
1:DE:16:ILE:HD11	1:DE:120:LYS:HE3	2.01	0.42
2:DU:116:ASN:OD1	2:DV:58:LYS:HE2	2.18	0.42
2:EH:63:PRO:HB2	2:EH:85:GLU:HG2	2.01	0.42
4:FL:133:SER:HB3	4:FL:177:TYR:CE1	2.55	0.42
5:GL:211:LYS:O	5:GL:215:ILE:HG13	2.19	0.42
5:HF:211:LYS:O	5:HF:215:ILE:HG13	2.20	0.42
5:IZ:200:THR:O	5:IZ:204:GLN:HG2	2.19	0.42
1:AB:49:TRP:CZ3	1:AB:74:SER:HB3	2.54	0.42
1:AC:126:ILE:O	1:AC:130:ILE:HG13	2.20	0.42
1:AE:49:TRP:CE3	1:AE:74:SER:HB3	2.55	0.42
1:AK:211:LEU:O	1:AK:214:VAL:HG22	2.20	0.42
1:AP:207:PRO:O	1:AP:211:LEU:HG	2.20	0.42
1:AU:35:GLU:O	1:AU:272:LYS:HA	2.18	0.42
1:AU:132:HIS:HA	1:AU:254:LEU:HD13	2.01	0.42
1:AV:96:GLU:O	1:AV:100:THR:HG23	2.20	0.42
1:BH:96:GLU:O	1:BH:100:THR:HG23	2.20	0.42
1:BI:107:ASP:HB3	1:BI:112:LEU:HB2	2.01	0.42
1:BR:150:ARG:HH12	4:FY:65:LEU:HG	1.85	0.42
1:CB:137:GLY:HA3	1:CB:160:ASN:OD1	2.19	0.42
1:CL:152:LEU:HD21	2:EZ:105:SER:HA	2.02	0.42
1:CN:163:GLU:HB3	1:CN:308:ARG:HG3	2.01	0.42
1:CO:96:GLU:O	1:CO:100:THR:HG23	2.19	0.42
1:CP:89:ARG:HH21	1:CP:112:LEU:HD21	1.84	0.42
1:CW:152:LEU:HD21	2:FG:105:SER:HA	2.00	0.42
1:CX:49:TRP:CE3	1:CX:74:SER:HB3	2.55	0.42
1:DC:34:ILE:HA	1:DC:271:PHE:O	2.20	0.42
1:DC:178:ASP:OD1	1:DC:178:ASP:N	2.52	0.42
1:DE:122:ALA:O	1:DE:126:ILE:HG13	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:DI:165:LYS:HE3	2:DI:168:GLU:HA	2.01	0.42
2:DN:76:SER:HB3	2:DN:87:GLU:HG2	2.02	0.42
2:EG:4:ILE:HG12	2:EG:8:LYS:HE3	2.01	0.42
2:ER:148:VAL:HG21	2:ER:155:VAL:HG12	2.02	0.42
2:FD:114:THR:O	2:FE:114:THR:HB	2.20	0.42
4:FM:141:LEU:HD11	4:FM:165:ALA:HB2	2.01	0.42
4:FN:64:PHE:CZ	4:FN:108:ILE:HD11	2.54	0.42
4:GJ:43:VAL:HG13	4:GJ:43:VAL:O	2.19	0.42
5:JK:200:THR:O	5:JK:204:GLN:HG2	2.19	0.42
1:AG:286:ASP:HB2	1:AG:294:HIS:HB2	2.02	0.42
1:AJ:108:ILE:O	2:DM:24:ASN:ND2	2.52	0.42
1:AM:112:LEU:HD12	1:AM:112:LEU:HA	1.92	0.42
1:AM:180:ILE:O	1:AM:184:ILE:HG13	2.20	0.42
1:AO:307:THR:HG22	4:FP:32:LEU:HB2	2.02	0.42
1:AQ:35:GLU:O	1:AQ:272:LYS:HA	2.19	0.42
1:AR:211:LEU:O	1:AR:214:VAL:HG22	2.19	0.42
1:AY:158:LEU:HB3	1:AY:260:LEU:HD21	2.02	0.42
1:BA:174:LYS:O	1:BA:212:LYS:NZ	2.53	0.42
1:BB:152:LEU:HD21	2:EA:105:SER:HA	2.02	0.42
1:BH:119:TYR:CE1	1:BH:281:PRO:HG3	2.55	0.42
1:BO:57:PRO:HG2	1:BS:84:LEU:HD13	2.00	0.42
1:BO:77:VAL:HA	2:EL:29:SER:O	2.20	0.42
1:BQ:195:ASP:HB2	4:FU:36:ASN:HB3	2.01	0.42
1:CB:257:HIS:CE1	1:CB:318:GLN:HG3	2.55	0.42
1:CK:43:TYR:HE2	1:CK:45:LYS:HE2	1.85	0.42
1:CO:45:LYS:HE2	1:CO:78:ARG:HD3	2.01	0.42
1:CO:159:LEU:HD12	1:CO:260:LEU:HD13	2.02	0.42
1:CR:77:VAL:HG11	1:CR:305:LEU:HD13	2.01	0.42
1:CT:35:GLU:O	1:CT:272:LYS:HA	2.19	0.42
1:CV:306:ALA:O	4:GG:31:LEU:HB2	2.20	0.42
2:DT:77:PHE:CE1	2:DT:84:LEU:HD13	2.55	0.42
2:EJ:137:LEU:HD13	2:EJ:145:LEU:HD13	2.01	0.42
2:ET:23:LYS:N	2:ET:67:TYR:OH	2.52	0.42
2:EX:59:ILE:HG22	2:EX:111:ILE:HG12	2.02	0.42
2:EY:137:LEU:HD11	2:EY:159:ALA:HB2	2.02	0.42
4:GD:142:ILE:HD11	4:GD:152:VAL:HG23	2.02	0.42
4:GH:23:LYS:N	4:GH:67:TYR:OH	2.51	0.42
5:GO:202:PHE:O	5:GO:206:ILE:HG13	2.19	0.42
5:GY:189:LEU:HD11	5:GY:206:ILE:HG12	2.02	0.42
5:HK:209:THR:O	5:HK:213:ARG:HG3	2.20	0.42
1:AG:308:ARG:O	2:DI:34:ASN:ND2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AN:57:PRO:HB2	1:AR:84:LEU:HD13	2.02	0.42
1:AP:96:GLU:O	1:AP:100:THR:HG23	2.19	0.42
1:AQ:77:VAL:HG11	1:AQ:305:LEU:HD13	2.00	0.42
1:AQ:97:LYS:HE2	1:AQ:97:LYS:HB3	1.89	0.42
1:AR:43:TYR:HA	1:AR:79:LEU:O	2.19	0.42
1:AU:169:VAL:HG22	1:AU:183:LYS:HG3	2.02	0.42
1:AW:231:GLU:O	1:AW:235:ILE:HG13	2.20	0.42
1:BA:85:GLN:HB3	1:CY:60:ILE:HD11	2.02	0.42
1:BB:210:SER:O	1:BB:214:VAL:HG13	2.20	0.42
1:BC:178:ASP:OD1	1:BC:179:LYS:N	2.53	0.42
1:BP:54:ASN:ND2	2:EG:47:ASN:HD21	2.17	0.42
1:BT:150:ARG:HE	2:EL:63:PRO:HB3	1.84	0.42
1:BU:178:ASP:N	1:BU:178:ASP:OD1	2.52	0.42
1:BZ:41:MET:HE2	1:BZ:83:LYS:H	1.85	0.42
1:CA:65:ASN:HB2	2:EK:59:ILE:H	1.83	0.42
1:CA:121:LEU:O	1:CA:125:GLU:HG2	2.20	0.42
1:CE:43:TYR:HE2	1:CE:45:LYS:HE2	1.84	0.42
1:CI:260:LEU:HD23	1:CI:260:LEU:HA	1.95	0.42
1:CL:101:SER:OG	1:CL:102:ASP:N	2.53	0.42
1:CP:277:MET:HA	1:CP:300:VAL:HB	2.01	0.42
1:CR:203:VAL:HA	1:CR:260:LEU:O	2.20	0.42
1:CX:178:ASP:OD1	1:CX:178:ASP:N	2.52	0.42
1:CZ:240:ALA:HB2	1:DC:214:VAL:HG11	2.02	0.42
1:DC:157:GLY:N	1:DC:160:ASN:OD1	2.46	0.42
2:EN:58:LYS:H	2:EN:115:ASN:ND2	2.18	0.42
2:EP:75:LEU:HD23	2:EP:75:LEU:HA	1.89	0.42
2:EV:69:TYR:HE1	2:EV:100:ASP:HA	1.84	0.42
4:FQ:43:VAL:HG13	4:FQ:43:VAL:O	2.19	0.42
4:GI:51:THR:HG21	4:GI:180:LYS:HE3	2.01	0.42
5:HH:200:THR:O	5:HH:204:GLN:HG2	2.19	0.42
1:AG:16:ILE:HD13	1:AG:116:ALA:HB1	2.01	0.42
1:AM:231:GLU:O	1:AM:235:ILE:HG13	2.20	0.42
1:AR:126:ILE:O	1:AR:130:ILE:HG13	2.20	0.42
1:AU:229:LYS:O	1:AU:233:VAL:HG23	2.20	0.42
1:AV:107:ASP:HB3	1:AV:112:LEU:HB2	2.01	0.42
1:AZ:203:VAL:HG13	1:AZ:261:ILE:HG12	2.01	0.42
1:BB:96:GLU:O	1:BB:100:THR:HG23	2.19	0.42
1:BE:130:ILE:HG12	1:BE:301:LEU:HD21	2.01	0.42
1:BH:244:ARG:NH1	1:BL:210:SER:OG	2.51	0.42
1:BI:257:HIS:CD2	1:BI:318:GLN:HG3	2.55	0.42
1:BN:158:LEU:HB3	1:BN:260:LEU:HD21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BQ:49:TRP:CE3	1:BQ:74:SER:HB3	2.54	0.42
1:BT:119:TYR:CZ	1:BT:281:PRO:HG3	2.55	0.42
1:BU:84:LEU:HD13	1:CA:57:PRO:HB2	2.01	0.42
1:BX:49:TRP:CZ3	1:BX:74:SER:HB3	2.55	0.42
1:BZ:203:VAL:HA	1:BZ:260:LEU:O	2.20	0.42
1:CD:286:ASP:HB2	1:CD:294:HIS:HB2	2.02	0.42
1:CI:178:ASP:N	1:CI:178:ASP:OD1	2.52	0.42
1:CS:79:LEU:HD11	1:CS:305:LEU:HB2	2.00	0.42
1:CV:23:PRO:HB2	1:CV:25:MET:HG2	2.01	0.42
1:CV:257:HIS:CE1	1:CV:318:GLN:HG3	2.54	0.42
1:DA:180:ILE:O	1:DA:184:ILE:HG13	2.20	0.42
1:DE:158:LEU:HB3	1:DE:260:LEU:HD21	2.02	0.42
2:DP:125:LYS:HD2	2:DP:169:ASP:HA	2.02	0.42
2:DV:58:LYS:H	2:DV:115:ASN:ND2	2.18	0.42
2:EM:77:PHE:CE1	2:EM:84:LEU:HD13	2.54	0.42
4:FQ:10:GLU:O	4:FQ:14:LYS:HG2	2.18	0.42
4:FV:142:ILE:HD11	4:FV:152:VAL:HG13	2.01	0.42
4:GH:133:SER:HB3	4:GH:177:TYR:CE1	2.55	0.42
5:JA:202:PHE:O	5:JA:206:ILE:HG13	2.20	0.42
5:JI:189:LEU:HD11	5:JI:206:ILE:HG12	2.01	0.42
1:AF:278:LEU:HD23	1:AF:278:LEU:HA	1.87	0.42
1:AG:132:HIS:HA	1:AG:254:LEU:HD13	2.02	0.42
1:AJ:28:TRP:CZ3	1:AJ:135:LEU:HB2	2.54	0.42
1:AK:164:GLN:HE22	1:AK:308:ARG:HA	1.85	0.42
1:AN:126:ILE:O	1:AN:130:ILE:HG13	2.20	0.42
1:AU:30:SER:HB3	1:AU:33:GLN:HG3	2.02	0.42
1:AV:8:TYR:CD2	1:AV:93:GLN:HG3	2.55	0.42
1:AV:214:VAL:HG11	1:AY:240:ALA:HB2	2.02	0.42
1:AW:205:VAL:HG12	1:AW:259:ILE:HG23	2.02	0.42
1:BK:256:LYS:HE3	1:BK:256:LYS:HB2	1.89	0.42
1:BL:96:GLU:O	1:BL:100:THR:HG23	2.20	0.42
1:BL:257:HIS:HB3	1:BL:316:ILE:HB	2.02	0.42
1:BP:81:TYR:OH	1:BP:272:LYS:O	2.30	0.42
1:BR:181:PHE:O	1:BR:185:GLU:HG3	2.20	0.42
1:CB:33:GLN:HG2	1:CB:266:SER:HA	2.02	0.42
1:CC:51:ALA:O	4:GD:41:LYS:NZ	2.45	0.42
1:CJ:286:ASP:HB2	1:CJ:294:HIS:HB2	2.01	0.42
1:CK:57:PRO:HB2	1:CN:84:LEU:HD13	2.02	0.42
1:CR:47:VAL:HG22	1:CR:76:VAL:HG22	2.01	0.42
1:CS:49:TRP:CH2	1:CS:74:SER:HB3	2.55	0.42
1:DE:277:MET:HA	1:DE:300:VAL:HB	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:DR:133:PRO:HG3	2:DR:161:SER:HA	2.01	0.42
2:DX:32:LEU:HD23	2:DX:32:LEU:HA	1.91	0.42
2:EE:113:ILE:HD12	2:EE:113:ILE:HA	1.90	0.42
2:EM:125:LYS:HD2	2:EM:169:ASP:HA	2.01	0.42
2:EN:77:PHE:CD2	4:FZ:138:LYS:HG2	2.55	0.42
2:EP:30:GLY:O	2:EP:31:LEU:HD23	2.20	0.42
2:EX:165:LYS:HE3	2:EX:168:GLU:HA	2.00	0.42
2:FC:116:ASN:ND2	4:GG:60:GLU:OE2	2.53	0.42
3:FJ:184:ASN:HB3	3:FJ:190:ILE:HD13	2.02	0.42
4:GC:120:ILE:HD12	4:GC:120:ILE:HA	1.94	0.42
5:JG:190:LEU:HG	5:JG:209:THR:HG23	2.02	0.42
5:JH:198:ASN:OD1	5:JH:201:GLU:HG3	2.20	0.42
1:AG:41:MET:HE2	1:AG:83:LYS:H	1.84	0.41
1:AJ:100:THR:HG22	1:AJ:105:ILE:HD13	2.01	0.41
1:AN:203:VAL:HG22	1:AN:261:ILE:HG23	2.02	0.41
1:AP:28:TRP:HB3	1:AP:262:TYR:OH	2.20	0.41
1:AP:90:HIS:HE2	1:AP:295:SER:HG	1.66	0.41
1:AT:209:THR:O	1:AT:213:LEU:HG	2.20	0.41
1:AX:124:SER:O	1:AX:128:LYS:HG3	2.20	0.41
1:AY:229:LYS:O	1:AY:233:VAL:HG23	2.19	0.41
1:BF:59:THR:O	2:EA:61:ASN:ND2	2.53	0.41
1:BJ:275:LYS:HE3	1:BJ:276:TYR:CZ	2.55	0.41
1:BO:196:GLU:HB3	1:BO:265:ASN:HD22	1.85	0.41
1:BV:165:ILE:HD13	1:BV:191:LEU:HD23	2.02	0.41
1:BY:178:ASP:OD1	1:BY:178:ASP:N	2.52	0.41
1:BZ:47:VAL:HG22	1:BZ:76:VAL:HG22	2.01	0.41
1:CC:132:HIS:HA	1:CC:254:LEU:HD13	2.01	0.41
1:CQ:84:LEU:HD13	1:DA:57:PRO:HB2	2.01	0.41
1:CW:66:THR:HG22	2:FE:52:CYS:HB3	2.02	0.41
1:CX:49:TRP:CZ3	1:CX:74:SER:HB3	2.55	0.41
1:DB:80:ASN:ND2	1:DB:154:ASN:HB2	2.34	0.41
1:DC:123:SER:O	1:DC:127:ILE:HG13	2.20	0.41
2:DO:98:CYS:SG	2:DO:108:ALA:HB1	2.60	0.41
2:EB:77:PHE:HD2	4:FU:138:LYS:HG3	1.85	0.41
2:EB:166:LEU:HB2	2:EB:170:LEU:HD23	2.02	0.41
2:EO:167:THR:HG22	2:EO:168:GLU:N	2.35	0.41
2:FC:58:LYS:H	2:FC:115:ASN:ND2	2.18	0.41
3:FJ:172:ASN:HB3	3:FJ:175:ILE:HD11	2.01	0.41
4:FT:93:VAL:HG21	4:FT:117:ILE:HD11	2.02	0.41
5:GS:200:THR:O	5:GS:204:GLN:HG2	2.20	0.41
5:IP:200:THR:O	5:IP:204:GLN:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AC:152:LEU:HD21	2:DH:105:SER:HA	2.02	0.41
1:AF:158:LEU:HB3	1:AF:260:LEU:HD21	2.02	0.41
1:AG:209:THR:O	1:AG:213:LEU:HG	2.20	0.41
1:AL:273:PRO:HA	1:AL:302:GLY:HA3	2.01	0.41
1:AN:66:THR:HG22	2:DQ:52:CYS:HB3	2.02	0.41
1:AN:169:VAL:HG22	1:AN:183:LYS:HG3	2.01	0.41
1:AQ:140:SER:HB2	1:AQ:148:GLN:HG2	2.02	0.41
1:AU:85:GLN:HB3	1:BA:60:ILE:HD11	2.01	0.41
1:AW:96:GLU:O	1:AW:100:THR:HG23	2.20	0.41
1:BG:165:ILE:HD13	1:BG:191:LEU:HD23	2.02	0.41
1:BK:203:VAL:HA	1:BK:260:LEU:O	2.20	0.41
1:BN:49:TRP:CZ3	1:BR:113:LEU:HD11	2.55	0.41
1:BN:49:TRP:CZ3	1:BN:74:SER:HB3	2.54	0.41
1:CB:84:LEU:HD13	1:CL:57:PRO:HB2	2.01	0.41
1:CC:178:ASP:N	1:CC:178:ASP:OD1	2.52	0.41
1:CD:79:LEU:HD11	1:CD:305:LEU:HB2	2.01	0.41
1:CJ:35:GLU:O	1:CJ:272:LYS:HA	2.20	0.41
1:CL:308:ARG:O	2:ET:34:ASN:ND2	2.43	0.41
1:CO:41:MET:HE2	1:CO:41:MET:HB2	1.94	0.41
1:CO:205:VAL:HG12	1:CO:259:ILE:HG23	2.02	0.41
1:CQ:113:LEU:HD11	1:DA:49:TRP:CE3	2.56	0.41
1:DA:101:SER:OG	1:DA:102:ASP:N	2.53	0.41
2:DK:140:ASN:HD21	2:DK:144:GLU:HB2	1.85	0.41
2:DM:28:ASP:OD1	2:DM:28:ASP:N	2.52	0.41
2:DT:58:LYS:HD3	4:FP:123:ASN:HD21	1.85	0.41
2:DZ:137:LEU:HB3	2:DZ:145:LEU:HD22	2.02	0.41
2:EI:76:SER:HB3	2:EI:87:GLU:HG2	2.02	0.41
4:GB:23:LYS:N	4:GB:67:TYR:OH	2.52	0.41
5:GL:189:LEU:HD11	5:GL:206:ILE:HG12	2.02	0.41
1:AA:13:VAL:HG11	1:AA:281:PRO:HG2	2.00	0.41
1:AE:150:ARG:HH22	2:DI:64:ALA:H	1.68	0.41
1:AE:203:VAL:HG22	1:AE:261:ILE:HG23	2.01	0.41
1:AF:197:PHE:CD2	1:AF:243:ASN:HB2	2.55	0.41
1:AG:36:ASP:CG	5:GQ:214:ARG:HH22	2.23	0.41
1:AI:39:LEU:O	1:AI:274:SER:OG	2.28	0.41
1:AK:169:VAL:HG22	1:AK:183:LYS:HG3	2.01	0.41
1:AK:256:LYS:HE3	1:AK:256:LYS:HB2	1.88	0.41
1:AP:80:ASN:HB2	1:AP:155:MET:HG3	2.01	0.41
1:AP:126:ILE:O	1:AP:130:ILE:HG13	2.20	0.41
1:AP:180:ILE:O	1:AP:184:ILE:HG13	2.20	0.41
1:AR:209:THR:O	1:AR:213:LEU:HG	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AW:123:SER:O	1:AW:127:ILE:HG13	2.20	0.41
1:BA:229:LYS:O	1:BA:233:VAL:HG23	2.20	0.41
1:BE:49:TRP:CE3	1:BE:74:SER:HB3	2.56	0.41
1:BI:52:PHE:CE1	1:BI:71:GLY:HA3	2.54	0.41
1:BM:97:LYS:HB3	1:BM:97:LYS:HE2	1.89	0.41
1:BP:16:ILE:HD11	1:BP:120:LYS:HE3	2.02	0.41
1:BR:35:GLU:O	1:BR:272:LYS:HA	2.19	0.41
1:BW:49:TRP:CZ3	1:BW:74:SER:HB3	2.56	0.41
1:BY:212:LYS:HA	1:BY:215:LYS:HE3	2.02	0.41
1:BZ:203:VAL:HG22	1:BZ:261:ILE:HG12	2.01	0.41
1:CG:317:LYS:NZ	1:CG:319:SER:OXT	2.53	0.41
1:CK:35:GLU:O	1:CK:272:LYS:HA	2.19	0.41
1:CL:203:VAL:HG22	1:CL:261:ILE:HG23	2.01	0.41
1:CR:28:TRP:O	1:CR:262:TYR:OH	2.34	0.41
1:CU:96:GLU:O	1:CU:100:THR:HG23	2.20	0.41
1:CU:277:MET:HA	1:CU:300:VAL:HB	2.01	0.41
1:DD:49:TRP:CH2	1:DD:74:SER:HB3	2.55	0.41
2:DJ:123:LEU:HD21	2:DJ:131:VAL:HG21	2.01	0.41
2:DO:167:THR:HG22	2:DO:168:GLU:H	1.86	0.41
2:DX:165:LYS:HB2	2:DX:171:PHE:CE2	2.55	0.41
2:EA:140:ASN:OD1	2:EA:144:GLU:N	2.44	0.41
2:EM:166:LEU:HB2	2:EM:170:LEU:HD23	2.02	0.41
2:EV:30:GLY:O	2:EV:31:LEU:HD23	2.20	0.41
4:FN:23:LYS:N	4:FN:67:TYR:OH	2.52	0.41
4:GA:25:PRO:HB2	4:GA:27:HIS:CD2	2.55	0.41
4:GC:20:LYS:HZ3	4:GC:21:PHE:HE1	1.67	0.41
5:GK:211:LYS:O	5:GK:214:ARG:HG2	2.20	0.41
5:HC:202:PHE:CE2	5:HC:206:ILE:HD11	2.56	0.41
5:HJ:209:THR:O	5:HJ:213:ARG:HG3	2.20	0.41
5:IL:202:PHE:O	5:IL:206:ILE:HG13	2.21	0.41
5:IR:190:LEU:HG	5:IR:209:THR:HG23	2.02	0.41
1:AC:67:ILE:HD12	1:AE:296:TYR:HE2	1.85	0.41
1:AH:135:LEU:HD21	1:AH:255:LEU:HG	2.03	0.41
1:AJ:20:VAL:O	5:GT:213:ARG:NH2	2.31	0.41
1:AR:130:ILE:O	1:AR:134:VAL:HG23	2.20	0.41
1:AU:27:LYS:O	5:HE:223:ARG:NH2	2.39	0.41
1:AY:203:VAL:HG22	1:AY:261:ILE:HG23	2.02	0.41
1:BG:84:LEU:HB3	1:BJ:57:PRO:HB2	2.01	0.41
1:BG:96:GLU:O	1:BG:100:THR:HG23	2.20	0.41
1:BJ:253:ASN:OD1	1:BJ:253:ASN:N	2.52	0.41
1:BQ:119:TYR:CE1	1:BQ:281:PRO:HG3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BS:59:THR:O	4:GB:61:ASN:ND2	2.54	0.41
1:BY:187:GLY:HA3	1:BY:312:LEU:HD13	2.01	0.41
1:CC:57:PRO:HG2	1:CF:84:LEU:HD13	2.02	0.41
1:CE:305:LEU:HD11	2:EY:32:LEU:HG	2.02	0.41
1:CF:92:LYS:O	1:CF:96:GLU:HG3	2.20	0.41
1:CG:306:ALA:O	4:GC:31:LEU:HB2	2.20	0.41
1:CH:96:GLU:O	1:CH:100:THR:HG23	2.21	0.41
1:CL:257:HIS:ND1	1:CL:318:GLN:HG3	2.35	0.41
1:CM:203:VAL:HG22	1:CM:261:ILE:HG23	2.02	0.41
1:CP:92:LYS:O	1:CP:96:GLU:HG3	2.20	0.41
1:CV:41:MET:HE2	1:CV:41:MET:HB2	1.94	0.41
1:CZ:79:LEU:HD11	1:CZ:305:LEU:HB2	2.02	0.41
1:DA:253:ASN:OD1	1:DA:253:ASN:N	2.54	0.41
1:DD:33:GLN:NE2	1:DD:269:ILE:O	2.48	0.41
2:DQ:140:ASN:OD1	2:DQ:144:GLU:N	2.52	0.41
2:DT:165:LYS:HE3	2:DT:168:GLU:HA	2.03	0.41
2:DU:158:ILE:HG13	2:DU:178:PHE:HE2	1.85	0.41
2:EC:23:LYS:N	2:EC:67:TYR:OH	2.52	0.41
4:FT:144:ASN:OD1	4:FT:148:ALA:N	2.46	0.41
4:GG:25:PRO:HB2	4:GG:27:HIS:CD2	2.55	0.41
5:IJ:200:THR:O	5:IJ:204:GLN:HG2	2.20	0.41
1:AA:169:VAL:HG22	1:AA:183:LYS:HG3	2.03	0.41
1:AD:186:ALA:O	1:AD:190:LYS:HG3	2.20	0.41
1:AG:260:LEU:HD23	1:AG:260:LEU:HA	1.95	0.41
1:AH:57:PRO:HB2	1:AL:84:LEU:HD13	2.02	0.41
1:AV:211:LEU:O	1:AV:214:VAL:HG22	2.21	0.41
1:BM:86:TYR:OH	1:BP:55:ALA:O	2.28	0.41
1:BR:180:ILE:O	1:BR:184:ILE:HG13	2.20	0.41
1:BV:174:LYS:O	1:BV:212:LYS:NZ	2.54	0.41
1:BX:257:HIS:CE1	1:BX:318:GLN:HG3	2.55	0.41
1:BY:203:VAL:HG13	1:BY:261:ILE:HG12	2.02	0.41
1:CB:113:LEU:HD11	1:CL:49:TRP:CE3	2.55	0.41
1:CC:62:ASN:ND2	2:EV:102:ASP:HB2	2.35	0.41
1:CF:180:ILE:O	1:CF:184:ILE:HG13	2.21	0.41
1:CL:188:LEU:HD23	1:CL:191:LEU:HD12	2.02	0.41
1:CN:57:PRO:HB2	1:CP:84:LEU:HB3	2.02	0.41
1:CX:123:SER:O	1:CX:127:ILE:HG13	2.20	0.41
1:DE:81:TYR:OH	1:DE:272:LYS:O	2.28	0.41
2:DS:58:LYS:HD3	2:DS:112:PRO:HG2	2.02	0.41
2:DY:74:LYS:HE2	2:DY:89:GLY:HA3	2.03	0.41
2:EE:28:ASP:N	2:EE:28:ASP:OD1	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:ER:116:ASN:HB3	2:ES:114:THR:HG21	2.02	0.41
2:ET:77:PHE:HB2	4:GC:138:LYS:HE2	2.03	0.41
2:FE:167:THR:HG22	2:FE:168:GLU:H	1.86	0.41
4:FX:37:GLU:HG3	4:FX:39:ARG:H	1.85	0.41
5:JO:200:THR:O	5:JO:204:GLN:HG2	2.20	0.41
1:AA:13:VAL:O	1:AA:17:ILE:HB	2.21	0.41
1:AA:186:ALA:O	1:AA:190:LYS:HG3	2.20	0.41
1:AB:209:THR:O	1:AB:213:LEU:HG	2.20	0.41
1:AD:77:VAL:HG11	1:AD:305:LEU:HD13	2.02	0.41
1:AP:133:PHE:CD2	1:AP:301:LEU:HD22	2.56	0.41
1:AR:203:VAL:HG22	1:AR:261:ILE:HG23	2.02	0.41
1:AY:130:ILE:O	1:AY:134:VAL:HG23	2.21	0.41
1:BB:49:TRP:CZ3	1:BB:74:SER:HB3	2.55	0.41
1:BD:14:ALA:HB2	5:HN:202:PHE:HE1	1.85	0.41
1:BD:142:GLN:NE2	1:BD:147:ASN:OD1	2.52	0.41
1:BH:203:VAL:HG13	1:BH:261:ILE:HG12	2.02	0.41
1:BJ:89:ARG:NH2	1:BJ:112:LEU:HD21	2.34	0.41
1:BO:211:LEU:HD23	1:BO:211:LEU:HA	1.89	0.41
1:BR:49:TRP:CZ3	1:BR:74:SER:HB3	2.55	0.41
1:CK:79:LEU:HD11	1:CK:305:LEU:HB2	2.02	0.41
1:CO:178:ASP:OD1	1:CO:178:ASP:N	2.52	0.41
1:CR:39:LEU:O	1:CR:274:SER:OG	2.24	0.41
1:CR:260:LEU:HD23	1:CR:260:LEU:HA	1.96	0.41
1:CT:77:VAL:HA	2:FG:29:SER:O	2.20	0.41
1:DE:169:VAL:HG22	1:DE:183:LYS:HG3	2.02	0.41
2:DK:153:LYS:HG3	2:DK:154:SER:H	1.86	0.41
2:DT:23:LYS:N	2:DT:67:TYR:OH	2.53	0.41
2:EB:129:ASN:OD1	2:EB:130:GLY:N	2.54	0.41
2:EL:133:PRO:HG3	2:EL:161:SER:HA	2.02	0.41
5:HC:202:PHE:CZ	5:HC:206:ILE:HD11	2.56	0.41
1:AU:282:ASN:OD1	1:AU:283:GLU:N	2.53	0.41
1:AV:140:SER:HB2	1:AV:148:GLN:HG2	2.02	0.41
1:AX:211:LEU:O	1:AX:214:VAL:HG22	2.21	0.41
1:AY:164:GLN:HE22	1:AY:308:ARG:HA	1.86	0.41
1:BE:142:GLN:OE1	1:BE:147:ASN:ND2	2.41	0.41
1:BG:7:ASN:HB3	1:BG:10:ALA:HB3	2.03	0.41
1:BG:196:GLU:HB3	1:BG:265:ASN:ND2	2.35	0.41
1:BT:196:GLU:HB3	1:BT:265:ASN:ND2	2.36	0.41
1:BW:96:GLU:O	1:BW:100:THR:HG23	2.20	0.41
1:CD:28:TRP:HB3	1:CD:262:TYR:OH	2.21	0.41
1:CK:255:LEU:HD22	1:CK:258:LYS:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CK:289:SER:HB2	1:CL:85:GLN:HE22	1.85	0.41
1:CP:169:VAL:HG22	1:CP:183:LYS:HG3	2.03	0.41
1:CQ:35:GLU:O	1:CQ:272:LYS:HA	2.21	0.41
1:CQ:135:LEU:HD21	1:CQ:255:LEU:HG	2.02	0.41
1:DC:260:LEU:HD23	1:DC:260:LEU:HA	1.94	0.41
2:DJ:65:LYS:HB2	2:DJ:85:GLU:OE1	2.21	0.41
2:DT:145:LEU:HD23	2:DT:145:LEU:HA	1.95	0.41
2:EN:69:TYR:CE2	2:EN:70:LYS:HG2	2.56	0.41
2:FH:23:LYS:N	2:FH:67:TYR:OH	2.49	0.41
3:FJ:140:ASP:OD1	3:FJ:140:ASP:N	2.53	0.41
4:FQ:142:ILE:HD11	4:FQ:152:VAL:HG23	2.01	0.41
5:HI:202:PHE:O	5:HI:206:ILE:HG13	2.21	0.41
5:JN:189:LEU:HD11	5:JN:206:ILE:HG12	2.02	0.41
1:AF:209:THR:O	1:AF:213:LEU:HG	2.20	0.41
1:AJ:91:LEU:HG	1:AJ:112:LEU:HG	2.02	0.41
1:AK:196:GLU:HB3	1:AK:265:ASN:HD22	1.84	0.41
1:AN:186:ALA:O	1:AN:190:LYS:HG3	2.21	0.41
1:AX:282:ASN:HB3	1:AX:296:TYR:HB2	2.03	0.41
1:BK:196:GLU:OE1	1:BK:265:ASN:ND2	2.48	0.41
1:BM:229:LYS:O	1:BM:233:VAL:HG23	2.20	0.41
1:BP:142:GLN:NE2	1:BP:147:ASN:OD1	2.51	0.41
1:BP:253:ASN:OD1	1:BP:253:ASN:N	2.53	0.41
1:BT:211:LEU:O	1:BT:214:VAL:HG22	2.20	0.41
1:CB:126:ILE:O	1:CB:130:ILE:HG13	2.20	0.41
1:CB:205:VAL:HG12	1:CB:259:ILE:HG23	2.02	0.41
1:CL:161:MET:SD	2:ET:31:LEU:HD21	2.61	0.41
1:CL:257:HIS:CE1	1:CL:318:GLN:HG3	2.55	0.41
1:CN:178:ASP:N	1:CN:178:ASP:OD1	2.52	0.41
1:CN:286:ASP:HB2	1:CN:294:HIS:HB2	2.03	0.41
1:CQ:126:ILE:O	1:CQ:130:ILE:HG13	2.20	0.41
1:CW:152:LEU:HD23	1:CW:152:LEU:HA	1.92	0.41
1:DB:23:PRO:HB2	1:DB:25:MET:HG2	2.02	0.41
1:DB:124:SER:O	1:DB:128:LYS:HG3	2.21	0.41
2:EA:123:LEU:HD13	2:EA:173:VAL:HG11	2.03	0.41
2:FD:74:LYS:HE2	2:FD:89:GLY:HA3	2.02	0.41
4:FS:35:SER:O	4:FS:41:LYS:HD2	2.21	0.41
4:GE:25:PRO:HB2	4:GE:27:HIS:CD2	2.56	0.41
4:GE:161:ILE:HA	4:GE:186:ASN:HA	2.01	0.41
4:GG:20:LYS:HZ1	4:GG:175:GLU:HB2	1.86	0.41
1:AC:124:SER:O	1:AC:128:LYS:HG3	2.20	0.41
1:AD:307:THR:HG22	4:FO:32:LEU:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:28:TRP:HB3	1:AG:262:TYR:OH	2.21	0.41
1:AH:65:ASN:ND2	2:DN:57:ASP:O	2.54	0.41
1:AJ:229:LYS:O	1:AJ:233:VAL:HG23	2.21	0.41
1:AK:130:ILE:O	1:AK:134:VAL:HG23	2.21	0.41
1:AL:36:ASP:CG	5:GV:214:ARG:HH22	2.24	0.41
1:AQ:97:LYS:NZ	5:HB:200:THR:HG21	2.35	0.41
1:AS:231:GLU:O	1:AS:235:ILE:HG13	2.21	0.41
1:AT:203:VAL:HG22	1:AT:261:ILE:HG23	2.02	0.41
1:AW:208:ALA:O	1:AW:212:LYS:HG3	2.21	0.41
1:AX:55:ALA:HA	1:DD:141:ILE:HD13	2.02	0.41
1:BD:77:VAL:HG11	1:BD:305:LEU:HD13	2.02	0.41
1:BD:307:THR:HG22	2:EI:32:LEU:HB2	2.03	0.41
1:BF:178:ASP:N	1:BF:178:ASP:OD1	2.53	0.41
1:BF:188:LEU:HD23	1:BF:191:LEU:HD12	2.03	0.41
1:BG:181:PHE:O	1:BG:185:GLU:HG3	2.21	0.41
1:BH:203:VAL:HA	1:BH:260:LEU:O	2.21	0.41
1:BI:34:ILE:HG12	1:BI:271:PHE:HB3	2.03	0.41
1:BI:159:LEU:HD11	1:BI:258:LYS:HD3	2.03	0.41
1:BN:54:ASN:OD1	2:EJ:47:ASN:ND2	2.34	0.41
1:BN:96:GLU:O	1:BN:100:THR:HG23	2.20	0.41
1:BQ:87:LYS:NZ	4:FY:53:THR:O	2.36	0.41
1:BQ:97:LYS:HE2	1:BQ:97:LYS:HB3	1.95	0.41
1:BQ:229:LYS:O	1:BQ:233:VAL:HG23	2.20	0.41
1:BU:27:LYS:HG3	5:IE:217:PHE:HZ	1.85	0.41
1:BV:203:VAL:HG22	1:BV:261:ILE:HG23	2.02	0.41
1:BW:107:ASP:OD2	1:BW:110:ASN:ND2	2.33	0.41
1:BY:209:THR:O	1:BY:213:LEU:HG	2.21	0.41
1:BY:277:MET:HA	1:BY:300:VAL:HB	2.03	0.41
1:BY:308:ARG:HG3	4:FZ:33:SER:HA	2.03	0.41
1:BZ:143:LYS:HA	2:ES:39:ARG:HE	1.86	0.41
1:CF:34:ILE:HG12	1:CF:271:PHE:HB3	2.03	0.41
1:CF:85:GLN:NE2	1:CF:298:ASP:OD1	2.52	0.41
1:CG:8:TYR:CD2	1:CG:93:GLN:HG3	2.56	0.41
1:CH:35:GLU:O	1:CH:272:LYS:HA	2.21	0.41
1:CH:66:THR:OG1	4:GD:58:LYS:NZ	2.50	0.41
1:CL:16:ILE:HD11	1:CL:120:LYS:HE3	2.02	0.41
1:CM:174:LYS:O	1:CM:212:LYS:NZ	2.54	0.41
1:CN:35:GLU:O	1:CN:272:LYS:HA	2.20	0.41
1:CO:152:LEU:HD21	2:EQ:105:SER:HA	2.03	0.41
1:CP:148:GLN:HG3	2:ER:81:THR:O	2.20	0.41
1:CP:205:VAL:HG12	1:CP:259:ILE:HG23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CQ:75:GLU:OE2	1:CQ:308:ARG:NH2	2.54	0.41
1:CR:194:GLY:HA3	4:GH:36:ASN:OD1	2.20	0.41
1:CT:49:TRP:CH2	1:CT:74:SER:HB3	2.56	0.41
1:CT:210:SER:O	1:CT:214:VAL:HG13	2.20	0.41
1:CT:289:SER:HB2	1:CU:85:GLN:HE22	1.85	0.41
1:CV:178:ASP:N	1:CV:178:ASP:OD1	2.53	0.41
1:CW:45:LYS:HE2	1:CW:78:ARG:HD3	2.03	0.41
1:CY:180:ILE:O	1:CY:184:ILE:HG13	2.21	0.41
1:CZ:35:GLU:O	1:CZ:272:LYS:HA	2.20	0.41
1:DD:35:GLU:O	1:DD:272:LYS:HA	2.20	0.41
2:DG:166:LEU:HD11	2:DG:172:ILE:HD13	2.02	0.41
2:DI:36:ILE:HG23	2:DI:36:ILE:O	2.21	0.41
2:DL:68:PRO:HD2	2:DL:101:ILE:HD11	2.03	0.41
2:DR:153:LYS:O	2:DR:181:ARG:NH2	2.54	0.41
2:DW:166:LEU:HB2	2:DW:170:LEU:HD23	2.03	0.41
2:EK:113:ILE:HD12	2:EK:113:ILE:HA	1.95	0.41
2:EO:23:LYS:HG3	2:EO:24:ASN:N	2.36	0.41
2:ER:120:TYR:CE1	2:ER:174:LEU:HB2	2.55	0.41
2:EU:69:TYR:HB2	2:EU:101:ILE:HD12	2.03	0.41
4:FN:65:LEU:HD23	4:FN:92:HIS:CG	2.55	0.41
4:FU:149:LEU:HD13	4:FU:181:VAL:HG11	2.02	0.41
4:GA:20:LYS:HZ1	4:GA:175:GLU:HB2	1.85	0.41
4:GB:107:ASP:OD1	4:GB:108:ILE:N	2.54	0.41
4:GD:107:ASP:OD1	4:GD:108:ILE:N	2.54	0.41
4:GG:23:LYS:N	4:GG:67:TYR:OH	2.54	0.41
4:GJ:142:ILE:HD11	4:GJ:152:VAL:HG23	2.02	0.41
5:GY:200:THR:O	5:GY:204:GLN:HG2	2.21	0.41
5:HC:215:ILE:O	5:HC:219:GLU:HG3	2.21	0.41
5:IC:198:ASN:OD1	5:IC:201:GLU:HG3	2.21	0.41
5:JG:202:PHE:O	5:JG:206:ILE:HG13	2.21	0.41
1:AA:112:LEU:HD12	1:AA:112:LEU:HA	1.91	0.41
1:AC:79:LEU:HD11	1:AC:305:LEU:HB2	2.03	0.41
1:AG:180:ILE:O	1:AG:184:ILE:HG13	2.20	0.41
1:AK:164:GLN:OE1	1:AK:311:ILE:N	2.54	0.41
1:AP:234:LEU:O	1:AP:238:ILE:HG13	2.21	0.41
1:AQ:162:PRO:HG2	2:DJ:31:LEU:HD11	2.02	0.41
1:AT:187:GLY:HA3	1:AT:312:LEU:HD13	2.03	0.41
1:BA:307:THR:HG22	2:DT:32:LEU:HB2	2.03	0.41
1:BD:208:ALA:O	1:BD:212:LYS:HG3	2.21	0.41
1:BG:119:TYR:CE1	1:BG:281:PRO:HG3	2.55	0.41
1:BJ:278:LEU:HD23	1:BJ:278:LEU:HA	1.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BK:132:HIS:HA	1:BK:254:LEU:HD13	2.03	0.41
1:BM:268:LEU:HD21	4:FW:36:ASN:HD21	1.86	0.41
1:BU:86:TYR:CD2	1:CA:70:ILE:HD11	2.56	0.41
1:BX:34:ILE:HA	1:BX:271:PHE:O	2.21	0.41
1:CF:152:LEU:HD21	2:EV:105:SER:HA	2.02	0.41
1:CM:8:TYR:CD2	1:CM:93:GLN:HG3	2.56	0.41
1:CO:109:ASN:O	2:EP:24:ASN:ND2	2.53	0.41
1:CR:57:PRO:HG2	1:CU:84:LEU:HD13	2.02	0.41
1:CS:70:ILE:HD11	1:CZ:86:TYR:CD2	2.56	0.41
1:CS:203:VAL:HA	1:CS:260:LEU:O	2.21	0.41
1:CT:196:GLU:HB3	1:CT:265:ASN:HD22	1.86	0.41
1:CV:169:VAL:HG22	1:CV:183:LYS:HG3	2.03	0.41
1:DC:317:LYS:HE2	1:DC:319:SER:HB2	2.03	0.41
2:EH:123:LEU:HD21	2:EH:131:VAL:HG21	2.03	0.41
2:EU:156:ASN:HB3	2:EU:178:PHE:CZ	2.57	0.41
4:FK:93:VAL:HG21	4:FK:117:ILE:HD11	2.03	0.41
4:FQ:93:VAL:HG21	4:FQ:117:ILE:HD11	2.03	0.41
4:GC:37:GLU:O	4:GC:41:LYS:HD2	2.20	0.41
4:GH:142:ILE:HD11	4:GH:152:VAL:HG23	2.02	0.41
5:HB:189:LEU:HD11	5:HB:206:ILE:HG12	2.03	0.41
1:AA:96:GLU:O	1:AA:100:THR:HG23	2.21	0.40
1:AC:57:PRO:HB2	1:AE:84:LEU:HB3	2.03	0.40
1:AC:306:ALA:O	4:FK:31:LEU:HB2	2.21	0.40
1:AF:133:PHE:CD2	1:AF:301:LEU:HD22	2.56	0.40
1:AN:158:LEU:HB3	1:AN:260:LEU:HD21	2.02	0.40
1:AS:255:LEU:HD23	1:AS:255:LEU:HA	1.93	0.40
1:AW:39:LEU:HD11	1:AW:81:TYR:CD2	2.48	0.40
1:AZ:146:LYS:HB3	4:FS:88:HIS:HD2	1.85	0.40
1:BB:158:LEU:HB3	1:BB:260:LEU:HD21	2.03	0.40
1:BI:50:ASP:HB3	1:BI:73:SER:OG	2.21	0.40
1:BJ:28:TRP:CZ3	1:BJ:135:LEU:HB2	2.56	0.40
1:BM:256:LYS:O	1:BM:258:LYS:HG2	2.21	0.40
1:BN:49:TRP:CE3	1:BR:113:LEU:HD11	2.56	0.40
1:BR:157:GLY:N	1:BR:160:ASN:OD1	2.39	0.40
1:BT:79:LEU:HD11	1:BT:305:LEU:HB2	2.02	0.40
1:CA:174:LYS:HE3	1:CA:318:GLN:HG3	2.02	0.40
1:CJ:107:ASP:OD2	1:CJ:110:ASN:ND2	2.43	0.40
1:CL:253:ASN:OD1	1:CL:253:ASN:N	2.54	0.40
1:CN:123:SER:O	1:CN:127:ILE:HG13	2.20	0.40
1:CS:91:LEU:HD21	1:CS:112:LEU:HD13	2.03	0.40
1:CS:119:TYR:CZ	1:CS:281:PRO:HG3	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CU:180:ILE:O	1:CU:184:ILE:HG13	2.21	0.40
1:CW:135:LEU:HD21	1:CW:255:LEU:HG	2.01	0.40
1:DA:59:THR:O	2:FC:61:ASN:ND2	2.54	0.40
1:DD:178:ASP:OD1	1:DD:178:ASP:N	2.52	0.40
2:DG:166:LEU:HB2	2:DG:170:LEU:HD23	2.03	0.40
2:DL:133:PRO:HG3	2:DL:161:SER:HA	2.04	0.40
2:EU:63:PRO:HB2	2:EU:85:GLU:HG2	2.03	0.40
2:EU:165:LYS:HB2	2:EU:171:PHE:CE2	2.56	0.40
2:EU:167:THR:HB	2:EU:170:LEU:HB3	2.03	0.40
2:FE:77:PHE:HE1	2:FE:84:LEU:HD22	1.86	0.40
5:HV:198:ASN:OD1	5:HV:201:GLU:HG3	2.20	0.40
5:II:200:THR:O	5:II:204:GLN:HG2	2.21	0.40
1:AI:209:THR:O	1:AI:213:LEU:HG	2.21	0.40
1:AN:84:LEU:HD13	1:AT:57:PRO:HB2	2.02	0.40
1:AU:203:VAL:HG13	1:AU:261:ILE:HG12	2.02	0.40
1:AX:35:GLU:O	1:AX:272:LYS:HA	2.22	0.40
1:AY:77:VAL:HG21	2:DU:32:LEU:HD23	2.03	0.40
1:BA:121:LEU:HB3	1:CY:51:ALA:HB2	2.04	0.40
1:BD:87:LYS:HD3	1:BD:296:TYR:CE2	2.56	0.40
1:BE:176:LYS:O	1:BE:180:ILE:HG13	2.21	0.40
1:BG:143:LYS:HE2	4:FV:37:GLU:HG2	2.02	0.40
1:BJ:92:LYS:O	1:BJ:96:GLU:HG3	2.21	0.40
1:BN:211:LEU:O	1:BN:214:VAL:HG22	2.22	0.40
1:BU:28:TRP:O	1:BU:262:TYR:OH	2.27	0.40
1:CD:180:ILE:O	1:CD:184:ILE:HG13	2.22	0.40
1:CJ:203:VAL:HG22	1:CJ:261:ILE:HG23	2.03	0.40
1:CL:180:ILE:O	1:CL:184:ILE:HG13	2.21	0.40
1:CR:62:ASN:ND2	2:FD:102:ASP:HB2	2.37	0.40
1:CZ:87:LYS:NZ	2:FH:53:THR:O	2.38	0.40
1:DC:47:VAL:HG22	1:DC:76:VAL:HG22	2.03	0.40
1:DD:82:LEU:HD12	1:DD:82:LEU:HA	1.95	0.40
2:DG:156:ASN:OD1	2:DG:181:ARG:HG3	2.20	0.40
2:DN:180:ASN:ND2	4:FM:186:ASN:O	2.52	0.40
2:EG:167:THR:HG22	2:EG:168:GLU:N	2.36	0.40
2:EK:23:LYS:HA	2:EK:45:PHE:CD2	2.56	0.40
2:EL:180:ASN:O	2:EM:180:ASN:ND2	2.55	0.40
2:EN:167:THR:HG22	2:EN:168:GLU:H	1.86	0.40
2:EP:22:MET:HA	2:EP:67:TYR:CZ	2.56	0.40
2:FA:181:ARG:HG2	2:FA:182:ALA:H	1.86	0.40
4:FR:144:ASN:HD21	4:FR:148:ALA:HB3	1.85	0.40
5:GU:211:LYS:O	5:GU:215:ILE:HG13	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:HD:211:LYS:O	5:HD:215:ILE:HG13	2.22	0.40
1:AA:85:GLN:HE22	1:AC:289:SER:HB2	1.86	0.40
1:AF:162:PRO:HG2	2:DH:31:LEU:HD11	2.04	0.40
1:AH:180:ILE:O	1:AH:184:ILE:HG13	2.22	0.40
1:AK:132:HIS:HA	1:AK:254:LEU:HD13	2.03	0.40
1:AL:57:PRO:HG2	1:AW:84:LEU:HD13	2.03	0.40
1:AM:150:ARG:HH22	2:DO:64:ALA:H	1.67	0.40
1:AN:86:TYR:OH	1:AT:55:ALA:O	2.30	0.40
1:AO:196:GLU:HB3	1:AO:265:ASN:ND2	2.36	0.40
1:AR:278:LEU:HD23	1:AR:278:LEU:HA	1.86	0.40
1:BI:41:MET:HE3	1:BI:83:LYS:HB3	2.04	0.40
1:BO:176:LYS:HB3	1:BO:178:ASP:OD1	2.21	0.40
1:BP:92:LYS:O	1:BP:96:GLU:HG3	2.20	0.40
1:BY:132:HIS:HA	1:BY:254:LEU:HD13	2.03	0.40
1:CB:124:SER:O	1:CB:128:LYS:HG3	2.21	0.40
1:CG:130:ILE:O	1:CG:134:VAL:HG23	2.21	0.40
1:CG:178:ASP:OD1	1:CG:178:ASP:N	2.53	0.40
1:CV:66:THR:HG22	4:GG:52:ARG:HB3	2.03	0.40
1:DB:150:ARG:CZ	4:GJ:63:PRO:HB3	2.52	0.40
1:DC:49:TRP:CZ3	1:DC:74:SER:HB3	2.56	0.40
1:DD:286:ASP:HB2	1:DD:294:HIS:HB2	2.03	0.40
2:DP:133:PRO:HG3	2:DP:161:SER:HA	2.04	0.40
2:DT:89:GLY:HA2	2:DT:141:GLN:O	2.22	0.40
2:EA:125:LYS:NZ	2:EA:169:ASP:OD1	2.45	0.40
2:EK:23:LYS:HG3	2:EK:24:ASN:N	2.36	0.40
2:EK:23:LYS:HE3	2:EK:23:LYS:HB2	1.95	0.40
2:EL:28:ASP:N	2:EL:28:ASP:OD1	2.54	0.40
2:ES:167:THR:HG22	2:ES:168:GLU:H	1.86	0.40
2:EV:114:THR:O	2:EW:114:THR:HB	2.20	0.40
2:EZ:114:THR:O	2:FA:114:THR:HB	2.21	0.40
2:FB:69:TYR:HE1	2:FB:100:ASP:HA	1.87	0.40
4:FW:37:GLU:O	4:FW:41:LYS:HD2	2.21	0.40
4:GE:120:ILE:HD12	4:GE:120:ILE:HA	1.95	0.40
1:AB:180:ILE:O	1:AB:184:ILE:HG13	2.21	0.40
1:AK:84:LEU:HD13	1:AV:57:PRO:HB2	2.03	0.40
1:AN:49:TRP:CE3	1:AN:74:SER:HB3	2.57	0.40
1:AO:232:ASP:O	1:AO:236:GLN:HG2	2.22	0.40
1:AR:121:LEU:O	1:AR:125:GLU:HG2	2.22	0.40
1:AR:231:GLU:O	1:AR:235:ILE:HG13	2.21	0.40
1:AV:158:LEU:HB3	1:AV:260:LEU:HD21	2.04	0.40
1:AW:97:LYS:HE2	1:AW:97:LYS:HB3	1.92	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:124:SER:O	1:BA:128:LYS:HG3	2.21	0.40
1:BB:36:ASP:CG	5:HL:214:ARG:HH22	2.24	0.40
1:BF:306:ALA:O	4:FT:31:LEU:HB2	2.20	0.40
1:BI:100:THR:HG22	1:BI:105:ILE:HG12	2.04	0.40
1:BK:164:GLN:OE1	1:BK:311:ILE:N	2.54	0.40
1:BL:7:ASN:HB3	1:BL:10:ALA:HB3	2.03	0.40
1:BR:229:LYS:O	1:BR:233:VAL:HG23	2.21	0.40
1:BV:96:GLU:O	1:BV:100:THR:HG23	2.20	0.40
1:CA:203:VAL:HG13	1:CA:261:ILE:HG12	2.03	0.40
1:CB:288:ASP:OD1	1:CB:289:SER:N	2.48	0.40
1:CD:169:VAL:HG22	1:CD:183:LYS:HG3	2.04	0.40
1:CH:16:ILE:HD11	1:CH:120:LYS:HE3	2.02	0.40
1:CH:78:ARG:O	1:CH:154:ASN:ND2	2.42	0.40
1:CO:277:MET:HA	1:CO:300:VAL:HB	2.04	0.40
1:CS:86:TYR:CD2	1:CV:70:ILE:HD11	2.55	0.40
1:CU:181:PHE:CZ	1:CU:233:VAL:HG12	2.57	0.40
1:CX:39:LEU:O	1:CX:274:SER:OG	2.24	0.40
1:DA:257:HIS:CG	1:DA:318:GLN:HG3	2.56	0.40
1:DB:277:MET:HA	1:DB:300:VAL:HB	2.04	0.40
1:DC:39:LEU:O	1:DC:274:SER:OG	2.23	0.40
1:DE:142:GLN:O	4:FS:39:ARG:HD2	2.21	0.40
2:DJ:133:PRO:HG3	2:DJ:161:SER:HA	2.03	0.40
2:DK:89:GLY:HA2	2:DK:141:GLN:O	2.21	0.40
2:EF:37:ASP:O	2:EF:41:GLN:NE2	2.55	0.40
2:EF:56:LYS:HD2	4:FW:56:PHE:HD1	1.86	0.40
2:EP:77:PHE:HB2	4:GA:138:LYS:HE2	2.02	0.40
2:EY:165:LYS:HB2	2:EY:171:PHE:CE2	2.57	0.40
2:FG:125:LYS:HD2	2:FG:169:ASP:HA	2.04	0.40
2:FH:74:LYS:HE2	2:FH:89:GLY:HA3	2.03	0.40
4:GF:35:SER:O	4:GF:41:LYS:HD2	2.21	0.40
4:GI:8:VAL:HG12	4:GI:12:GLN:NE2	2.36	0.40
5:HY:211:LYS:O	5:HY:214:ARG:HG2	2.21	0.40
5:IN:200:THR:O	5:IN:204:GLN:HG2	2.22	0.40
1:AB:158:LEU:HB3	1:AB:260:LEU:HD21	2.03	0.40
1:AC:209:THR:O	1:AC:213:LEU:HG	2.21	0.40
1:AG:231:GLU:O	1:AG:235:ILE:HG13	2.21	0.40
1:AJ:84:LEU:HB3	1:AM:57:PRO:HB2	2.03	0.40
1:AT:25:MET:SD	1:AT:134:VAL:HG21	2.62	0.40
1:AV:194:GLY:HA3	2:DN:36:ILE:HD12	2.03	0.40
1:BB:203:VAL:HA	1:BB:260:LEU:O	2.21	0.40
1:BO:41:MET:HG2	4:FX:111:PHE:HE2	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BP:196:GLU:HB3	1:BP:265:ASN:ND2	2.36	0.40
1:BQ:101:SER:OG	1:BQ:102:ASP:N	2.55	0.40
1:BU:286:ASP:HB2	1:BU:294:HIS:HB2	2.03	0.40
1:CA:79:LEU:HD11	1:CA:305:LEU:HB2	2.03	0.40
1:CF:16:ILE:HD11	1:CF:120:LYS:HE3	2.03	0.40
1:CG:277:MET:HA	1:CG:300:VAL:HB	2.03	0.40
1:CI:123:SER:O	1:CI:127:ILE:HG13	2.21	0.40
1:CP:197:PHE:CD2	1:CP:243:ASN:HB2	2.57	0.40
1:CW:178:ASP:N	1:CW:178:ASP:OD1	2.55	0.40
1:DC:267:GLU:H	1:DC:267:GLU:HG2	1.71	0.40
2:DK:133:PRO:HG3	2:DK:161:SER:HA	2.03	0.40
2:DS:140:ASN:HD21	2:DS:144:GLU:HB2	1.86	0.40
2:EC:136:LYS:HD3	2:EC:155:VAL:HG21	2.04	0.40
2:ED:167:THR:HG22	2:ED:168:GLU:H	1.86	0.40
2:EG:23:LYS:HG3	2:EG:24:ASN:H	1.86	0.40
4:FL:65:LEU:HD23	4:FL:65:LEU:HA	1.92	0.40
4:FY:141:LEU:HB3	4:FY:149:LEU:HD22	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	305/319 (96%)	302 (99%)	3 (1%)	0	100	100
1	AB	309/319 (97%)	302 (98%)	7 (2%)	0	100	100
1	AC	309/319 (97%)	303 (98%)	6 (2%)	0	100	100
1	AD	305/319 (96%)	302 (99%)	3 (1%)	0	100	100
1	AE	309/319 (97%)	305 (99%)	4 (1%)	0	100	100
1	AF	309/319 (97%)	305 (99%)	4 (1%)	0	100	100
1	AG	305/319 (96%)	301 (99%)	4 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AH	309/319 (97%)	305 (99%)	4 (1%)	0	100	100
1	AI	309/319 (97%)	307 (99%)	2 (1%)	0	100	100
1	AJ	305/319 (96%)	300 (98%)	5 (2%)	0	100	100
1	AK	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	AL	309/319 (97%)	304 (98%)	5 (2%)	0	100	100
1	AM	305/319 (96%)	301 (99%)	4 (1%)	0	100	100
1	AN	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	AO	309/319 (97%)	304 (98%)	5 (2%)	0	100	100
1	AP	305/319 (96%)	301 (99%)	4 (1%)	0	100	100
1	AQ	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	AR	309/319 (97%)	304 (98%)	5 (2%)	0	100	100
1	AS	309/319 (97%)	303 (98%)	6 (2%)	0	100	100
1	AT	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	AU	309/319 (97%)	305 (99%)	4 (1%)	0	100	100
1	AV	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	AW	309/319 (97%)	307 (99%)	2 (1%)	0	100	100
1	AX	309/319 (97%)	307 (99%)	2 (1%)	0	100	100
1	AY	309/319 (97%)	302 (98%)	7 (2%)	0	100	100
1	AZ	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	BA	309/319 (97%)	307 (99%)	2 (1%)	0	100	100
1	BB	309/319 (97%)	305 (99%)	4 (1%)	0	100	100
1	BC	294/319 (92%)	286 (97%)	8 (3%)	0	100	100
1	BD	305/319 (96%)	301 (99%)	4 (1%)	0	100	100
1	BE	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	BF	309/319 (97%)	304 (98%)	5 (2%)	0	100	100
1	BG	305/319 (96%)	300 (98%)	5 (2%)	0	100	100
1	BH	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	BI	309/319 (97%)	304 (98%)	5 (2%)	0	100	100
1	BJ	305/319 (96%)	299 (98%)	6 (2%)	0	100	100
1	BK	309/319 (97%)	305 (99%)	4 (1%)	0	100	100
1	BL	309/319 (97%)	305 (99%)	4 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BM	307/319 (96%)	304 (99%)	3 (1%)	0	100	100
1	BN	309/319 (97%)	304 (98%)	5 (2%)	0	100	100
1	BO	309/319 (97%)	304 (98%)	5 (2%)	0	100	100
1	BP	305/319 (96%)	302 (99%)	3 (1%)	0	100	100
1	BQ	309/319 (97%)	307 (99%)	2 (1%)	0	100	100
1	BR	307/319 (96%)	302 (98%)	5 (2%)	0	100	100
1	BS	309/319 (97%)	303 (98%)	6 (2%)	0	100	100
1	BT	293/319 (92%)	290 (99%)	3 (1%)	0	100	100
1	BU	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	BV	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	BW	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	BX	293/319 (92%)	289 (99%)	4 (1%)	0	100	100
1	BY	309/319 (97%)	304 (98%)	5 (2%)	0	100	100
1	BZ	309/319 (97%)	305 (99%)	4 (1%)	0	100	100
1	CA	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	CB	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	CC	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	CD	309/319 (97%)	304 (98%)	5 (2%)	0	100	100
1	CE	309/319 (97%)	302 (98%)	7 (2%)	0	100	100
1	CF	309/319 (97%)	305 (99%)	4 (1%)	0	100	100
1	CG	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	CH	309/319 (97%)	305 (99%)	4 (1%)	0	100	100
1	CI	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	CJ	309/319 (97%)	305 (99%)	4 (1%)	0	100	100
1	CK	309/319 (97%)	302 (98%)	7 (2%)	0	100	100
1	CL	309/319 (97%)	305 (99%)	4 (1%)	0	100	100
1	CM	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	CN	309/319 (97%)	307 (99%)	2 (1%)	0	100	100
1	CO	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	CP	309/319 (97%)	305 (99%)	4 (1%)	0	100	100
1	CQ	309/319 (97%)	306 (99%)	3 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CR	309/319 (97%)	307 (99%)	2 (1%)	0	100	100
1	CS	309/319 (97%)	304 (98%)	5 (2%)	0	100	100
1	CT	309/319 (97%)	303 (98%)	6 (2%)	0	100	100
1	CU	309/319 (97%)	307 (99%)	2 (1%)	0	100	100
1	CV	309/319 (97%)	305 (99%)	4 (1%)	0	100	100
1	CW	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	CX	309/319 (97%)	307 (99%)	2 (1%)	0	100	100
1	CY	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	CZ	309/319 (97%)	302 (98%)	7 (2%)	0	100	100
1	DA	309/319 (97%)	305 (99%)	4 (1%)	0	100	100
1	DB	309/319 (97%)	305 (99%)	4 (1%)	0	100	100
1	DC	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	DD	309/319 (97%)	306 (99%)	3 (1%)	0	100	100
1	DE	309/319 (97%)	304 (98%)	5 (2%)	0	100	100
2	DF	149/185 (80%)	148 (99%)	1 (1%)	0	100	100
2	DG	146/185 (79%)	145 (99%)	1 (1%)	0	100	100
2	DH	148/185 (80%)	147 (99%)	1 (1%)	0	100	100
2	DI	147/185 (80%)	143 (97%)	4 (3%)	0	100	100
2	DJ	148/185 (80%)	146 (99%)	2 (1%)	0	100	100
2	DK	147/185 (80%)	145 (99%)	2 (1%)	0	100	100
2	DL	148/185 (80%)	148 (100%)	0	0	100	100
2	DM	148/185 (80%)	146 (99%)	2 (1%)	0	100	100
2	DN	148/185 (80%)	146 (99%)	2 (1%)	0	100	100
2	DO	147/185 (80%)	144 (98%)	3 (2%)	0	100	100
2	DP	147/185 (80%)	145 (99%)	2 (1%)	0	100	100
2	DQ	146/185 (79%)	145 (99%)	1 (1%)	0	100	100
2	DR	148/185 (80%)	147 (99%)	1 (1%)	0	100	100
2	DS	162/185 (88%)	160 (99%)	2 (1%)	0	100	100
2	DT	148/185 (80%)	145 (98%)	3 (2%)	0	100	100
2	DU	147/185 (80%)	145 (99%)	2 (1%)	0	100	100
2	DV	147/185 (80%)	146 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	DW	147/185 (80%)	145 (99%)	2 (1%)	0	100	100
2	DX	154/185 (83%)	153 (99%)	1 (1%)	0	100	100
2	DY	145/185 (78%)	142 (98%)	3 (2%)	0	100	100
2	DZ	148/185 (80%)	147 (99%)	1 (1%)	0	100	100
2	EA	114/185 (62%)	113 (99%)	1 (1%)	0	100	100
2	EB	154/185 (83%)	152 (99%)	2 (1%)	0	100	100
2	EC	147/185 (80%)	146 (99%)	1 (1%)	0	100	100
2	ED	156/185 (84%)	153 (98%)	3 (2%)	0	100	100
2	EE	154/185 (83%)	153 (99%)	1 (1%)	0	100	100
2	EF	148/185 (80%)	146 (99%)	2 (1%)	0	100	100
2	EG	171/185 (92%)	168 (98%)	3 (2%)	0	100	100
2	EH	147/185 (80%)	146 (99%)	1 (1%)	0	100	100
2	EI	153/185 (83%)	152 (99%)	1 (1%)	0	100	100
2	EJ	160/185 (86%)	159 (99%)	1 (1%)	0	100	100
2	EK	162/185 (88%)	161 (99%)	1 (1%)	0	100	100
2	EL	146/185 (79%)	144 (99%)	2 (1%)	0	100	100
2	EM	148/185 (80%)	146 (99%)	2 (1%)	0	100	100
2	EN	147/185 (80%)	145 (99%)	2 (1%)	0	100	100
2	EO	164/185 (89%)	163 (99%)	1 (1%)	0	100	100
2	EP	147/185 (80%)	145 (99%)	2 (1%)	0	100	100
2	EQ	154/185 (83%)	153 (99%)	1 (1%)	0	100	100
2	ER	145/185 (78%)	142 (98%)	3 (2%)	0	100	100
2	ES	148/185 (80%)	146 (99%)	2 (1%)	0	100	100
2	ET	147/185 (80%)	145 (99%)	2 (1%)	0	100	100
2	EU	154/185 (83%)	153 (99%)	1 (1%)	0	100	100
2	EV	145/185 (78%)	143 (99%)	2 (1%)	0	100	100
2	EW	148/185 (80%)	145 (98%)	3 (2%)	0	100	100
2	EX	147/185 (80%)	146 (99%)	1 (1%)	0	100	100
2	EY	154/185 (83%)	152 (99%)	2 (1%)	0	100	100
2	EZ	145/185 (78%)	144 (99%)	1 (1%)	0	100	100
2	FA	148/185 (80%)	147 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	FB	147/185 (80%)	146 (99%)	1 (1%)	0	100	100
2	FC	154/185 (83%)	152 (99%)	2 (1%)	0	100	100
2	FD	145/185 (78%)	142 (98%)	3 (2%)	0	100	100
2	FE	148/185 (80%)	147 (99%)	1 (1%)	0	100	100
2	FF	147/185 (80%)	146 (99%)	1 (1%)	0	100	100
2	FG	154/185 (83%)	152 (99%)	2 (1%)	0	100	100
2	FH	145/185 (78%)	142 (98%)	3 (2%)	0	100	100
2	FI	148/185 (80%)	147 (99%)	1 (1%)	0	100	100
3	FJ	153/254 (60%)	152 (99%)	1 (1%)	0	100	100
4	FK	146/190 (77%)	144 (99%)	2 (1%)	0	100	100
4	FL	146/190 (77%)	145 (99%)	1 (1%)	0	100	100
4	FM	147/190 (77%)	144 (98%)	3 (2%)	0	100	100
4	FN	146/190 (77%)	145 (99%)	1 (1%)	0	100	100
4	FO	150/190 (79%)	146 (97%)	4 (3%)	0	100	100
4	FP	146/190 (77%)	145 (99%)	1 (1%)	0	100	100
4	FQ	165/190 (87%)	160 (97%)	5 (3%)	0	100	100
4	FR	165/190 (87%)	162 (98%)	3 (2%)	0	100	100
4	FS	165/190 (87%)	162 (98%)	3 (2%)	0	100	100
4	FT	138/190 (73%)	136 (99%)	2 (1%)	0	100	100
4	FU	145/190 (76%)	141 (97%)	4 (3%)	0	100	100
4	FV	148/190 (78%)	145 (98%)	3 (2%)	0	100	100
4	FW	148/190 (78%)	145 (98%)	3 (2%)	0	100	100
4	FX	145/190 (76%)	141 (97%)	4 (3%)	0	100	100
4	FY	145/190 (76%)	142 (98%)	3 (2%)	0	100	100
4	FZ	146/190 (77%)	145 (99%)	1 (1%)	0	100	100
4	GA	165/190 (87%)	164 (99%)	1 (1%)	0	100	100
4	GB	165/190 (87%)	161 (98%)	4 (2%)	0	100	100
4	GC	165/190 (87%)	164 (99%)	1 (1%)	0	100	100
4	GD	165/190 (87%)	163 (99%)	2 (1%)	0	100	100
4	GE	165/190 (87%)	163 (99%)	2 (1%)	0	100	100
4	GF	165/190 (87%)	163 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	GG	165/190 (87%)	163 (99%)	2 (1%)	0	100	100
4	GH	165/190 (87%)	163 (99%)	2 (1%)	0	100	100
4	GI	165/190 (87%)	164 (99%)	1 (1%)	0	100	100
4	GJ	165/190 (87%)	162 (98%)	3 (2%)	0	100	100
5	GK	28/230 (12%)	28 (100%)	0	0	100	100
5	GL	35/230 (15%)	35 (100%)	0	0	100	100
5	GM	35/230 (15%)	35 (100%)	0	0	100	100
5	GN	35/230 (15%)	35 (100%)	0	0	100	100
5	GO	35/230 (15%)	35 (100%)	0	0	100	100
5	GP	35/230 (15%)	35 (100%)	0	0	100	100
5	GQ	35/230 (15%)	35 (100%)	0	0	100	100
5	GR	35/230 (15%)	35 (100%)	0	0	100	100
5	GS	35/230 (15%)	35 (100%)	0	0	100	100
5	GT	35/230 (15%)	35 (100%)	0	0	100	100
5	GU	35/230 (15%)	35 (100%)	0	0	100	100
5	GV	35/230 (15%)	35 (100%)	0	0	100	100
5	GW	28/230 (12%)	28 (100%)	0	0	100	100
5	GX	35/230 (15%)	35 (100%)	0	0	100	100
5	GY	35/230 (15%)	35 (100%)	0	0	100	100
5	GZ	35/230 (15%)	35 (100%)	0	0	100	100
5	HA	35/230 (15%)	35 (100%)	0	0	100	100
5	HB	35/230 (15%)	35 (100%)	0	0	100	100
5	HC	35/230 (15%)	35 (100%)	0	0	100	100
5	HD	28/230 (12%)	28 (100%)	0	0	100	100
5	HE	35/230 (15%)	35 (100%)	0	0	100	100
5	HF	35/230 (15%)	35 (100%)	0	0	100	100
5	HG	35/230 (15%)	35 (100%)	0	0	100	100
5	HH	28/230 (12%)	28 (100%)	0	0	100	100
5	HI	28/230 (12%)	28 (100%)	0	0	100	100
5	HJ	28/230 (12%)	28 (100%)	0	0	100	100
5	HK	28/230 (12%)	28 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	HL	35/230 (15%)	35 (100%)	0	0	100	100
5	HM	27/230 (12%)	27 (100%)	0	0	100	100
5	HN	35/230 (15%)	35 (100%)	0	0	100	100
5	HO	35/230 (15%)	35 (100%)	0	0	100	100
5	HP	35/230 (15%)	35 (100%)	0	0	100	100
5	HQ	35/230 (15%)	35 (100%)	0	0	100	100
5	HR	35/230 (15%)	35 (100%)	0	0	100	100
5	HS	35/230 (15%)	35 (100%)	0	0	100	100
5	HT	35/230 (15%)	35 (100%)	0	0	100	100
5	HU	35/230 (15%)	35 (100%)	0	0	100	100
5	HV	35/230 (15%)	35 (100%)	0	0	100	100
5	HW	26/230 (11%)	26 (100%)	0	0	100	100
5	HX	35/230 (15%)	35 (100%)	0	0	100	100
5	HY	35/230 (15%)	35 (100%)	0	0	100	100
5	HZ	35/230 (15%)	35 (100%)	0	0	100	100
5	IA	35/230 (15%)	35 (100%)	0	0	100	100
5	IB	27/230 (12%)	27 (100%)	0	0	100	100
5	IC	35/230 (15%)	35 (100%)	0	0	100	100
5	ID	27/230 (12%)	27 (100%)	0	0	100	100
5	IE	35/230 (15%)	35 (100%)	0	0	100	100
5	IF	35/230 (15%)	35 (100%)	0	0	100	100
5	IG	35/230 (15%)	35 (100%)	0	0	100	100
5	IH	27/230 (12%)	27 (100%)	0	0	100	100
5	II	28/230 (12%)	28 (100%)	0	0	100	100
5	IJ	28/230 (12%)	28 (100%)	0	0	100	100
5	IK	28/230 (12%)	28 (100%)	0	0	100	100
5	IL	38/230 (16%)	38 (100%)	0	0	100	100
5	IM	35/230 (15%)	35 (100%)	0	0	100	100
5	IN	35/230 (15%)	35 (100%)	0	0	100	100
5	IO	38/230 (16%)	38 (100%)	0	0	100	100
5	IP	35/230 (15%)	35 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	IQ	35/230 (15%)	35 (100%)	0	0	100	100
5	IR	38/230 (16%)	38 (100%)	0	0	100	100
5	IS	35/230 (15%)	35 (100%)	0	0	100	100
5	IT	35/230 (15%)	35 (100%)	0	0	100	100
5	IU	38/230 (16%)	38 (100%)	0	0	100	100
5	IV	35/230 (15%)	35 (100%)	0	0	100	100
5	IW	35/230 (15%)	35 (100%)	0	0	100	100
5	IX	35/230 (15%)	35 (100%)	0	0	100	100
5	IY	38/230 (16%)	38 (100%)	0	0	100	100
5	IZ	35/230 (15%)	35 (100%)	0	0	100	100
5	JA	38/230 (16%)	38 (100%)	0	0	100	100
5	JB	35/230 (15%)	35 (100%)	0	0	100	100
5	JC	35/230 (15%)	35 (100%)	0	0	100	100
5	JD	38/230 (16%)	38 (100%)	0	0	100	100
5	JE	35/230 (15%)	35 (100%)	0	0	100	100
5	JF	35/230 (15%)	35 (100%)	0	0	100	100
5	JG	38/230 (16%)	38 (100%)	0	0	100	100
5	JH	35/230 (15%)	35 (100%)	0	0	100	100
5	JI	35/230 (15%)	35 (100%)	0	0	100	100
5	JJ	38/230 (16%)	38 (100%)	0	0	100	100
5	JK	35/230 (15%)	35 (100%)	0	0	100	100
5	JL	35/230 (15%)	35 (100%)	0	0	100	100
5	JM	35/230 (15%)	35 (100%)	0	0	100	100
5	JN	38/230 (16%)	38 (100%)	0	0	100	100
5	JO	35/230 (15%)	35 (100%)	0	0	100	100
All	All	40930/61121 (67%)	40441 (99%)	489 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM

entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AA	281/286 (98%)	281 (100%)	0	100	100
1	AB	283/286 (99%)	283 (100%)	0	100	100
1	AC	283/286 (99%)	283 (100%)	0	100	100
1	AD	281/286 (98%)	281 (100%)	0	100	100
1	AE	283/286 (99%)	283 (100%)	0	100	100
1	AF	283/286 (99%)	283 (100%)	0	100	100
1	AG	281/286 (98%)	281 (100%)	0	100	100
1	AH	283/286 (99%)	283 (100%)	0	100	100
1	AI	283/286 (99%)	283 (100%)	0	100	100
1	AJ	281/286 (98%)	281 (100%)	0	100	100
1	AK	283/286 (99%)	283 (100%)	0	100	100
1	AL	283/286 (99%)	283 (100%)	0	100	100
1	AM	281/286 (98%)	281 (100%)	0	100	100
1	AN	283/286 (99%)	283 (100%)	0	100	100
1	AO	283/286 (99%)	283 (100%)	0	100	100
1	AP	281/286 (98%)	281 (100%)	0	100	100
1	AQ	283/286 (99%)	283 (100%)	0	100	100
1	AR	283/286 (99%)	283 (100%)	0	100	100
1	AS	283/286 (99%)	283 (100%)	0	100	100
1	AT	283/286 (99%)	283 (100%)	0	100	100
1	AU	283/286 (99%)	283 (100%)	0	100	100
1	AV	283/286 (99%)	283 (100%)	0	100	100
1	AW	283/286 (99%)	283 (100%)	0	100	100
1	AX	283/286 (99%)	283 (100%)	0	100	100
1	AY	283/286 (99%)	283 (100%)	0	100	100
1	AZ	283/286 (99%)	283 (100%)	0	100	100
1	BA	283/286 (99%)	283 (100%)	0	100	100
1	BB	283/286 (99%)	283 (100%)	0	100	100
1	BC	271/286 (95%)	271 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BD	281/286 (98%)	281 (100%)	0	100	100
1	BE	283/286 (99%)	283 (100%)	0	100	100
1	BF	283/286 (99%)	283 (100%)	0	100	100
1	BG	281/286 (98%)	281 (100%)	0	100	100
1	BH	283/286 (99%)	283 (100%)	0	100	100
1	BI	283/286 (99%)	283 (100%)	0	100	100
1	BJ	281/286 (98%)	281 (100%)	0	100	100
1	BK	283/286 (99%)	283 (100%)	0	100	100
1	BL	283/286 (99%)	283 (100%)	0	100	100
1	BM	283/286 (99%)	283 (100%)	0	100	100
1	BN	283/286 (99%)	283 (100%)	0	100	100
1	BO	283/286 (99%)	283 (100%)	0	100	100
1	BP	281/286 (98%)	281 (100%)	0	100	100
1	BQ	283/286 (99%)	283 (100%)	0	100	100
1	BR	283/286 (99%)	283 (100%)	0	100	100
1	BS	283/286 (99%)	283 (100%)	0	100	100
1	BT	271/286 (95%)	271 (100%)	0	100	100
1	BU	283/286 (99%)	283 (100%)	0	100	100
1	BV	283/286 (99%)	283 (100%)	0	100	100
1	BW	283/286 (99%)	283 (100%)	0	100	100
1	BX	271/286 (95%)	271 (100%)	0	100	100
1	BY	283/286 (99%)	283 (100%)	0	100	100
1	BZ	283/286 (99%)	283 (100%)	0	100	100
1	CA	283/286 (99%)	283 (100%)	0	100	100
1	CB	283/286 (99%)	283 (100%)	0	100	100
1	CC	283/286 (99%)	283 (100%)	0	100	100
1	CD	283/286 (99%)	283 (100%)	0	100	100
1	CE	283/286 (99%)	283 (100%)	0	100	100
1	CF	283/286 (99%)	283 (100%)	0	100	100
1	CG	283/286 (99%)	283 (100%)	0	100	100
1	CH	283/286 (99%)	283 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CI	283/286 (99%)	283 (100%)	0	100	100
1	CJ	283/286 (99%)	283 (100%)	0	100	100
1	CK	283/286 (99%)	283 (100%)	0	100	100
1	CL	283/286 (99%)	283 (100%)	0	100	100
1	CM	283/286 (99%)	283 (100%)	0	100	100
1	CN	283/286 (99%)	283 (100%)	0	100	100
1	CO	283/286 (99%)	283 (100%)	0	100	100
1	CP	283/286 (99%)	283 (100%)	0	100	100
1	CQ	283/286 (99%)	283 (100%)	0	100	100
1	CR	283/286 (99%)	283 (100%)	0	100	100
1	CS	283/286 (99%)	283 (100%)	0	100	100
1	CT	283/286 (99%)	283 (100%)	0	100	100
1	CU	283/286 (99%)	283 (100%)	0	100	100
1	CV	283/286 (99%)	283 (100%)	0	100	100
1	CW	283/286 (99%)	283 (100%)	0	100	100
1	CX	283/286 (99%)	283 (100%)	0	100	100
1	CY	283/286 (99%)	283 (100%)	0	100	100
1	CZ	283/286 (99%)	283 (100%)	0	100	100
1	DA	283/286 (99%)	283 (100%)	0	100	100
1	DB	283/286 (99%)	283 (100%)	0	100	100
1	DC	283/286 (99%)	283 (100%)	0	100	100
1	DD	283/286 (99%)	283 (100%)	0	100	100
1	DE	283/286 (99%)	283 (100%)	0	100	100
2	DF	130/154 (84%)	130 (100%)	0	100	100
2	DG	129/154 (84%)	129 (100%)	0	100	100
2	DH	130/154 (84%)	130 (100%)	0	100	100
2	DI	129/154 (84%)	129 (100%)	0	100	100
2	DJ	130/154 (84%)	130 (100%)	0	100	100
2	DK	129/154 (84%)	129 (100%)	0	100	100
2	DL	130/154 (84%)	130 (100%)	0	100	100
2	DM	129/154 (84%)	129 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	DN	130/154 (84%)	130 (100%)	0	100	100
2	DO	129/154 (84%)	129 (100%)	0	100	100
2	DP	129/154 (84%)	129 (100%)	0	100	100
2	DQ	129/154 (84%)	129 (100%)	0	100	100
2	DR	130/154 (84%)	130 (100%)	0	100	100
2	DS	142/154 (92%)	142 (100%)	0	100	100
2	DT	130/154 (84%)	130 (100%)	0	100	100
2	DU	128/154 (83%)	128 (100%)	0	100	100
2	DV	129/154 (84%)	129 (100%)	0	100	100
2	DW	128/154 (83%)	128 (100%)	0	100	100
2	DX	132/154 (86%)	132 (100%)	0	100	100
2	DY	127/154 (82%)	127 (100%)	0	100	100
2	DZ	130/154 (84%)	130 (100%)	0	100	100
2	EA	99/154 (64%)	99 (100%)	0	100	100
2	EB	132/154 (86%)	132 (100%)	0	100	100
2	EC	129/154 (84%)	129 (100%)	0	100	100
2	ED	133/154 (86%)	133 (100%)	0	100	100
2	EE	131/154 (85%)	131 (100%)	0	100	100
2	EF	130/154 (84%)	130 (100%)	0	100	100
2	EG	147/154 (96%)	147 (100%)	0	100	100
2	EH	129/154 (84%)	129 (100%)	0	100	100
2	EI	131/154 (85%)	131 (100%)	0	100	100
2	EJ	141/154 (92%)	141 (100%)	0	100	100
2	EK	142/154 (92%)	142 (100%)	0	100	100
2	EL	129/154 (84%)	129 (100%)	0	100	100
2	EM	130/154 (84%)	130 (100%)	0	100	100
2	EN	129/154 (84%)	129 (100%)	0	100	100
2	EO	144/154 (94%)	144 (100%)	0	100	100
2	EP	128/154 (83%)	128 (100%)	0	100	100
2	EQ	132/154 (86%)	132 (100%)	0	100	100
2	ER	127/154 (82%)	127 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	ES	130/154 (84%)	130 (100%)	0	100	100
2	ET	128/154 (83%)	128 (100%)	0	100	100
2	EU	132/154 (86%)	132 (100%)	0	100	100
2	EV	127/154 (82%)	127 (100%)	0	100	100
2	EW	130/154 (84%)	130 (100%)	0	100	100
2	EX	128/154 (83%)	128 (100%)	0	100	100
2	EY	132/154 (86%)	132 (100%)	0	100	100
2	EZ	127/154 (82%)	127 (100%)	0	100	100
2	FA	130/154 (84%)	130 (100%)	0	100	100
2	FB	128/154 (83%)	128 (100%)	0	100	100
2	FC	132/154 (86%)	132 (100%)	0	100	100
2	FD	127/154 (82%)	127 (100%)	0	100	100
2	FE	130/154 (84%)	130 (100%)	0	100	100
2	FF	128/154 (83%)	128 (100%)	0	100	100
2	FG	132/154 (86%)	132 (100%)	0	100	100
2	FH	127/154 (82%)	127 (100%)	0	100	100
2	FI	130/154 (84%)	130 (100%)	0	100	100
3	FJ	141/218 (65%)	141 (100%)	0	100	100
4	FK	130/163 (80%)	130 (100%)	0	100	100
4	FL	130/163 (80%)	130 (100%)	0	100	100
4	FM	131/163 (80%)	131 (100%)	0	100	100
4	FN	130/163 (80%)	130 (100%)	0	100	100
4	FO	133/163 (82%)	133 (100%)	0	100	100
4	FP	129/163 (79%)	129 (100%)	0	100	100
4	FQ	148/163 (91%)	148 (100%)	0	100	100
4	FR	148/163 (91%)	148 (100%)	0	100	100
4	FS	148/163 (91%)	148 (100%)	0	100	100
4	FT	124/163 (76%)	124 (100%)	0	100	100
4	FU	130/163 (80%)	130 (100%)	0	100	100
4	FV	131/163 (80%)	131 (100%)	0	100	100
4	FW	131/163 (80%)	131 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	FX	129/163 (79%)	129 (100%)	0	100	100
4	FY	129/163 (79%)	129 (100%)	0	100	100
4	FZ	130/163 (80%)	130 (100%)	0	100	100
4	GA	148/163 (91%)	148 (100%)	0	100	100
4	GB	148/163 (91%)	148 (100%)	0	100	100
4	GC	148/163 (91%)	148 (100%)	0	100	100
4	GD	148/163 (91%)	148 (100%)	0	100	100
4	GE	148/163 (91%)	148 (100%)	0	100	100
4	GF	148/163 (91%)	148 (100%)	0	100	100
4	GG	148/163 (91%)	148 (100%)	0	100	100
4	GH	148/163 (91%)	148 (100%)	0	100	100
4	GI	148/163 (91%)	148 (100%)	0	100	100
4	GJ	148/163 (91%)	148 (100%)	0	100	100
5	GK	29/210 (14%)	29 (100%)	0	100	100
5	GL	35/210 (17%)	35 (100%)	0	100	100
5	GM	35/210 (17%)	35 (100%)	0	100	100
5	GN	35/210 (17%)	35 (100%)	0	100	100
5	GO	35/210 (17%)	35 (100%)	0	100	100
5	GP	35/210 (17%)	35 (100%)	0	100	100
5	GQ	35/210 (17%)	35 (100%)	0	100	100
5	GR	35/210 (17%)	35 (100%)	0	100	100
5	GS	35/210 (17%)	35 (100%)	0	100	100
5	GT	35/210 (17%)	35 (100%)	0	100	100
5	GU	35/210 (17%)	35 (100%)	0	100	100
5	GV	35/210 (17%)	35 (100%)	0	100	100
5	GW	29/210 (14%)	29 (100%)	0	100	100
5	GX	35/210 (17%)	35 (100%)	0	100	100
5	GY	35/210 (17%)	35 (100%)	0	100	100
5	GZ	35/210 (17%)	35 (100%)	0	100	100
5	HA	35/210 (17%)	35 (100%)	0	100	100
5	HB	35/210 (17%)	35 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	HC	35/210 (17%)	35 (100%)	0	100	100
5	HD	29/210 (14%)	29 (100%)	0	100	100
5	HE	35/210 (17%)	35 (100%)	0	100	100
5	HF	35/210 (17%)	35 (100%)	0	100	100
5	HG	35/210 (17%)	35 (100%)	0	100	100
5	HH	29/210 (14%)	29 (100%)	0	100	100
5	HI	29/210 (14%)	29 (100%)	0	100	100
5	HJ	29/210 (14%)	29 (100%)	0	100	100
5	HK	29/210 (14%)	29 (100%)	0	100	100
5	HL	35/210 (17%)	35 (100%)	0	100	100
5	HM	28/210 (13%)	28 (100%)	0	100	100
5	HN	35/210 (17%)	35 (100%)	0	100	100
5	HO	35/210 (17%)	35 (100%)	0	100	100
5	HP	35/210 (17%)	35 (100%)	0	100	100
5	HQ	35/210 (17%)	35 (100%)	0	100	100
5	HR	35/210 (17%)	35 (100%)	0	100	100
5	HS	35/210 (17%)	35 (100%)	0	100	100
5	HT	35/210 (17%)	35 (100%)	0	100	100
5	HU	35/210 (17%)	35 (100%)	0	100	100
5	HV	35/210 (17%)	35 (100%)	0	100	100
5	HW	27/210 (13%)	27 (100%)	0	100	100
5	HX	35/210 (17%)	35 (100%)	0	100	100
5	HY	35/210 (17%)	35 (100%)	0	100	100
5	HZ	35/210 (17%)	35 (100%)	0	100	100
5	IA	35/210 (17%)	35 (100%)	0	100	100
5	IB	28/210 (13%)	28 (100%)	0	100	100
5	IC	35/210 (17%)	35 (100%)	0	100	100
5	ID	28/210 (13%)	28 (100%)	0	100	100
5	IE	35/210 (17%)	35 (100%)	0	100	100
5	IF	35/210 (17%)	35 (100%)	0	100	100
5	IG	35/210 (17%)	35 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	IH	28/210 (13%)	28 (100%)	0	100	100
5	II	29/210 (14%)	29 (100%)	0	100	100
5	IJ	29/210 (14%)	29 (100%)	0	100	100
5	IK	29/210 (14%)	29 (100%)	0	100	100
5	IL	38/210 (18%)	38 (100%)	0	100	100
5	IM	35/210 (17%)	35 (100%)	0	100	100
5	IN	35/210 (17%)	35 (100%)	0	100	100
5	IO	38/210 (18%)	38 (100%)	0	100	100
5	IP	35/210 (17%)	35 (100%)	0	100	100
5	IQ	35/210 (17%)	35 (100%)	0	100	100
5	IR	38/210 (18%)	38 (100%)	0	100	100
5	IS	35/210 (17%)	35 (100%)	0	100	100
5	IT	35/210 (17%)	35 (100%)	0	100	100
5	IU	38/210 (18%)	38 (100%)	0	100	100
5	IV	35/210 (17%)	35 (100%)	0	100	100
5	IW	35/210 (17%)	35 (100%)	0	100	100
5	IX	35/210 (17%)	35 (100%)	0	100	100
5	IY	38/210 (18%)	38 (100%)	0	100	100
5	IZ	35/210 (17%)	35 (100%)	0	100	100
5	JA	38/210 (18%)	38 (100%)	0	100	100
5	JB	35/210 (17%)	35 (100%)	0	100	100
5	JC	35/210 (17%)	35 (100%)	0	100	100
5	JD	38/210 (18%)	38 (100%)	0	100	100
5	JE	35/210 (17%)	35 (100%)	0	100	100
5	JF	35/210 (17%)	35 (100%)	0	100	100
5	JG	38/210 (18%)	38 (100%)	0	100	100
5	JH	35/210 (17%)	35 (100%)	0	100	100
5	JI	35/210 (17%)	35 (100%)	0	100	100
5	JJ	38/210 (18%)	38 (100%)	0	100	100
5	JK	35/210 (17%)	35 (100%)	0	100	100
5	JL	35/210 (17%)	35 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	JM	35/210 (17%)	35 (100%)	0	100	100
5	JN	38/210 (18%)	38 (100%)	0	100	100
5	JO	35/210 (17%)	35 (100%)	0	100	100
All	All	37314/54248 (69%)	37314 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (56) such sidechains are listed below:

Mol	Chain	Res	Type
1	AB	54	ASN
1	AF	257	HIS
1	AF	318	GLN
1	AK	85	GLN
1	AK	110	ASN
1	AN	110	ASN
1	AN	142	GLN
1	AN	147	ASN
1	AS	62	ASN
1	AU	80	ASN
1	AW	54	ASN
1	AY	85	GLN
1	AY	110	ASN
1	AZ	110	ASN
1	BA	54	ASN
1	BA	110	ASN
1	BB	313	GLN
1	BL	44	GLN
1	BO	109	ASN
1	BS	257	HIS
1	BS	318	GLN
1	BT	318	GLN
1	BX	54	ASN
1	BX	85	GLN
1	BY	85	GLN
1	BY	110	ASN
1	BZ	110	ASN
1	CA	110	ASN
1	CH	62	ASN
1	CJ	85	GLN
1	CK	62	ASN

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Mol	Chain	Res	Type
1	CP	110	ASN
1	CY	54	ASN
1	DC	62	ASN
1	DE	110	ASN
2	DV	115	ASN
2	DX	115	ASN
2	EG	47	ASN
2	EH	41	GLN
2	EI	24	ASN
2	EI	34	ASN
2	EN	115	ASN
2	EO	156	ASN
2	EP	61	ASN
2	ER	180	ASN
2	FF	156	ASN
2	FF	180	ASN
3	FJ	162	ASN
4	FM	88	HIS
4	FO	162	ASN
4	FS	88	HIS
4	FT	24	ASN
4	FW	186	ASN
4	GF	88	HIS
4	GH	88	HIS
4	GJ	88	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

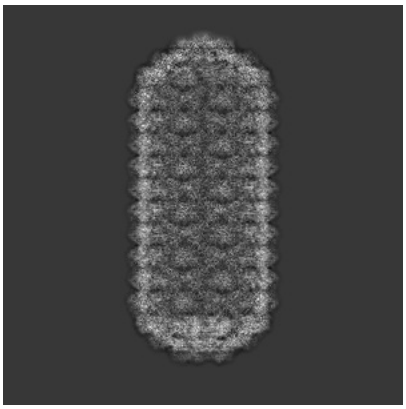
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-17739. These allow visual inspection of the internal detail of the map and identification of artifacts.

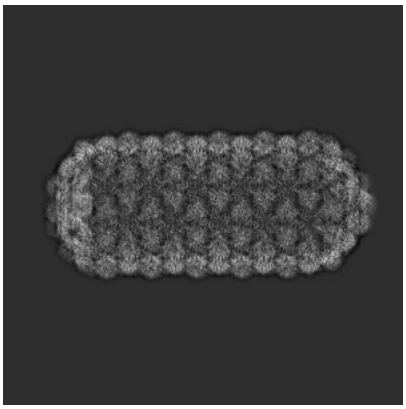
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

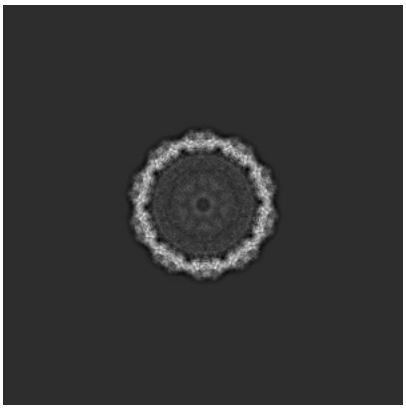
6.1.1 Primary map



X

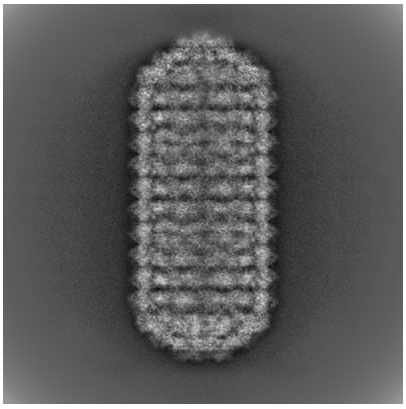


Y

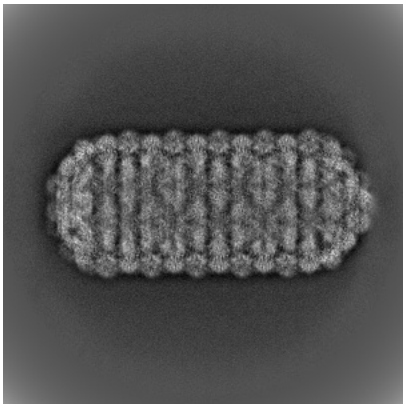


Z

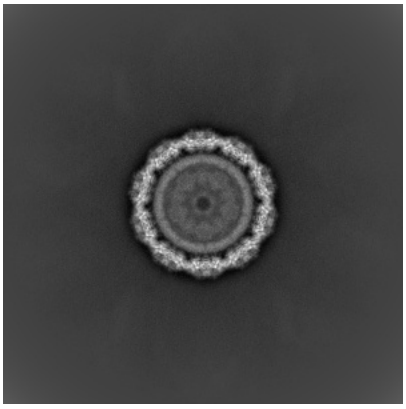
6.1.2 Raw map



X



Y

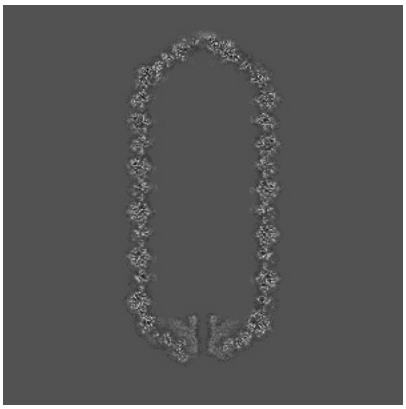


Z

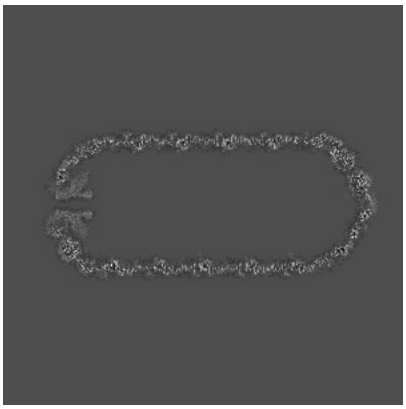
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

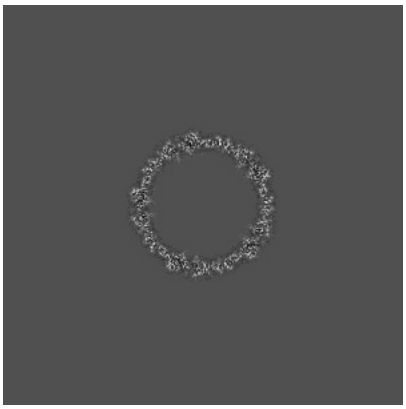
6.2.1 Primary map



X Index: 360

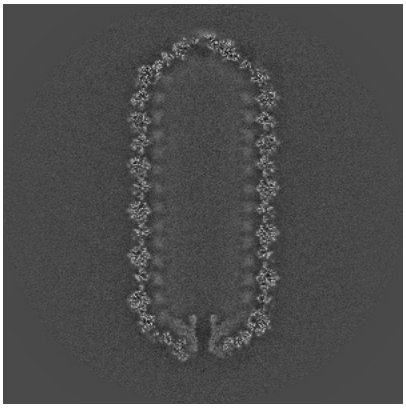


Y Index: 360

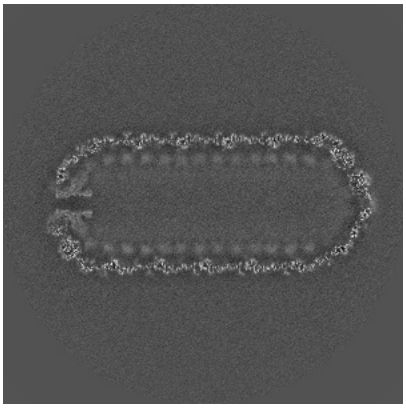


Z Index: 360

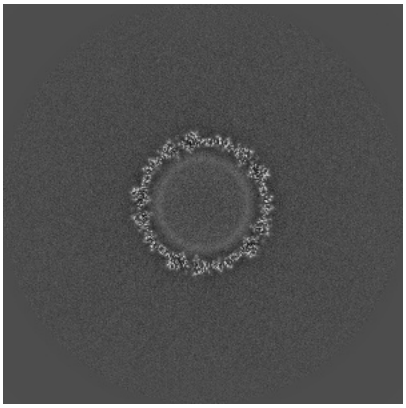
6.2.2 Raw map



X Index: 360



Y Index: 360

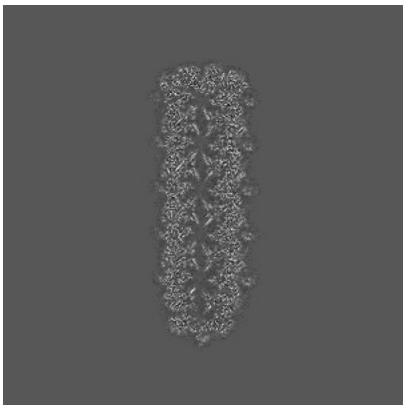


Z Index: 360

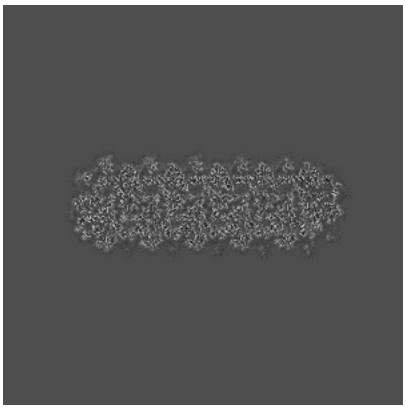
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

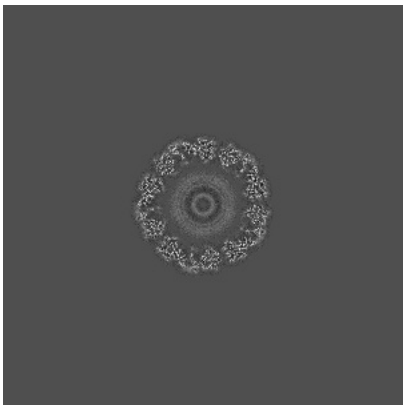
6.3.1 Primary map



X Index: 260

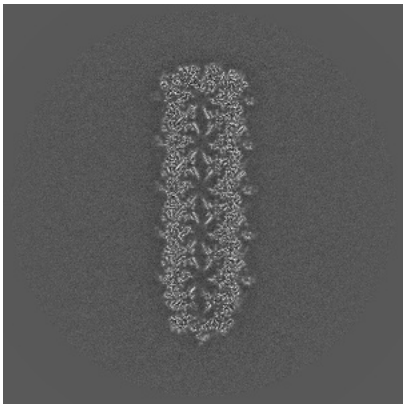


Y Index: 465

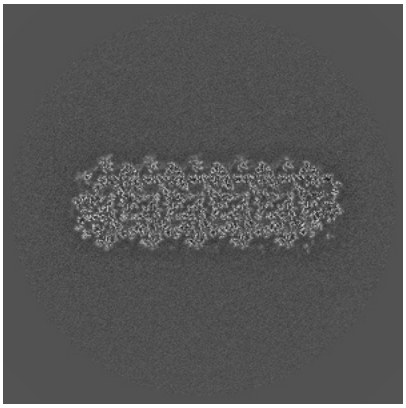


Z Index: 145

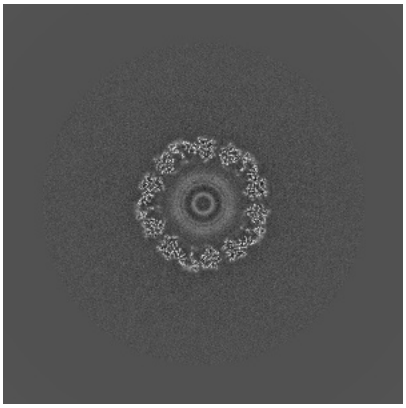
6.3.2 Raw map



X Index: 260



Y Index: 465

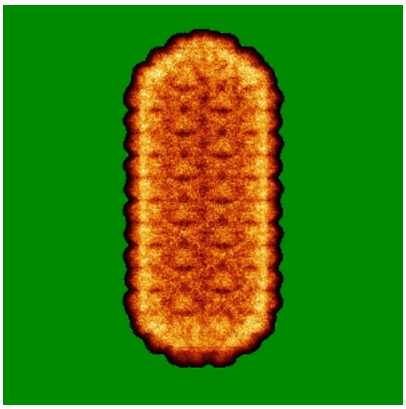


Z Index: 145

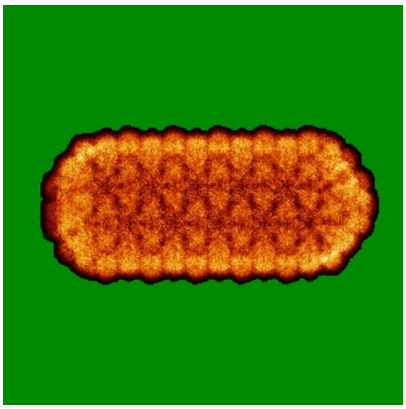
The images above show the largest variance slices of the map in three orthogonal directions.

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

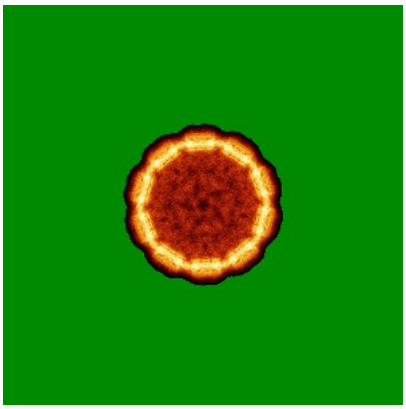
6.4.1 Primary map



X

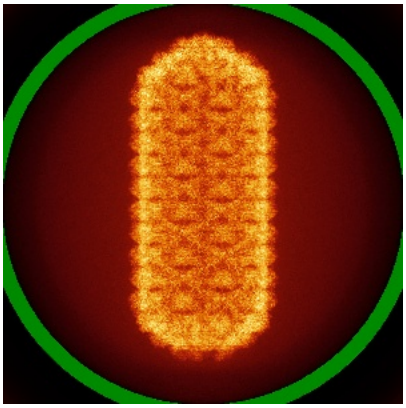


Y

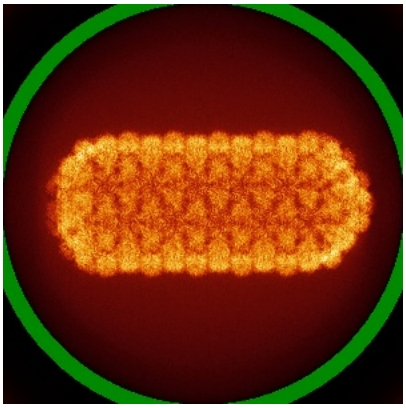


Z

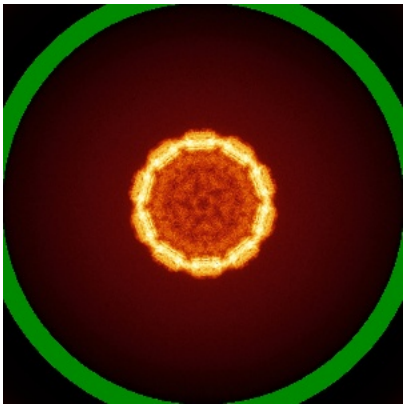
6.4.2 Raw map



X



Y

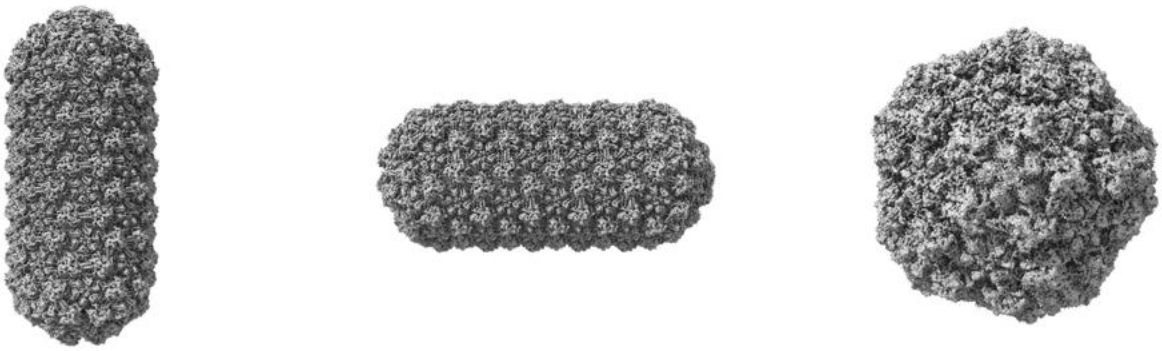


Z

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)

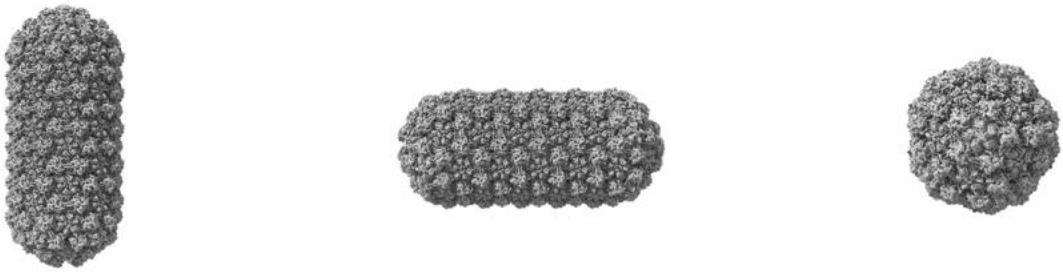
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

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

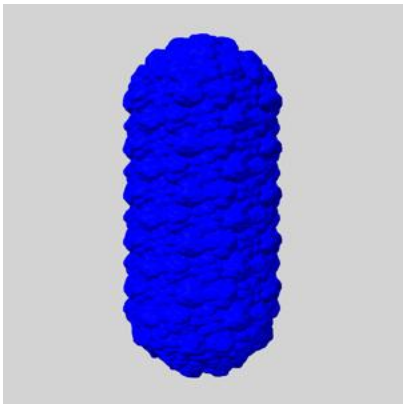
6.6 Mask visualisation

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

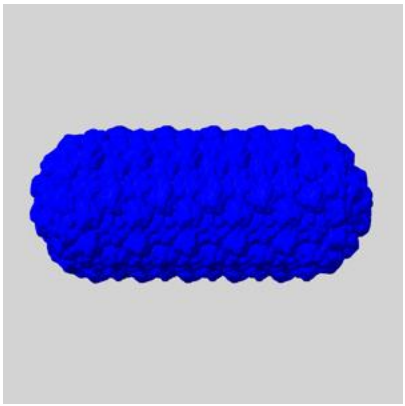
A mask typically either:

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

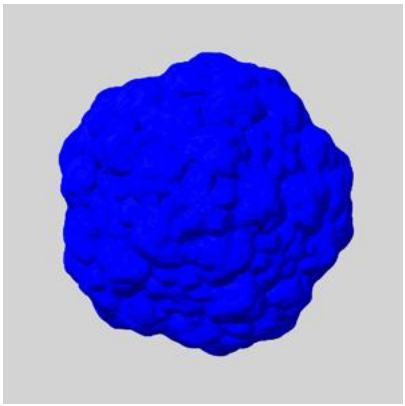
6.6.1 emd_17739_msk_1.map



X



Y

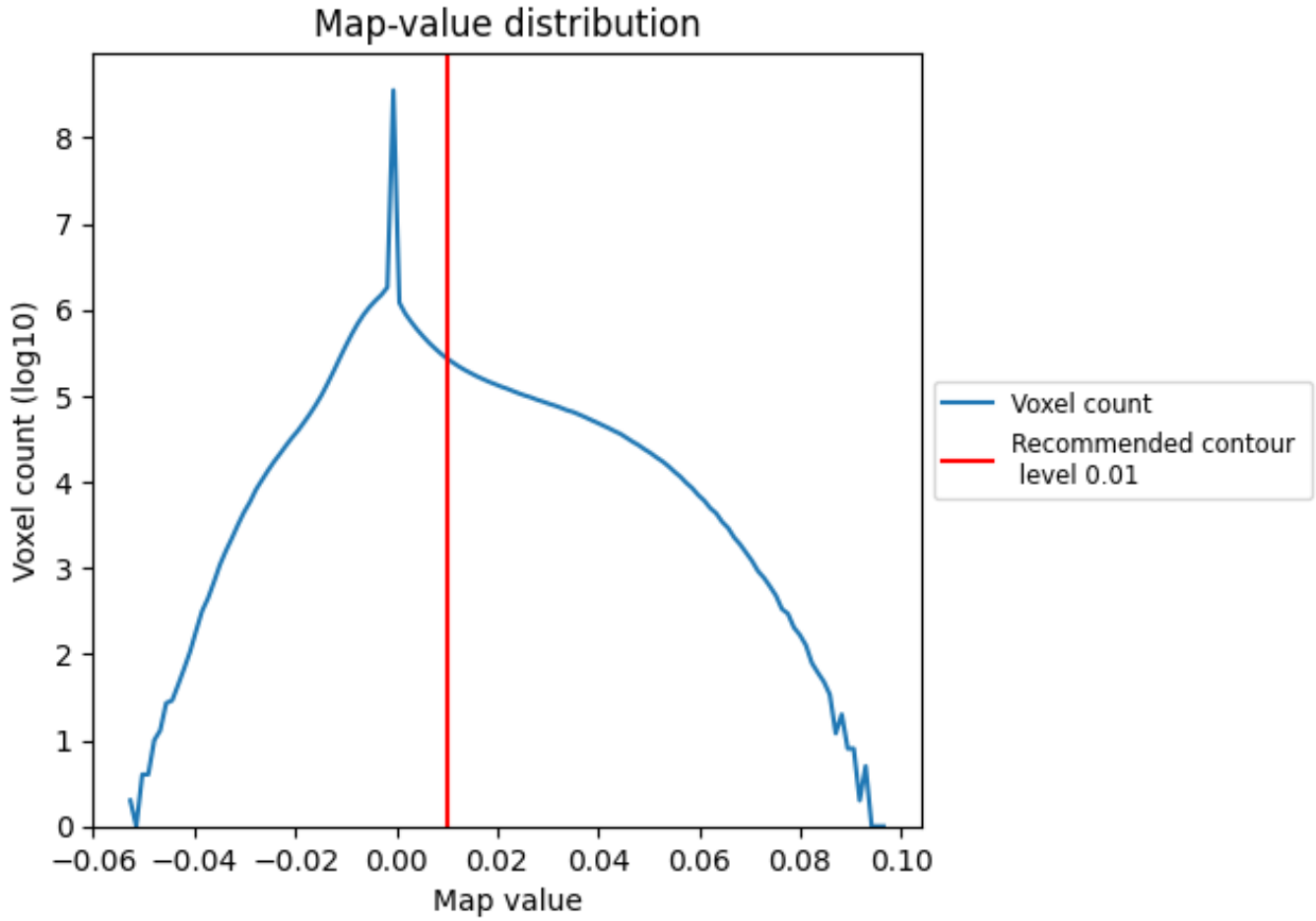


Z

7 Map analysis

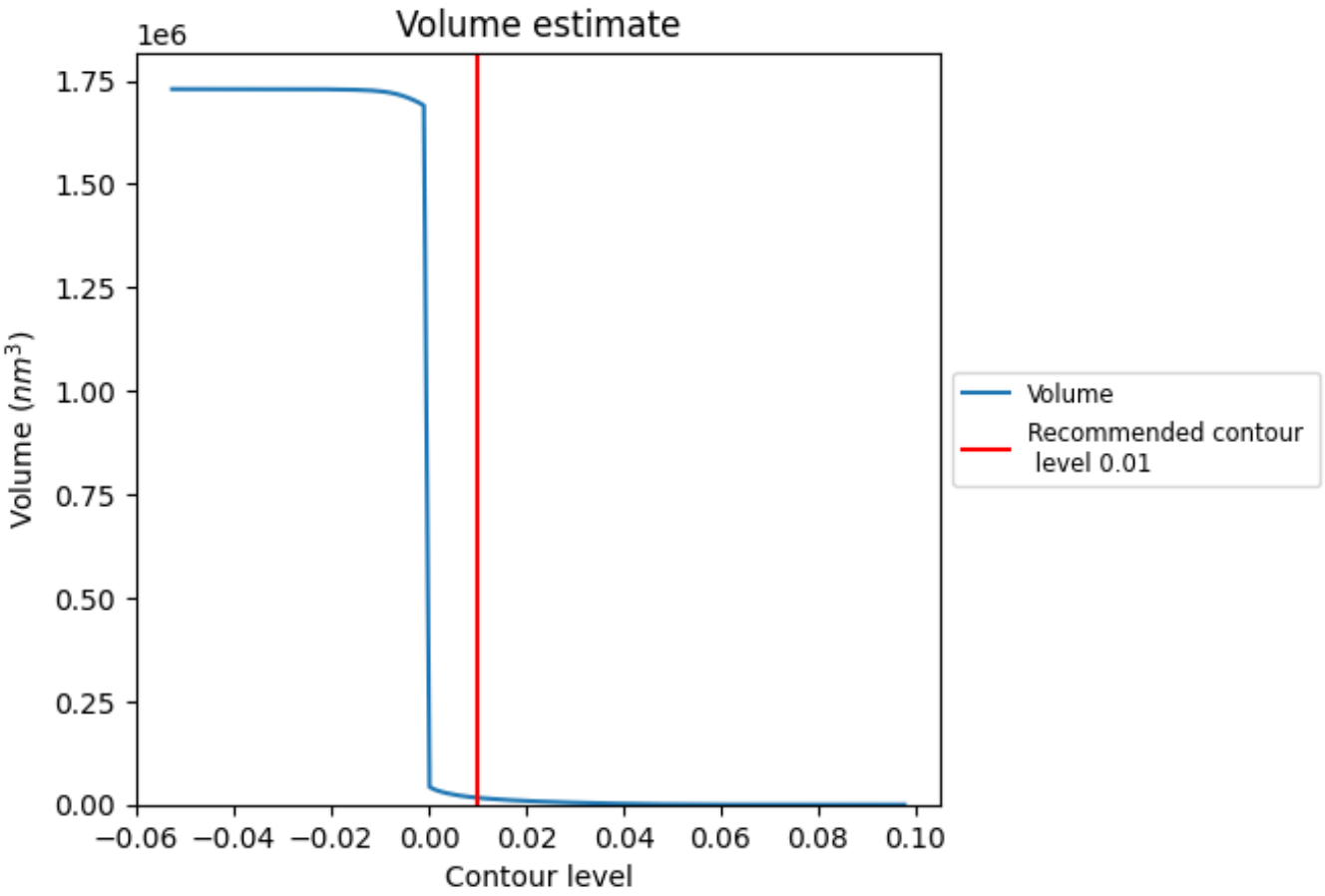
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

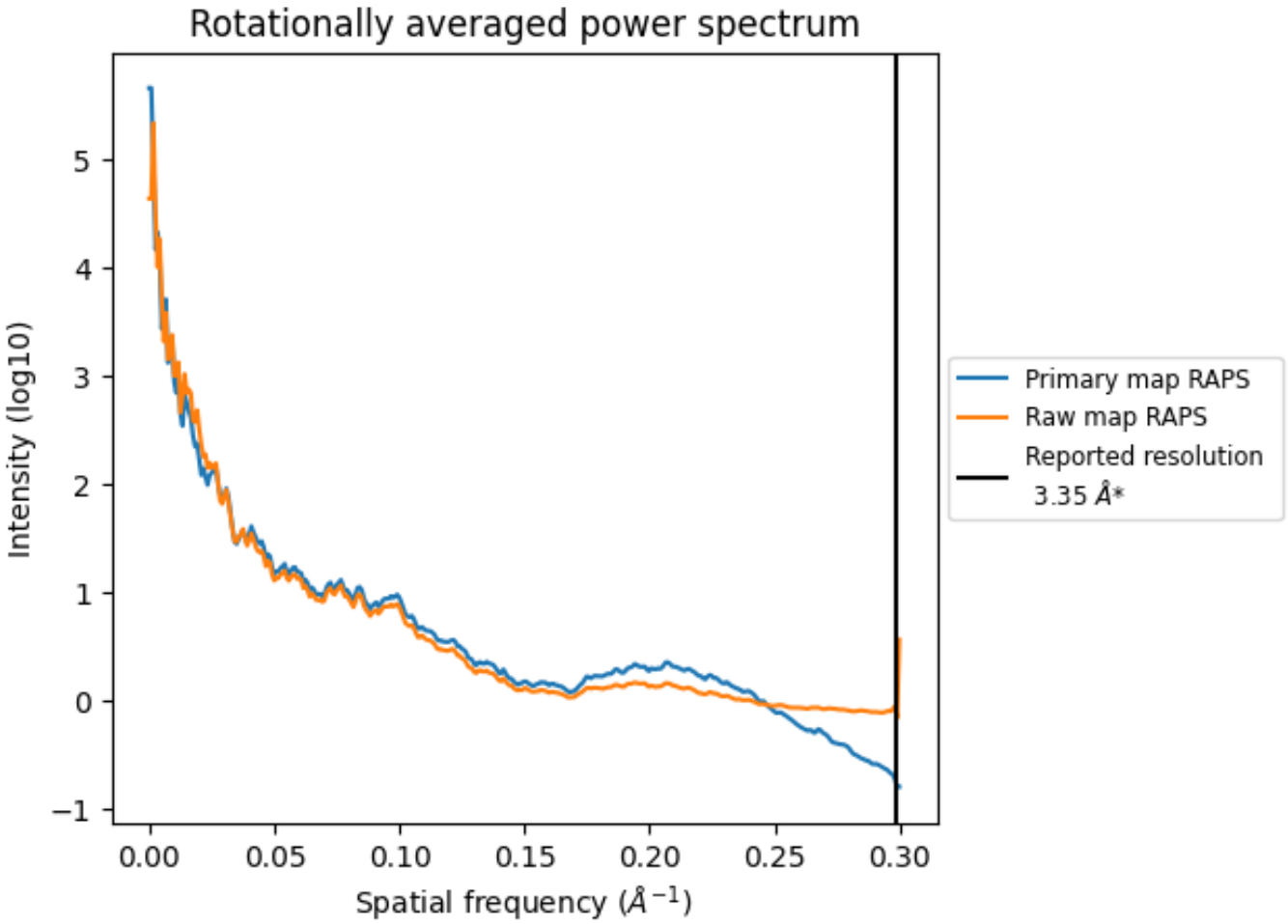
7.2 Volume estimate



The volume at the recommended contour level is 16709 nm^3; this corresponds to an approximate mass of 15093 kDa.

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

7.3 Rotationally averaged power spectrum (i)

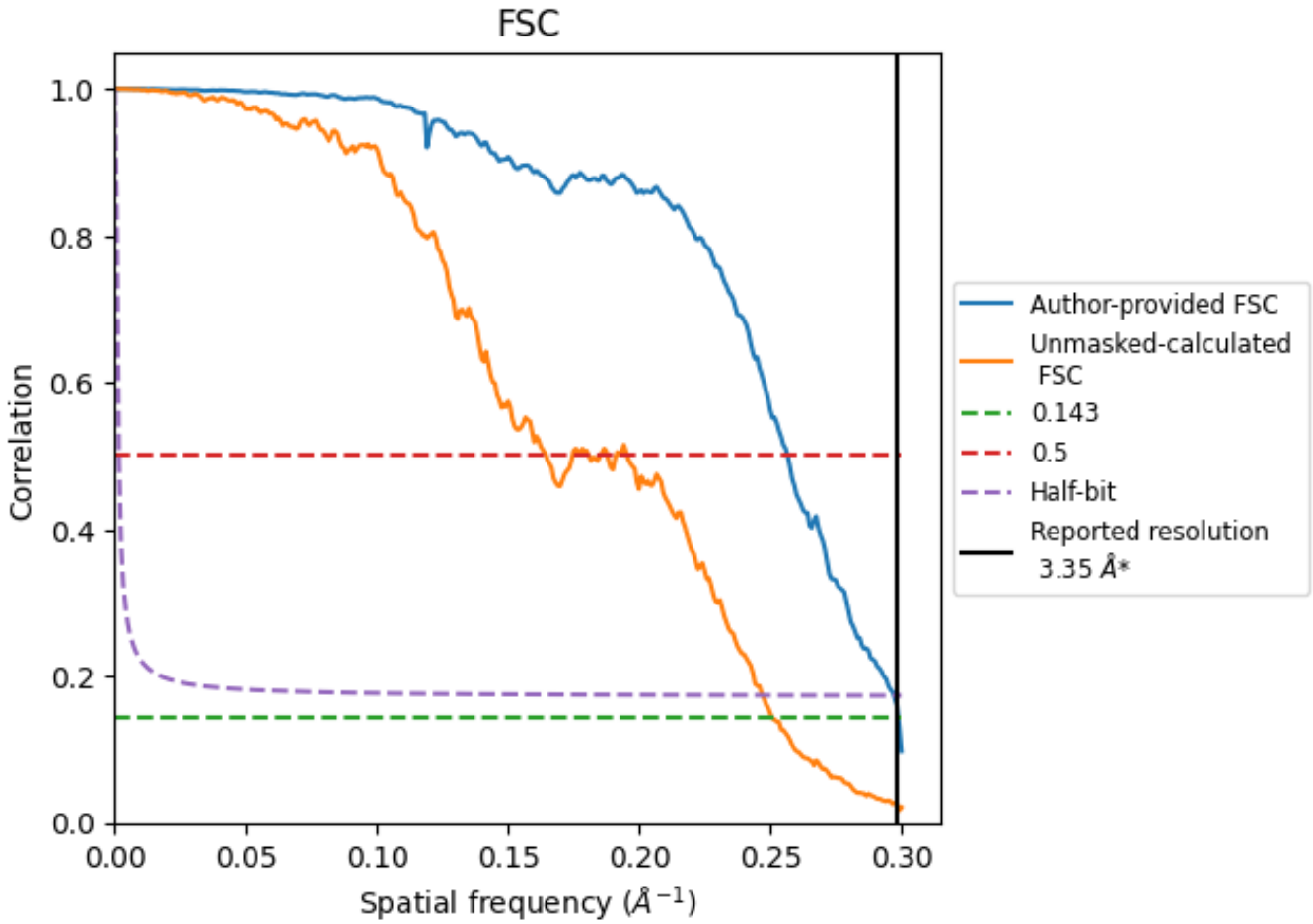


*Reported resolution corresponds to spatial frequency of 0.299 Å^{-1}

8 Fourier-Shell correlation

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

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.299 Å^{-1}

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.35	-	-
Author-provided FSC curve	3.35	3.90	3.37
Unmasked-calculated*	3.99	6.08	4.05

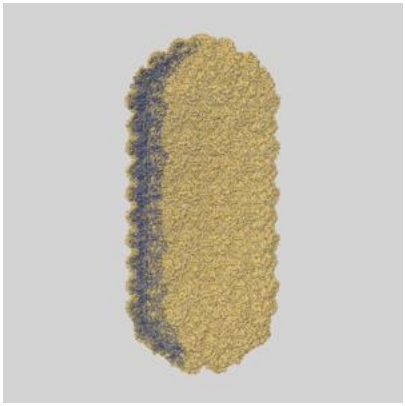
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.99 differs from the reported value 3.35 by more than 10 %

9 Map-model fit

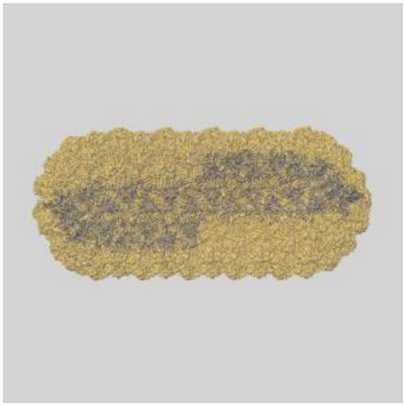
This section contains information regarding the fit between EMDB map EMD-17739 and PDB model 8PKH. Per-residue inclusion information can be found in section 3 on page 26.

9.1 Map-model overlays

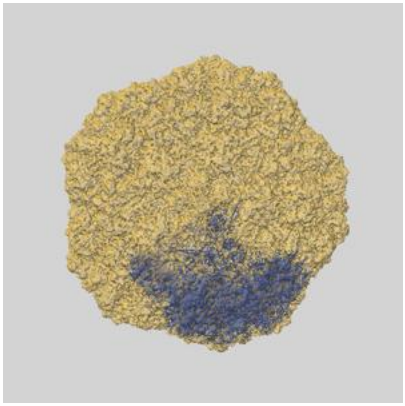
9.1.1 Map-model overlay



X

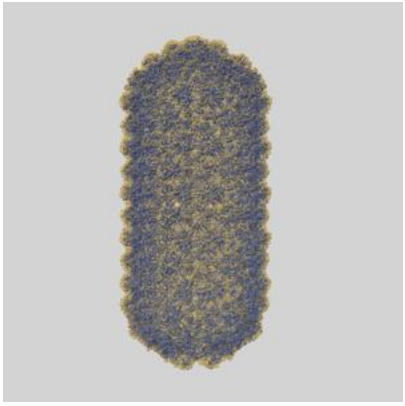


Y

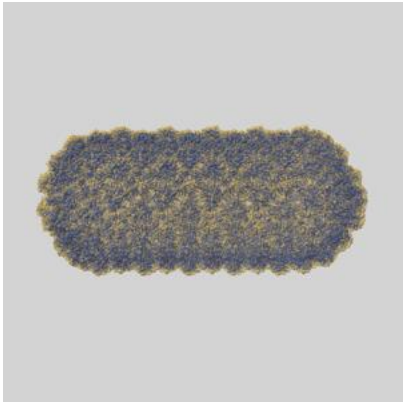


Z

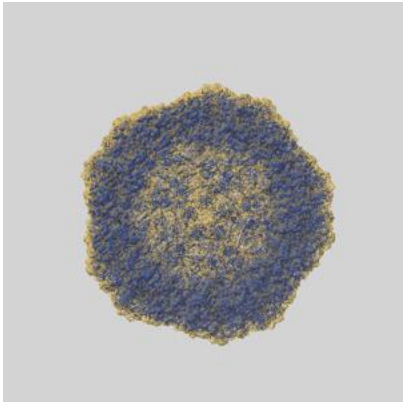
9.1.2 Map-model assembly overlay



X



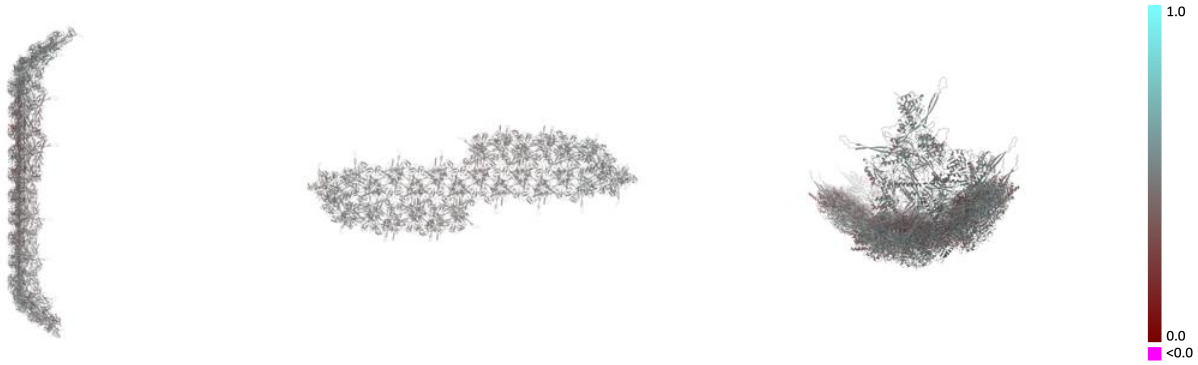
Y



Z

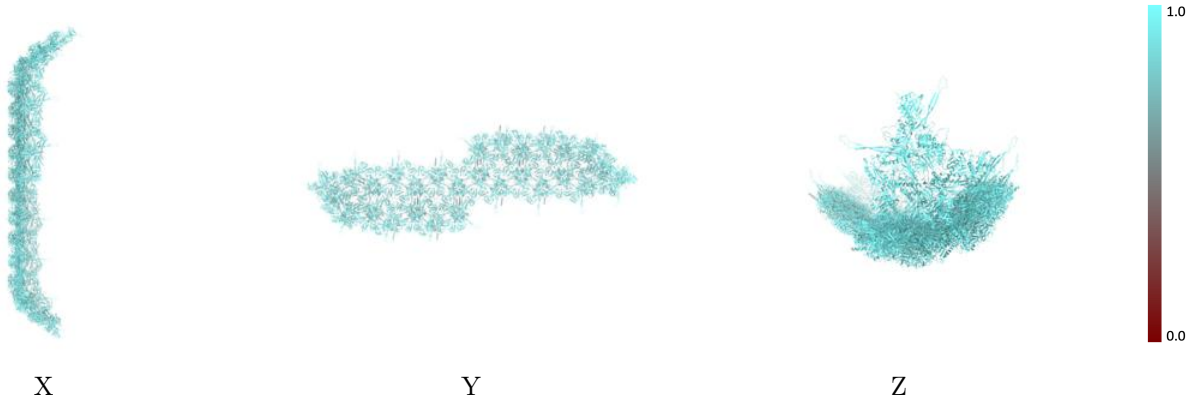
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model



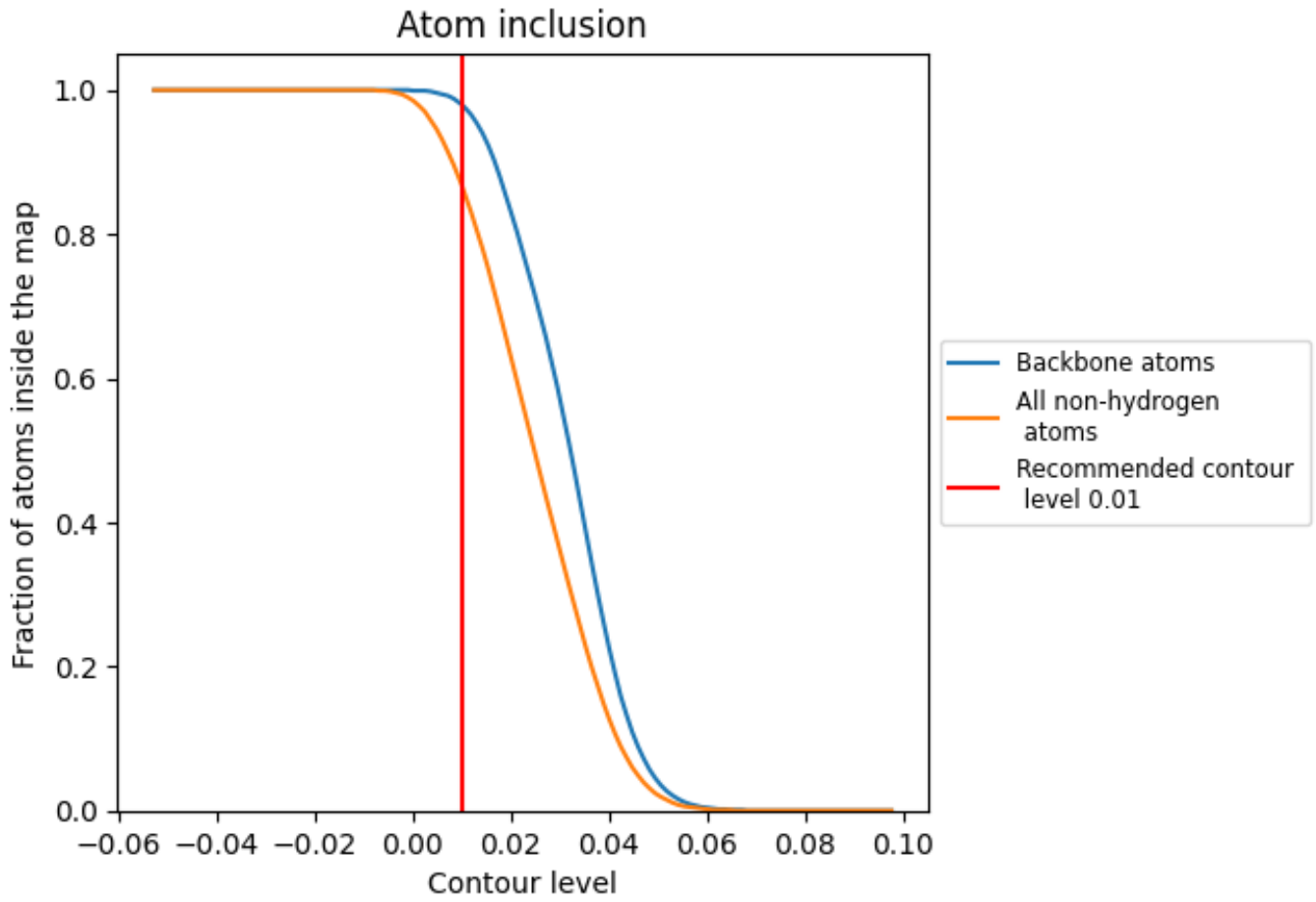
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).

9.4 Atom inclusion (i)



At the recommended contour level, 98% of all backbone atoms, 87% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8690	0.4550
AA	0.8950	0.4860
AB	0.8860	0.4790
AC	0.8930	0.4840
AD	0.8850	0.4920
AE	0.8880	0.4860
AF	0.8930	0.4880
AG	0.8900	0.4880
AH	0.8820	0.4790
AI	0.8860	0.4850
AJ	0.8840	0.4840
AK	0.8740	0.4650
AL	0.8800	0.4740
AM	0.8830	0.4910
AN	0.8850	0.4820
AO	0.8710	0.4740
AP	0.8950	0.4920
AQ	0.8850	0.4810
AR	0.8890	0.4880
AS	0.8660	0.4530
AT	0.8610	0.4650
AU	0.8600	0.4460
AV	0.8710	0.4600
AW	0.8650	0.4660
AX	0.8650	0.4590
AY	0.8590	0.4530
AZ	0.8540	0.4440
BA	0.8600	0.4510
BB	0.8580	0.4510
BC	0.8660	0.4510
BD	0.8770	0.4820
BE	0.8730	0.4720
BF	0.8850	0.4770
BG	0.8940	0.4880
BH	0.8810	0.4800

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Chain	Atom inclusion	Q-score
BI	0.8920	0.4780
BJ	0.8950	0.4900
BK	0.8790	0.4760
BL	0.8900	0.4790
BM	0.8890	0.4860
BN	0.8900	0.4820
BO	0.8870	0.4750
BP	0.8930	0.4850
BQ	0.8790	0.4760
BR	0.8630	0.4690
BS	0.8760	0.4590
BT	0.8780	0.4720
BU	0.8780	0.4590
BV	0.8890	0.4690
BW	0.8790	0.4660
BX	0.8620	0.4540
BY	0.8890	0.4740
BZ	0.8810	0.4520
CA	0.8730	0.4530
CB	0.8670	0.4440
CC	0.8590	0.4430
CD	0.8670	0.4510
CE	0.8720	0.4490
CF	0.8530	0.4400
CG	0.8590	0.4370
CH	0.8650	0.4470
CI	0.8610	0.4470
CJ	0.8730	0.4480
CK	0.8680	0.4430
CL	0.8560	0.4450
CM	0.8660	0.4460
CN	0.8670	0.4470
CO	0.8660	0.4510
CP	0.8690	0.4470
CQ	0.8660	0.4390
CR	0.8580	0.4410
CS	0.8520	0.4400
CT	0.8610	0.4380
CU	0.8680	0.4440
CV	0.8540	0.4380
CW	0.8590	0.4470
CX	0.8650	0.4410

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Chain	Atom inclusion	Q-score
CY	0.8530	0.4430
CZ	0.8580	0.4390
DA	0.8650	0.4500
DB	0.8530	0.4430
DC	0.8670	0.4430
DD	0.8700	0.4520
DE	0.8700	0.4480
DF	0.9060	0.4760
DG	0.8910	0.4710
DH	0.8650	0.4710
DI	0.8760	0.4800
DJ	0.8850	0.4710
DK	0.8880	0.4830
DL	0.8820	0.4760
DM	0.8340	0.4460
DN	0.8600	0.4720
DO	0.8640	0.4720
DP	0.8760	0.4790
DQ	0.9020	0.4870
DR	0.8810	0.4830
DS	0.8390	0.4190
DT	0.8700	0.4600
DU	0.8700	0.4640
DV	0.8570	0.4650
DW	0.8500	0.4140
DX	0.8640	0.4470
DY	0.8790	0.4490
DZ	0.8570	0.4410
EA	0.8070	0.3940
EB	0.8660	0.4690
EC	0.9020	0.4880
ED	0.8730	0.4660
EE	0.8990	0.4780
EF	0.8710	0.4690
EG	0.8680	0.4740
EH	0.8440	0.4430
EI	0.8870	0.4760
EJ	0.8760	0.4760
EK	0.8790	0.4450
EL	0.8830	0.4650
EM	0.8820	0.4530
EN	0.8640	0.4610

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Chain	Atom inclusion	Q-score
EO	0.8650	0.4430
EP	0.8760	0.4580
EQ	0.8720	0.4560
ER	0.8460	0.4240
ES	0.8670	0.4490
ET	0.8890	0.4530
EU	0.8710	0.4540
EV	0.8440	0.4130
EW	0.8810	0.4480
EX	0.8650	0.4510
EY	0.8790	0.4550
EZ	0.8450	0.4190
FA	0.8740	0.4580
FB	0.8390	0.4060
FC	0.8690	0.4540
FD	0.8760	0.4470
FE	0.8690	0.4490
FF	0.8380	0.4210
FG	0.8700	0.4500
FH	0.8660	0.4530
FI	0.8630	0.4500
FJ	0.8660	0.4640
FK	0.8880	0.4770
FL	0.8830	0.4810
FM	0.8690	0.4690
FN	0.8580	0.4730
FO	0.8820	0.4810
FP	0.8730	0.4610
FQ	0.8430	0.4410
FR	0.7830	0.3770
FS	0.8260	0.4130
FT	0.8570	0.4530
FU	0.8690	0.4690
FV	0.8750	0.4670
FW	0.8690	0.4680
FX	0.8770	0.4740
FY	0.8710	0.4580
FZ	0.8700	0.4380
GA	0.8230	0.4120
GB	0.8030	0.3970
GC	0.8360	0.4250
GD	0.7890	0.3740

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Chain	Atom inclusion	Q-score
GE	0.8460	0.4230
GF	0.8050	0.3810
GG	0.7830	0.3850
GH	0.8230	0.4150
GI	0.8060	0.3890
GJ	0.8260	0.4160
GK	0.8450	0.4430
GL	0.8630	0.4520
GM	0.8340	0.4410
GN	0.8370	0.4490
GO	0.8860	0.4550
GP	0.8760	0.4290
GQ	0.7950	0.4300
GR	0.8700	0.4480
GS	0.8700	0.4290
GT	0.8760	0.4550
GU	0.8730	0.4430
GV	0.8890	0.4410
GW	0.8570	0.4560
GX	0.8760	0.4350
GY	0.8630	0.4380
GZ	0.8890	0.4490
HA	0.8600	0.4450
HB	0.8370	0.4480
HC	0.8990	0.4180
HD	0.8640	0.4230
HE	0.8730	0.4200
HF	0.8760	0.4120
HG	0.8660	0.4260
HH	0.8490	0.4240
HI	0.8610	0.3990
HJ	0.8800	0.3940
HK	0.8950	0.3990
HL	0.7590	0.3960
HM	0.8300	0.3880
HN	0.8790	0.4560
HO	0.8760	0.4460
HP	0.8600	0.4340
HQ	0.8400	0.4290
HR	0.9120	0.4650
HS	0.8140	0.4200
HT	0.8830	0.4590

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Chain	Atom inclusion	Q-score
HU	0.8730	0.4420
HV	0.9020	0.4500
HW	0.7830	0.4290
HX	0.8860	0.4450
HY	0.8920	0.4530
HZ	0.8760	0.4370
IA	0.8440	0.4320
IB	0.7730	0.4380
IC	0.8920	0.4360
ID	0.8580	0.4180
IE	0.8960	0.4490
IF	0.8990	0.4330
IG	0.8760	0.4440
IH	0.8620	0.3980
II	0.8840	0.4400
IJ	0.9030	0.4130
IK	0.9190	0.4140
IL	0.8780	0.4070
IM	0.8890	0.4240
IN	0.8630	0.4090
IO	0.8660	0.3970
IP	0.8730	0.4010
IQ	0.8790	0.4020
IR	0.8570	0.4000
IS	0.8700	0.4130
IT	0.8830	0.4230
IU	0.8540	0.4070
IV	0.8370	0.4000
IW	0.8860	0.4240
IX	0.8790	0.4120
IY	0.8780	0.4060
IZ	0.8660	0.4200
JA	0.8720	0.4130
JB	0.8760	0.4020
JC	0.8600	0.4000
JD	0.8870	0.4080
JE	0.8530	0.4110
JF	0.8730	0.3960
JG	0.8570	0.3960
JH	0.8790	0.4010
JI	0.8470	0.4310
JJ	0.8720	0.4050

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Chain	Atom inclusion	Q-score
JK	0.8700	0.4090
JL	0.8790	0.4350
JM	0.8660	0.4050
JN	0.8780	0.4070
JO	0.8600	0.4140