



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 04:24 PM UTC

PDB ID : 7MUV / pdb_00007muv
EMDB ID : EMD-24023
Title : Reconstruction of the Legionella pneumophila Dot/Icm T4SS 3DVA Map 3
Authors : Sheedlo, M.J.; Durie, C.L.; Swanson, M.; Lacy, D.B.; Ohi, M.D.
Deposited on : 2021-05-14
Resolution : 4.60 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

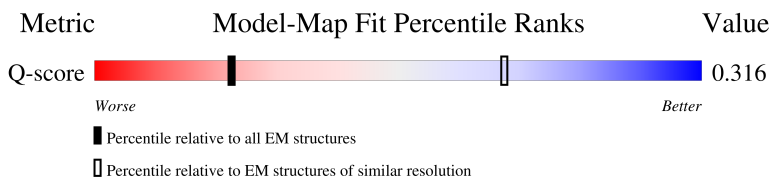
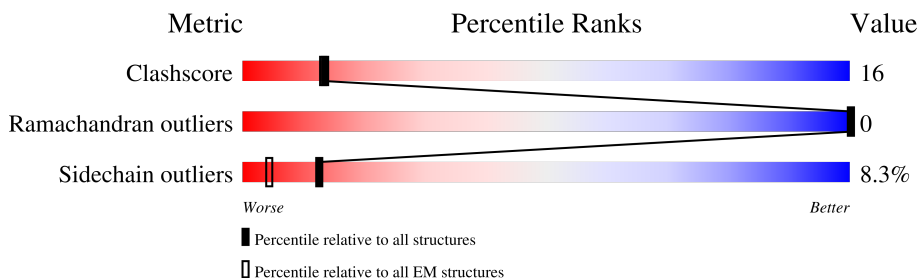
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.60 Å.

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



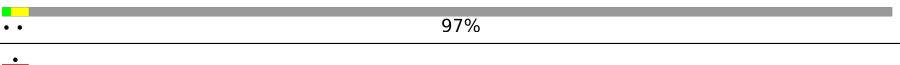
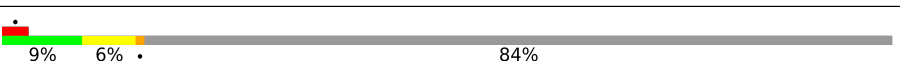
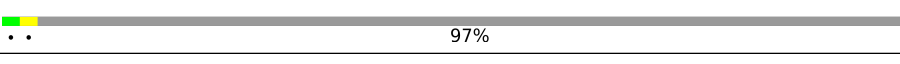
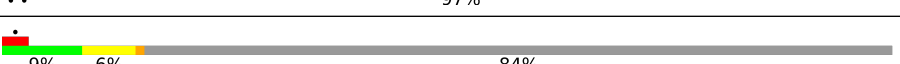
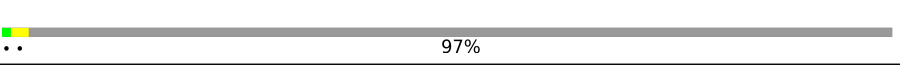
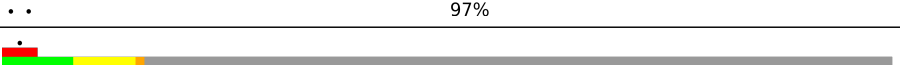
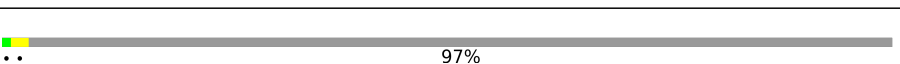
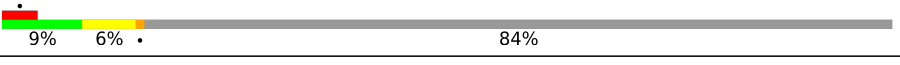
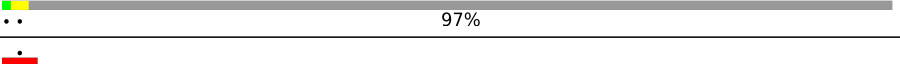
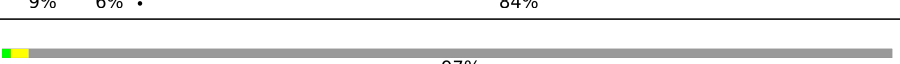
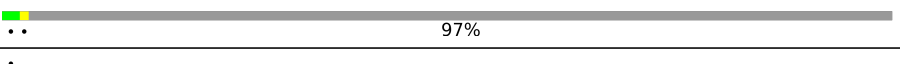
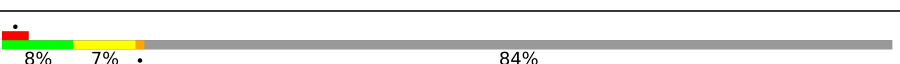
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2407 (4.10 - 5.10)

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

Mol	Chain	Length	Quality of chain
1	AG	1048	9% 6% . 84%
1	Ag	1048	. . 97%
1	BG	1048	10% 6% . 84%
1	Bg	1048	. . 97%

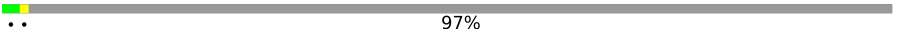
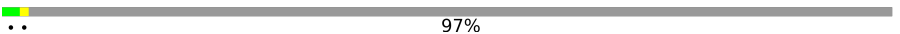
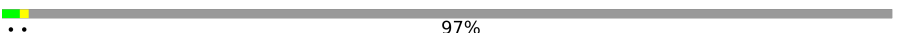
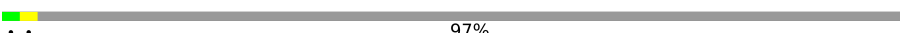
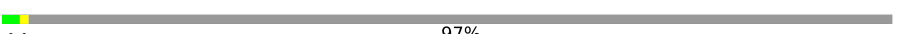
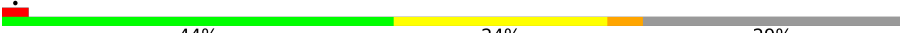
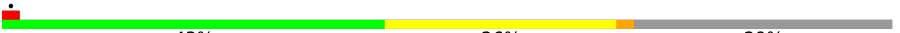
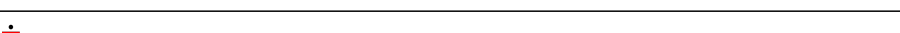
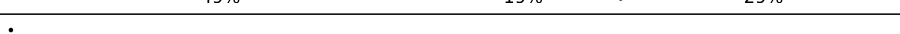
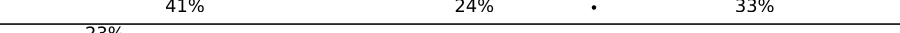
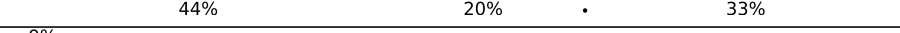
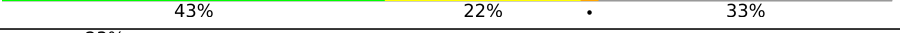
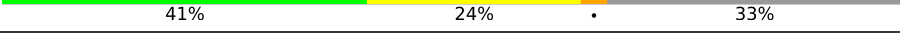
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Mol	Chain	Length	Quality of chain
1	CG	1048	 9% 6% . 84%
1	Cg	1048	 97%
1	DG	1048	 9% 6% . 84%
1	Dg	1048	 97%
1	EG	1048	 9% 6% . 84%
1	Eg	1048	 97%
1	FG	1048	 9% 6% . 84%
1	Fg	1048	 97%
1	GG	1048	 9% 6% . 84%
1	Gg	1048	 97%
1	HG	1048	 8% 7% . 84%
1	Hg	1048	 97%
1	IG	1048	 8% 7% . 84%
1	Ig	1048	 97%
1	JG	1048	 9% 6% . 84%
1	Jg	1048	 97%
1	KG	1048	 9% 6% . 84%
1	Kg	1048	 97%
1	LG	1048	 9% 6% . 84%
1	Lg	1048	 97%
1	MG	1048	 10% 6% . 84%
1	Mg	1048	 97%
1	NG	1048	 8% 7% . 84%
1	OG	1048	8% 7% . 84%
1	PG	1048	9% 6% . 84%

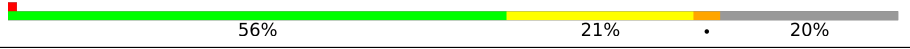
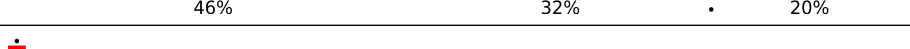
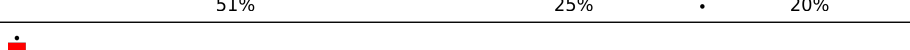
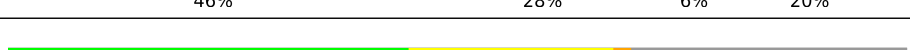
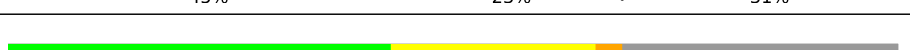
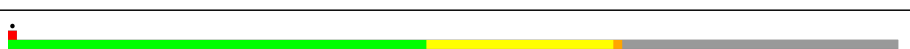
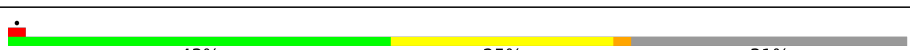
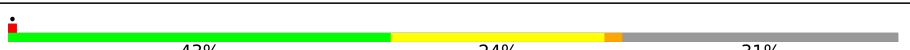
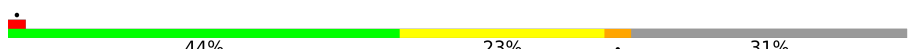
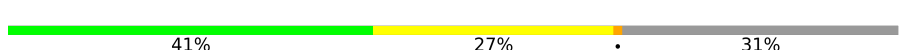
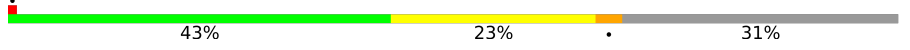
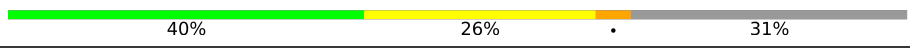
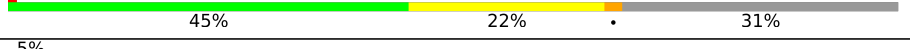
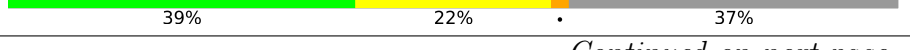
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Mol	Chain	Length	Quality of chain
1	VG	1048	 97%
1	WG	1048	 97%
1	XG	1048	 97%
1	YG	1048	 97%
1	ZG	1048	 97%
2	AH	361	 44% 24% . 29%
2	BH	361	 43% 26% . 29%
2	CH	361	 48% 22% . 29%
2	DH	361	 45% 25% . 29%
2	EH	361	 41% 26% . 29%
2	FH	361	 45% 25% . 29%
2	GH	361	 47% 23% . 29%
2	HH	361	 47% 23% . 29%
2	IH	361	 47% 22% . 29%
2	JH	361	 49% 19% . 29%
2	KH	361	 47% 21% . 29%
2	LH	361	 44% 24% . 29%
2	MH	361	 45% 24% . 29%
2	VH	361	 12% 41% . 33%
2	WH	361	 23% 44% . 33%
2	XH	361	 9% 43% . 33%
2	YH	361	 23% 41% . 33%
2	ZH	361	 14% 44% . 33%
3	AK	189	 52% 26% . 20%
3	BK	189	 53% 25% . 20%

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Mol	Chain	Length	Quality of chain
3	CK	189	
3	DK	189	
3	EK	189	
3	FK	189	
3	GK	189	
3	HK	189	
3	IK	189	
3	JK	189	
3	KK	189	
3	LK	189	
3	MK	189	
4	AL	249	
4	BL	249	
4	CL	249	
4	DL	249	
4	EL	249	
4	FL	249	
4	GL	249	
4	HL	249	
4	IL	249	
4	JL	249	
4	KL	249	
4	LL	249	
4	ML	249	
5	AN	124	

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Mol	Chain	Length	Quality of chain
5	BN	124	
5	CN	124	
5	DN	124	
5	EN	124	
5	FN	124	
5	GN	124	
5	HN	124	
5	IN	124	
5	JN	124	
5	KN	124	
5	LN	124	
5	MN	124	
6	AU	9	
6	BU	9	
6	CU	9	
6	DU	9	
6	EU	9	
6	FU	9	
6	GU	9	
6	HU	9	
6	IU	9	
6	JU	9	
6	KU	9	
6	LU	9	
6	MU	9	

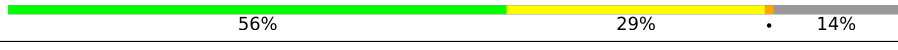
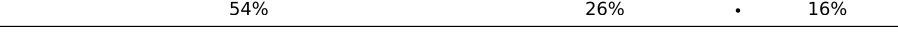
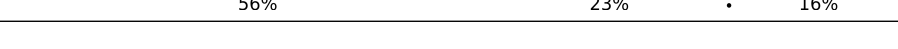
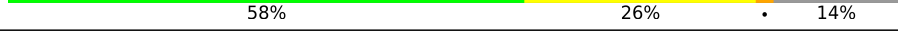
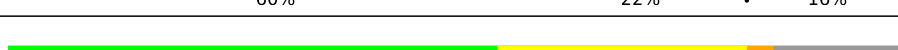
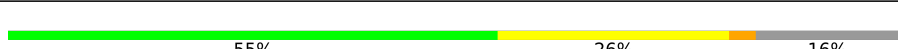
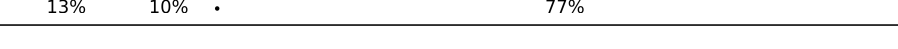
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Mol	Chain	Length	Quality of chain
7	AX	48	31% 92% 8%
7	BX	48	35% 85% 15%
7	CX	48	40% 96% .
7	DX	48	42% 98% .
7	EX	48	46% 100% .
7	FX	48	29% 100% .
7	GX	48	33% 100% .
7	HX	48	44% 96% .
7	IX	48	46% 98% .
7	JX	48	31% 96% .
7	KX	48	42% 98% .
7	LX	48	29% 100% .
7	MX	48	31% 90% 10%
7	VX	48	42% 98% .
7	WX	48	40% 96% .
7	XX	48	29% 98% .
7	YX	48	40% 88% 12%
7	ZX	48	38% 96% .
8	AD	163	51% 33% 14%
8	Ad	163	52% 30% 16%
8	BD	163	58% 27% 14%
8	Bd	163	56% 26% 16%
8	CD	163	63% 22% 14%
8	Cd	163	54% 28% 16%
8	DD	163	55% 29% 14%

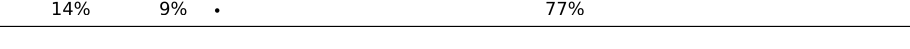
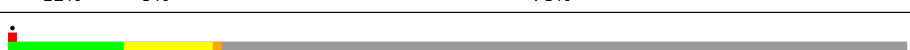
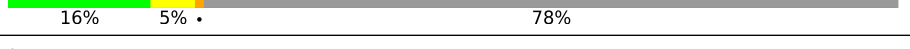
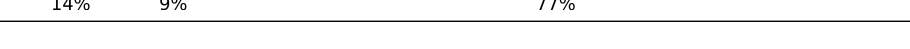
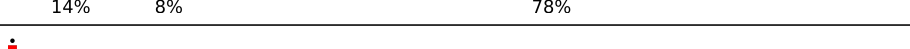
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Mol	Chain	Length	Quality of chain
8	Dd	163	
8	ED	163	
8	Ed	163	
8	FD	163	
8	Fd	163	
8	GD	163	
8	Gd	163	
8	HD	163	
8	Hd	163	
8	ID	163	
8	Id	163	
8	JD	163	
8	Jd	163	
8	KD	163	
8	Kd	163	
8	LD	163	
8	Ld	163	
8	MD	163	
8	Md	163	
9	AF	269	
9	Af	269	
9	BF	269	
9	Bf	269	
9	CF	269	
9	Cf	269	

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Mol	Chain	Length	Quality of chain
9	DF	269	
9	Df	269	
9	EF	269	
9	Ef	269	
9	FF	269	
9	Ff	269	
9	GF	269	
9	Gf	269	
9	HF	269	
9	Hf	269	
9	IF	269	
9	If	269	
9	JF	269	
9	Jf	269	
9	KF	269	
9	Kf	269	
9	LF	269	
9	Lf	269	
9	MF	269	
9	Mf	269	
9	VF	269	
9	WF	269	
9	XF	269	
9	YF	269	
9	ZF	269	

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Mol	Chain	Length	Quality of chain
10	AC	303	
10	BC	303	
10	CC	303	
10	DC	303	
10	EC	303	
10	FC	303	
10	GC	303	
10	HC	303	
10	IC	303	
10	JC	303	
10	KC	303	
10	LC	303	
10	MC	303	
11	AM	320	
11	BM	320	
11	CM	320	
11	DM	320	
11	EM	320	
11	FM	320	
11	GM	320	
11	HM	320	
11	IM	320	
11	JM	320	
11	KM	320	
11	LM	320	

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Mol	Chain	Length	Quality of chain
11	MM	320	

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 192370 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 IcmE protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AG	165	Total	C	N	O	S	0	0
			1229	780	203	242	4		
1	Fg	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
1	Gg	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
1	BG	165	Total	C	N	O	S	0	0
			1229	780	203	242	4		
1	Hg	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
1	Bg	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
1	Ig	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
1	CG	165	Total	C	N	O	S	0	0
			1229	780	203	242	4		
1	Jg	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
1	Kg	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
1	DG	165	Total	C	N	O	S	0	0
			1229	780	203	242	4		
1	Lg	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
1	Mg	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
1	EG	165	Total	C	N	O	S	0	0
			1229	780	203	242	4		
1	VG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
1	WG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
1	XG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	YG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
1	ZG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
1	FG	165	Total	C	N	O	S	0	0
			1229	780	203	242	4		
1	Cg	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
1	GG	165	Total	C	N	O	S	0	0
			1229	780	203	242	4		
1	Dg	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
1	HG	165	Total	C	N	O	S	0	0
			1229	780	203	242	4		
1	IG	165	Total	C	N	O	S	0	0
			1229	780	203	242	4		
1	JG	165	Total	C	N	O	S	0	0
			1229	780	203	242	4		
1	KG	165	Total	C	N	O	S	0	0
			1229	780	203	242	4		
1	LG	165	Total	C	N	O	S	0	0
			1229	780	203	242	4		
1	MG	165	Total	C	N	O	S	0	0
			1229	780	203	242	4		
1	NG	165	Total	C	N	O	S	0	0
			1229	780	203	242	4		
1	OG	165	Total	C	N	O	S	0	0
			1229	780	203	242	4		
1	PG	165	Total	C	N	O	S	0	0
			1229	780	203	242	4		
1	Ag	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
1	Eg	34	Total	C	N	O	S	0	0
			276	168	47	60	1		

- Molecule 2 is a protein called Type IV secretion protein IcmK.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	EH	258	Total	C	N	O	S	0	0
			1983	1268	336	371	8		
2	FH	258	Total	C	N	O	S	0	0
			1983	1268	336	371	8		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	GH	258	Total	C	N	O	S	0	0
			1983	1268	336	371	8		
2	HH	258	Total	C	N	O	S	0	0
			1983	1268	336	371	8		
2	IH	258	Total	C	N	O	S	0	0
			1983	1268	336	371	8		
2	JH	258	Total	C	N	O	S	0	0
			1983	1268	336	371	8		
2	AH	258	Total	C	N	O	S	0	0
			1983	1268	336	371	8		
2	KH	258	Total	C	N	O	S	0	0
			1983	1268	336	371	8		
2	LH	258	Total	C	N	O	S	0	0
			1983	1268	336	371	8		
2	MH	258	Total	C	N	O	S	0	0
			1983	1268	336	371	8		
2	VH	243	Total	C	N	O	S	0	0
			1875	1201	319	348	7		
2	WH	243	Total	C	N	O	S	0	0
			1875	1201	319	348	7		
2	XH	243	Total	C	N	O	S	0	0
			1875	1201	319	348	7		
2	YH	243	Total	C	N	O	S	0	0
			1875	1201	319	348	7		
2	ZH	243	Total	C	N	O	S	0	0
			1875	1201	319	348	7		
2	BH	258	Total	C	N	O	S	0	0
			1983	1268	336	371	8		
2	CH	258	Total	C	N	O	S	0	0
			1983	1268	336	371	8		
2	DH	258	Total	C	N	O	S	0	0
			1983	1268	336	371	8		

- Molecule 3 is a protein called Inner membrane lipoprotein YiaD.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	EK	151	Total	C	N	O	S	0	0
			1175	747	209	215	4		
3	FK	151	Total	C	N	O	S	0	0
			1175	747	209	215	4		
3	GK	151	Total	C	N	O	S	0	0
			1175	747	209	215	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	HK	151	Total	C	N	O	S	0	0
			1175	747	209	215	4		
3	IK	151	Total	C	N	O	S	0	0
			1175	747	209	215	4		
3	JK	151	Total	C	N	O	S	0	0
			1175	747	209	215	4		
3	KK	151	Total	C	N	O	S	0	0
			1175	747	209	215	4		
3	LK	151	Total	C	N	O	S	0	0
			1175	747	209	215	4		
3	AK	151	Total	C	N	O	S	0	0
			1175	747	209	215	4		
3	MK	151	Total	C	N	O	S	0	0
			1175	747	209	215	4		
3	BK	151	Total	C	N	O	S	0	0
			1175	747	209	215	4		
3	CK	151	Total	C	N	O	S	0	0
			1175	747	209	215	4		
3	DK	151	Total	C	N	O	S	0	0
			1175	747	209	215	4		

- Molecule 4 is a protein called Outer membrane protein, OmpA family protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	EL	173	Total	C	N	O	S	0	0
			1388	877	253	253	5		
4	FL	173	Total	C	N	O	S	0	0
			1388	877	253	253	5		
4	GL	173	Total	C	N	O	S	0	0
			1388	877	253	253	5		
4	HL	173	Total	C	N	O	S	0	0
			1388	877	253	253	5		
4	IL	173	Total	C	N	O	S	0	0
			1388	877	253	253	5		
4	JL	173	Total	C	N	O	S	0	0
			1388	877	253	253	5		
4	KL	173	Total	C	N	O	S	0	0
			1388	877	253	253	5		
4	LL	173	Total	C	N	O	S	0	0
			1388	877	253	253	5		
4	ML	173	Total	C	N	O	S	0	0
			1388	877	253	253	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	AL	173	Total	C	N	O	S	0	0
			1388	877	253	253	5		
4	BL	173	Total	C	N	O	S	0	0
			1388	877	253	253	5		
4	CL	173	Total	C	N	O	S	0	0
			1388	877	253	253	5		
4	DL	173	Total	C	N	O	S	0	0
			1388	877	253	253	5		

- Molecule 5 is a protein called Neurogenic locus notch.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	EN	78	Total	C	N	O	S	0	0
			582	357	99	113	13		
5	FN	78	Total	C	N	O	S	0	0
			582	357	99	113	13		
5	GN	78	Total	C	N	O	S	0	0
			582	357	99	113	13		
5	HN	78	Total	C	N	O	S	0	0
			582	357	99	113	13		
5	IN	78	Total	C	N	O	S	0	0
			582	357	99	113	13		
5	JN	78	Total	C	N	O	S	0	0
			582	357	99	113	13		
5	KN	78	Total	C	N	O	S	0	0
			582	357	99	113	13		
5	LN	78	Total	C	N	O	S	0	0
			582	357	99	113	13		
5	MN	78	Total	C	N	O	S	0	0
			582	357	99	113	13		
5	AN	78	Total	C	N	O	S	0	0
			582	357	99	113	13		
5	BN	78	Total	C	N	O	S	0	0
			582	357	99	113	13		
5	CN	78	Total	C	N	O	S	0	0
			582	357	99	113	13		
5	DN	78	Total	C	N	O	S	0	0
			582	357	99	113	13		

- Molecule 6 is a protein called Unknown protein fragment.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	EU	9	Total	C	N	O	0	0
			45	27	9	9		
6	FU	9	Total	C	N	O	0	0
			45	27	9	9		
6	GU	9	Total	C	N	O	0	0
			45	27	9	9		
6	HU	9	Total	C	N	O	0	0
			45	27	9	9		
6	IU	9	Total	C	N	O	0	0
			45	27	9	9		
6	JU	9	Total	C	N	O	0	0
			45	27	9	9		
6	KU	9	Total	C	N	O	0	0
			45	27	9	9		
6	LU	9	Total	C	N	O	0	0
			45	27	9	9		
6	MU	9	Total	C	N	O	0	0
			45	27	9	9		
6	AU	9	Total	C	N	O	0	0
			45	27	9	9		
6	BU	9	Total	C	N	O	0	0
			45	27	9	9		
6	CU	9	Total	C	N	O	0	0
			45	27	9	9		
6	DU	9	Total	C	N	O	0	0
			45	27	9	9		

- Molecule 7 is a protein called Unknown protein fragment.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	EX	48	Total	C	N	O	0	0
			240	144	48	48		
7	FX	48	Total	C	N	O	0	0
			240	144	48	48		
7	GX	48	Total	C	N	O	0	0
			240	144	48	48		
7	HX	48	Total	C	N	O	0	0
			240	144	48	48		
7	IX	48	Total	C	N	O	0	0
			240	144	48	48		
7	JX	48	Total	C	N	O	0	0
			240	144	48	48		
7	KX	48	Total	C	N	O	0	0
			240	144	48	48		

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Mol	Chain	Residues	Atoms				AltConf	Trace
7	LX	48	Total	C	N	O	0	0
			240	144	48	48		
7	MX	48	Total	C	N	O	0	0
			240	144	48	48		
7	VX	48	Total	C	N	O	0	0
			240	144	48	48		
7	WX	48	Total	C	N	O	0	0
			240	144	48	48		
7	XX	48	Total	C	N	O	0	0
			240	144	48	48		
7	YX	48	Total	C	N	O	0	0
			240	144	48	48		
7	ZX	48	Total	C	N	O	0	0
			240	144	48	48		
7	AX	48	Total	C	N	O	0	0
			240	144	48	48		
7	BX	48	Total	C	N	O	0	0
			240	144	48	48		
7	CX	48	Total	C	N	O	0	0
			240	144	48	48		
7	DX	48	Total	C	N	O	0	0
			240	144	48	48		

- Molecule 8 is a protein called DotD.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Ed	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
8	FD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
8	Fd	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
8	GD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
8	Gd	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
8	HD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
8	Hd	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
8	ID	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
8	Id	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
8	JD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
8	Jd	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
8	KD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
8	Kd	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
8	LD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
8	CD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
8	Ld	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
8	MD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
8	Md	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
8	Ad	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
8	BD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
8	Bd	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
8	Cd	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
8	DD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
8	Dd	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
8	AD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
8	ED	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		

- Molecule 9 is a protein called DotF.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Ef	59	Total	C	N	O	S	0	0
			449	290	77	81	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	FF	63	Total 483	C 308	N 84	O 90	S 1	0	0
9	Ff	59	Total 449	C 290	N 77	O 81	S 1	0	0
9	AF	63	Total 483	C 308	N 84	O 90	S 1	0	0
9	GF	63	Total 483	C 308	N 84	O 90	S 1	0	0
9	Gf	59	Total 449	C 290	N 77	O 81	S 1	0	0
9	HF	63	Total 483	C 308	N 84	O 90	S 1	0	0
9	Hf	59	Total 449	C 290	N 77	O 81	S 1	0	0
9	IF	63	Total 483	C 308	N 84	O 90	S 1	0	0
9	If	59	Total 449	C 290	N 77	O 81	S 1	0	0
9	JF	63	Total 483	C 308	N 84	O 90	S 1	0	0
9	Jf	59	Total 449	C 290	N 77	O 81	S 1	0	0
9	KF	63	Total 483	C 308	N 84	O 90	S 1	0	0
9	Kf	59	Total 449	C 290	N 77	O 81	S 1	0	0
9	LF	63	Total 483	C 308	N 84	O 90	S 1	0	0
9	Lf	59	Total 449	C 290	N 77	O 81	S 1	0	0
9	MF	63	Total 483	C 308	N 84	O 90	S 1	0	0
9	Mf	59	Total 449	C 290	N 77	O 81	S 1	0	0
9	VF	63	Total 483	C 308	N 84	O 90	S 1	0	0
9	CF	63	Total 483	C 308	N 84	O 90	S 1	0	0
9	WF	63	Total 483	C 308	N 84	O 90	S 1	0	0
9	XF	63	Total 483	C 308	N 84	O 90	S 1	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
9	YF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
9	ZF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
9	Af	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
9	BF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
9	Bf	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
9	Cf	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
9	DF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
9	Df	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
9	EF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		

- Molecule 10 is a protein called DotC.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	BC	243	Total	C	N	O	S	0	0
			1921	1216	340	357	8		
10	CC	209	Total	C	N	O	S	0	0
			1667	1061	292	309	5		
10	DC	209	Total	C	N	O	S	0	0
			1667	1061	292	309	5		
10	EC	209	Total	C	N	O	S	0	0
			1667	1061	292	309	5		
10	FC	243	Total	C	N	O	S	0	0
			1921	1216	340	357	8		
10	GC	209	Total	C	N	O	S	0	0
			1667	1061	292	309	5		
10	HC	209	Total	C	N	O	S	0	0
			1667	1061	292	309	5		
10	IC	209	Total	C	N	O	S	0	0
			1667	1061	292	309	5		
10	JC	243	Total	C	N	O	S	0	0
			1921	1216	340	357	8		
10	KC	243	Total	C	N	O	S	0	0
			1921	1216	340	357	8		

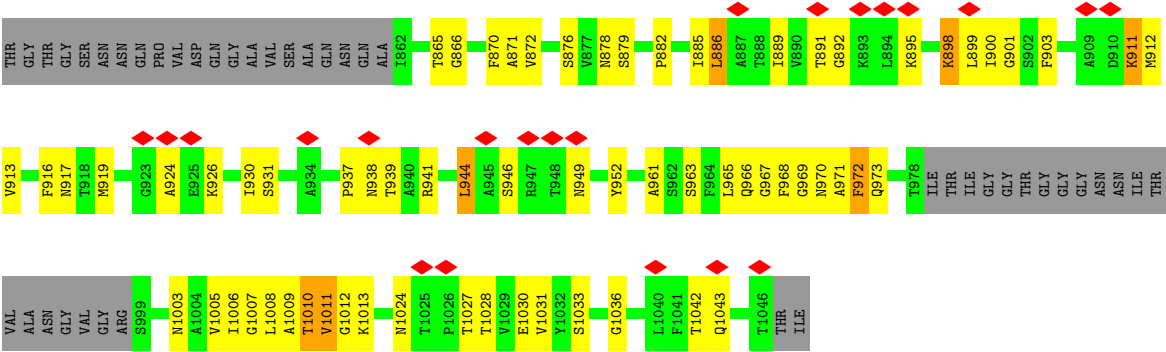
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Mol	Chain	Residues	Atoms					AltConf	Trace
10	LC	209	Total	C	N	O	S	0	0
			1667	1061	292	309	5		
10	MC	209	Total	C	N	O	S	0	0
			1667	1061	292	309	5		
10	AC	243	Total	C	N	O	S	0	0
			1921	1216	340	357	8		

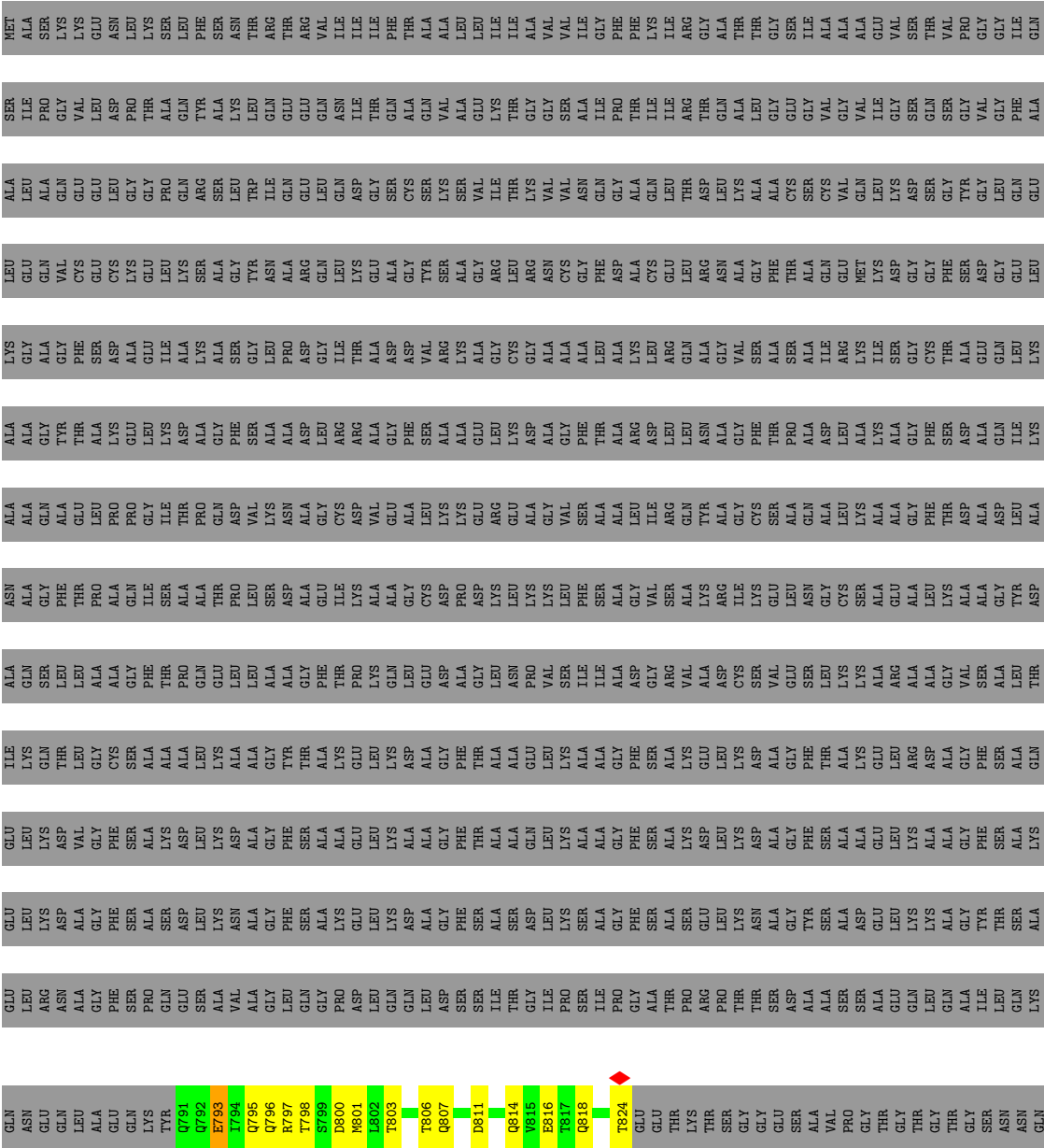
- Molecule 11 is a protein called DUF2807 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	HM	208	Total	C	N	O	S	0	0
			1650	1046	293	308	3		
11	IM	208	Total	C	N	O	S	0	0
			1650	1046	293	308	3		
11	KM	208	Total	C	N	O	S	0	0
			1650	1046	293	308	3		
11	LM	208	Total	C	N	O	S	0	0
			1650	1046	293	308	3		
11	MM	208	Total	C	N	O	S	0	0
			1650	1046	293	308	3		
11	AM	208	Total	C	N	O	S	0	0
			1650	1046	293	308	3		
11	BM	208	Total	C	N	O	S	0	0
			1650	1046	293	308	3		
11	EM	208	Total	C	N	O	S	0	0
			1650	1046	293	308	3		
11	FM	208	Total	C	N	O	S	0	0
			1650	1046	293	308	3		
11	GM	208	Total	C	N	O	S	0	0
			1650	1046	293	308	3		
11	JM	208	Total	C	N	O	S	0	0
			1650	1046	293	308	3		
11	CM	208	Total	C	N	O	S	0	0
			1650	1046	293	308	3		
11	DM	208	Total	C	N	O	S	0	0
			1650	1046	293	308	3		



● Molecule 1: IcmE protein

Chain Fg: .. 97%



[illegible]

- Molecule 1: IcmE protein

Chain Gg: 97%

[illegible]

THR
THR
VAL
GLU
VAL
TYR
SER
GLY
THR
GLY
LEU
GLY
ILE
LEU
PHE
THR
GLN
ASP
VAL
THR
THR
ILE

- Molecule 1: IcmE protein



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

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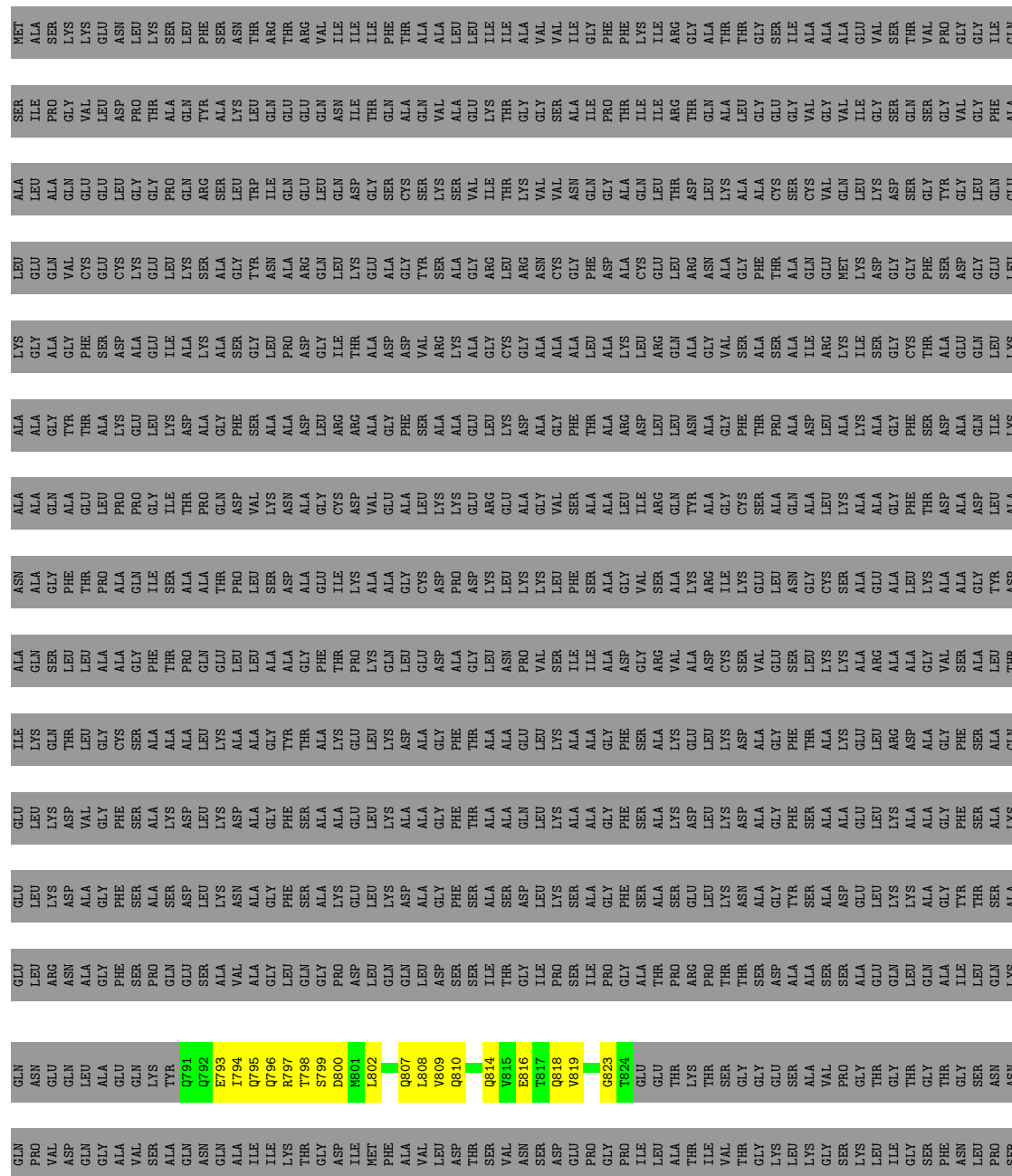
GLU LEU LYS ASP ALA GLY PHE SER SER SER ASP LEU LYS ASN ALA GLY PHE SER LEU LYS ASP ALA GLY PHE SER SER SER ASP LEU LYS ASN ALA GLY TYR THR SER LEU LYS ASP ALA GLY PHE SER SER SER ASP LEU LYS ASN ALA GLY TYR THR SER

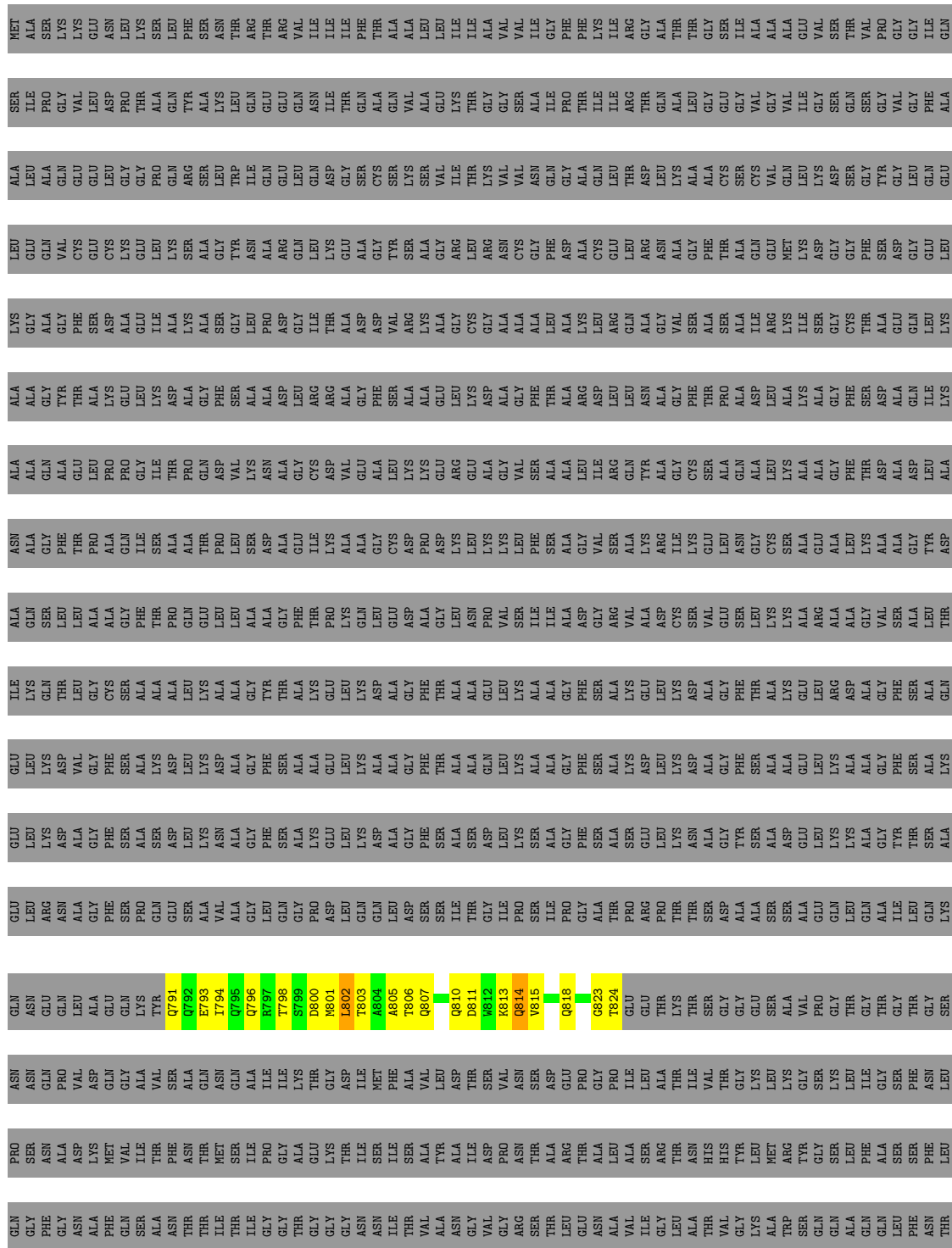
GLN	ASN	GLU	GLN	LEU	ALA	GLU	GLN	LYS	TYR	THR	GLN	GLN	GLU	GLU	ILE	GLN	GLN	ARG	THR	ASP	SER	MET	LEU	LEU	THR	ALA	ALA	THR	THR	GLN	GLN	LEU	VAL	VAL	GLN	ASP	TRP	TRP	GLN	VAL	VAL	GLY	THR	THR	THR	GLU	GLY	GLU	GLU	THR	LYS	THR	SER	GLY	GLY	GLY	GLY	GLU	GLU	SER	VAL	VAL	PRO	PRO	GLY	GLY	THR	THR	Y
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[illegible]

- Molecule 1: IcmE protein

Chain Hg: 97%



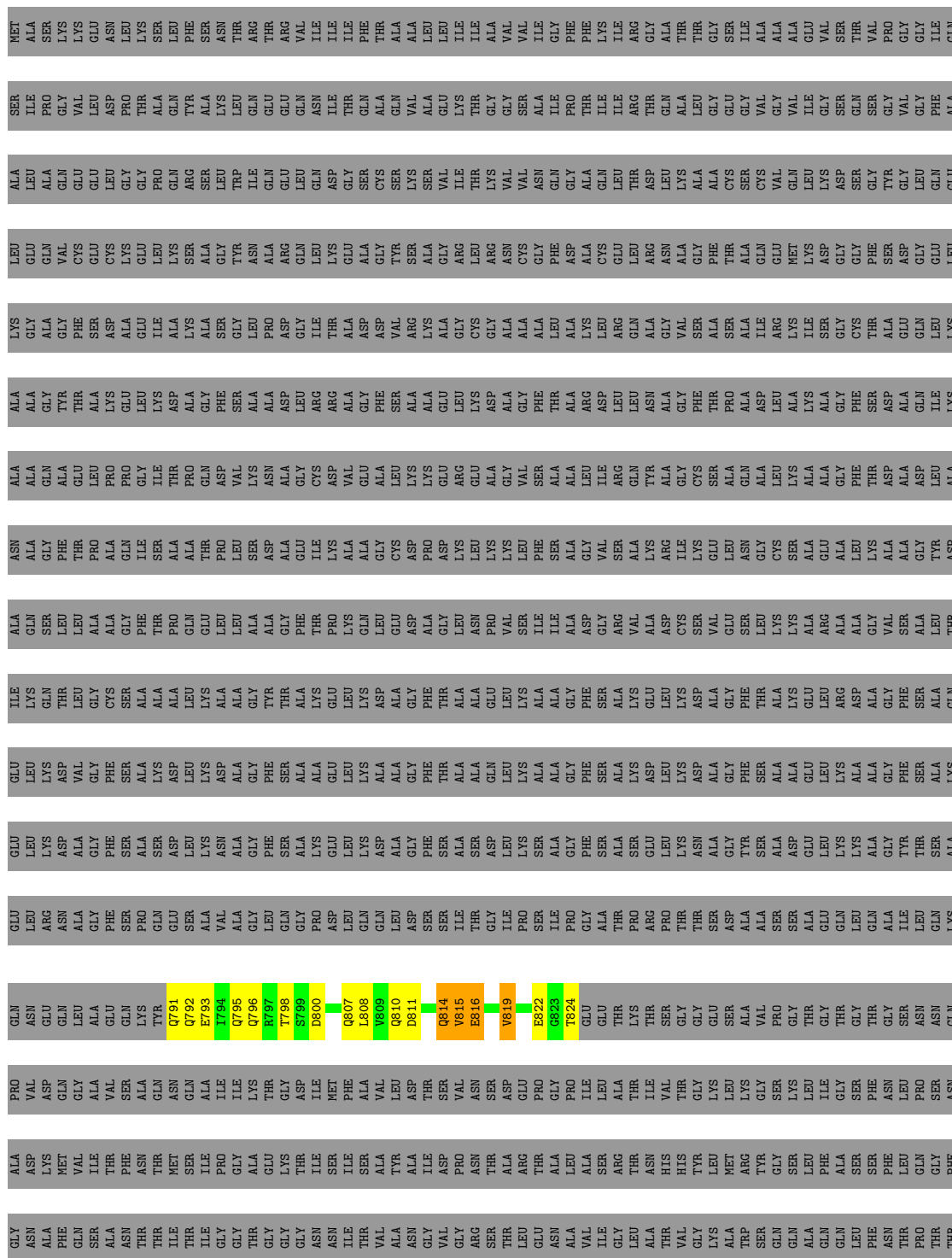


Chain Kg: .. 97%



- Molecule 1: IcmE protein

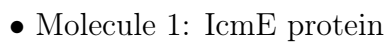
Chain Lg: 97%



Chain Mg: .. 97%



Chain EG: 9% 6% 84%



97%

- Molecule 1: IcmE protein

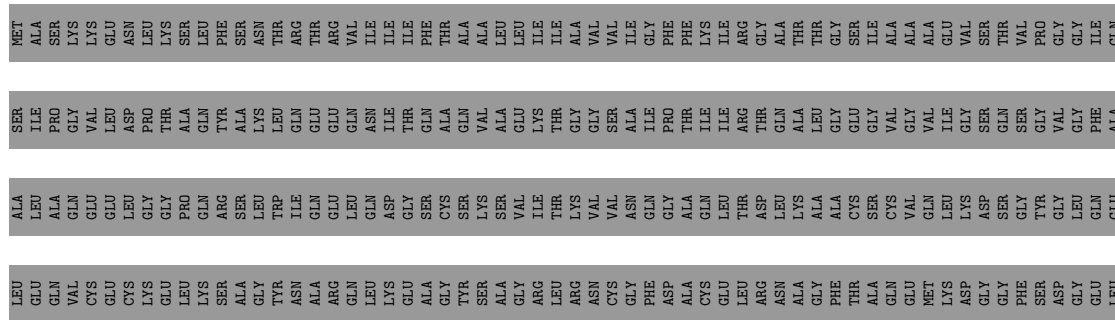
97%





WORLDWIDE
PDB
PROTEIN DATA BANK

- Molecule 1: IcmE protein



V1045	THR
T1046	ILE

Chain IG: 8% 7% 84%

[illegible]



- Molecule 1: IcmE protein

[illegible]





- Molecule 1: IcmE protein

[illegible]

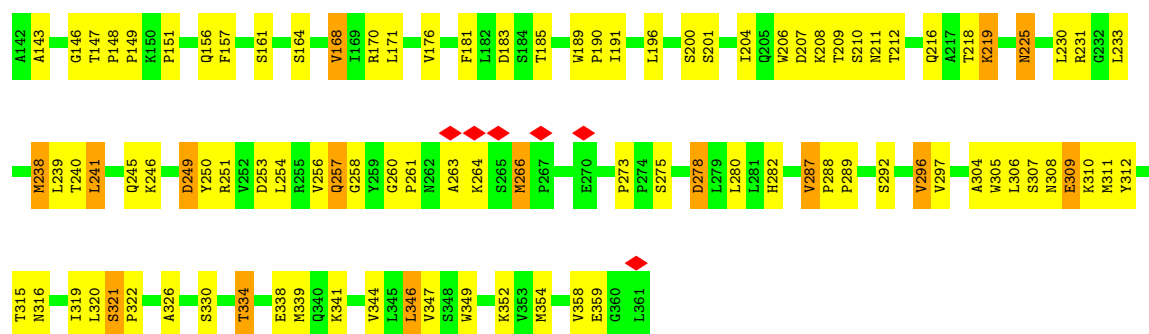
RET	ALA	SER	LYS	GLU	ASN	LEU	LYS	SER	PRE	SER	THR	THR	ARG	ARG	ILE	ILE	ILE	PRE	THR	THR	ALA	ALA	VAL	VAL	ILE	ILE	GLY	PRE	PRE	LYS	LYS	ILE	ILE	ARG	GLY	ALA	ALA	THR	THR	GLY	SER	SER	ILE	ALA	ALA	ALA	GLU	VAL	SER	SER	THR	THR	VAL	PRO	GLY	GLY	ILE	ILE	GLN
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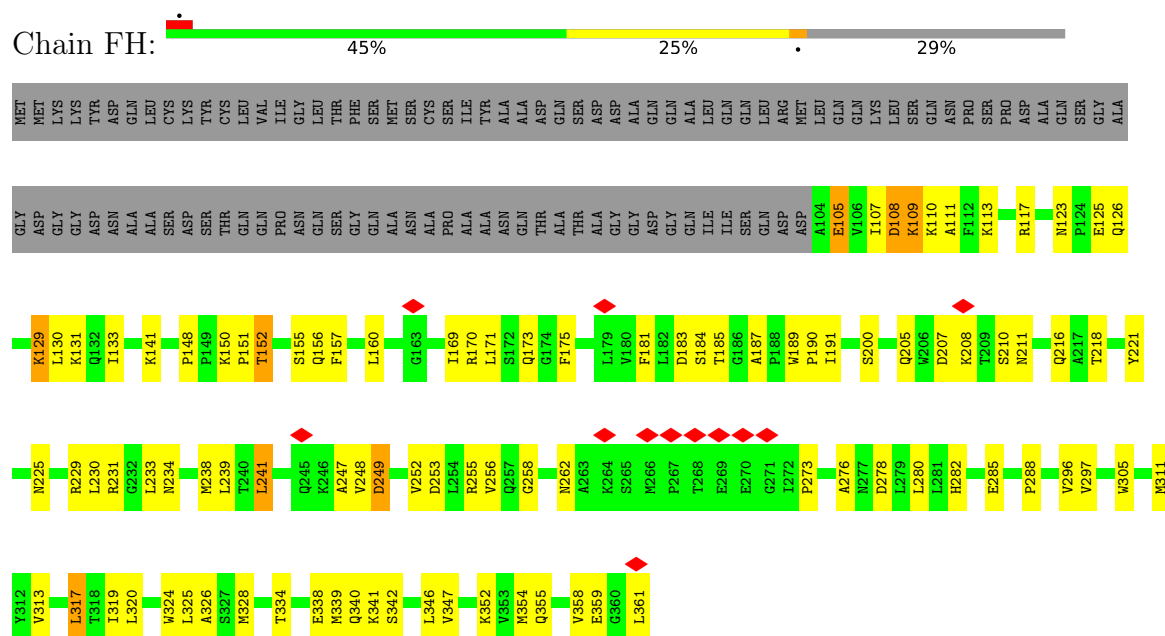


[illegible]

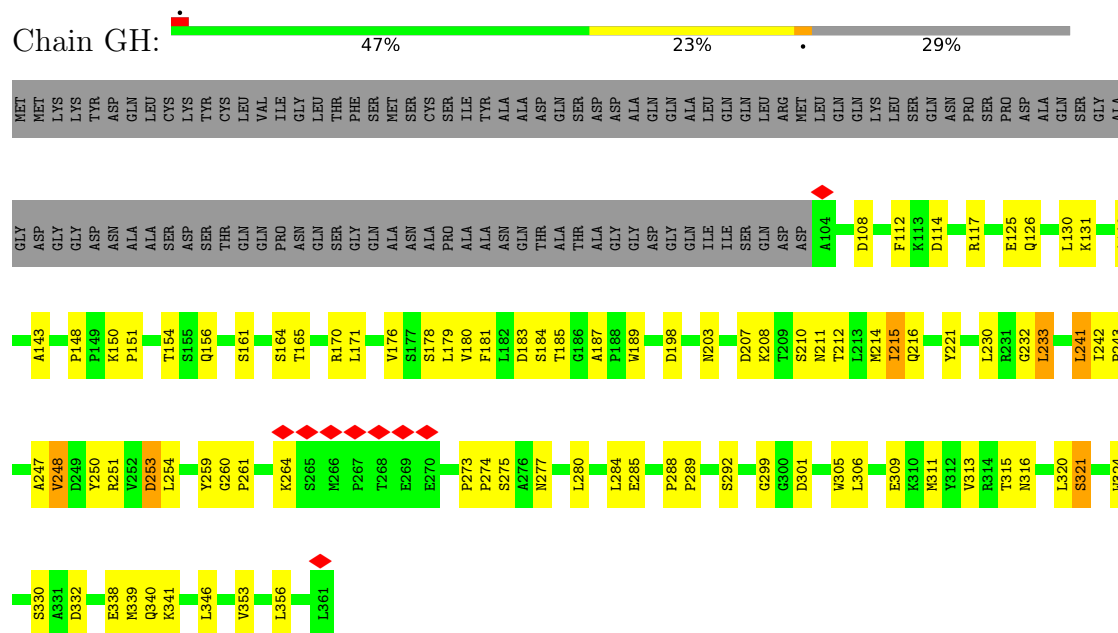
- Molecule 2: Type IV secretion protein IcmK



- Molecule 2: Type IV secretion protein IcmK



- Molecule 2: Type IV secretion protein IcmK



Chain HH:

47% 23% 29%

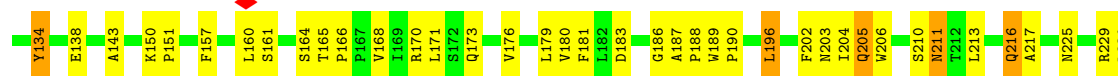
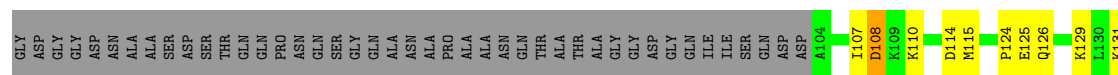
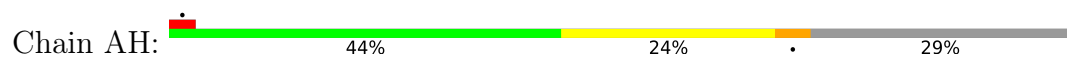
Category	Value
47%	47%
23%	23%
29%	29%

Chain IH:

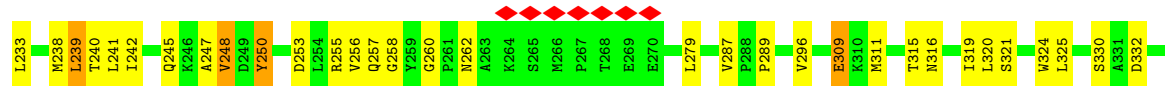
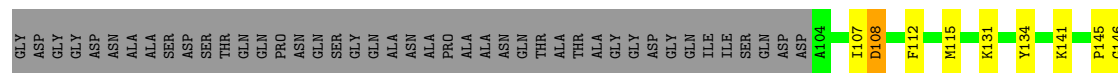
Category	Percentage	Amino Acids
Green	47%	MET, ASP, GLY, LYS, TYR, ASP, ASN, ALA, LEU, CYS, SER, THR, CYS, LEU, VAL, ILE, GLY, ASN, LEU, THR
Yellow	22%	GLY, ASP, GLY, LYS, TYR, ASP, ASN, ALA, LEU, CYS, SER, THR, CYS, LEU, VAL, ILE, GLY, ASN, LEU, THR
Grey	29%	MET, ASP, GLY, LYS, TYR, ASP, ASN, ALA, LEU, CYS, SER, THR, CYS, LEU, VAL, ILE, GLY, ASN, LEU, THR

[illegible]

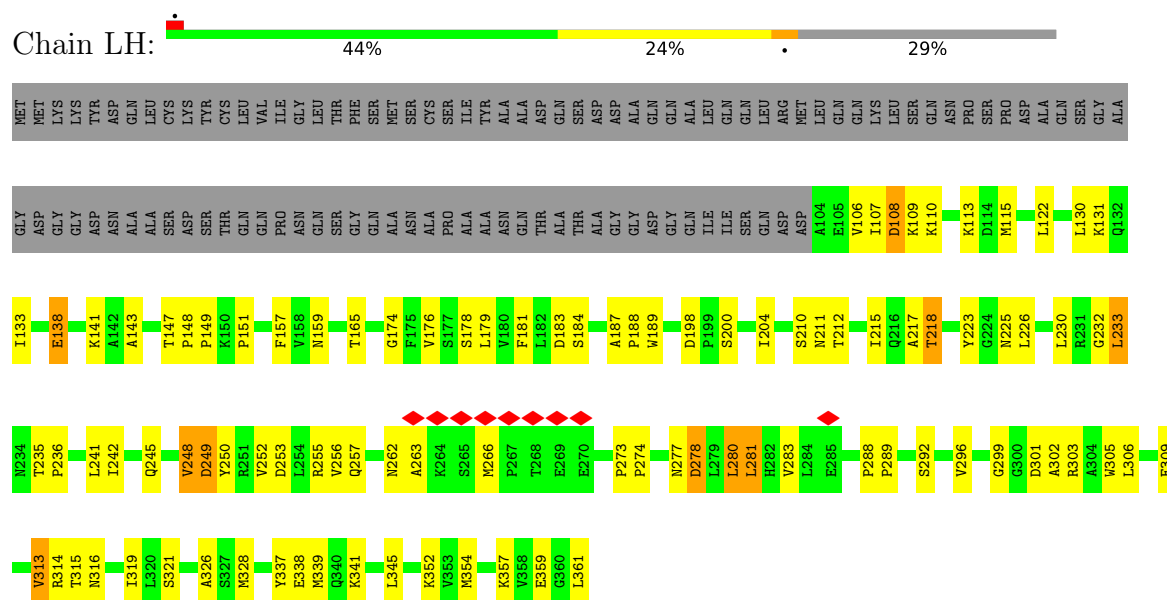
- Molecule 2: Type IV secretion protein IcmK



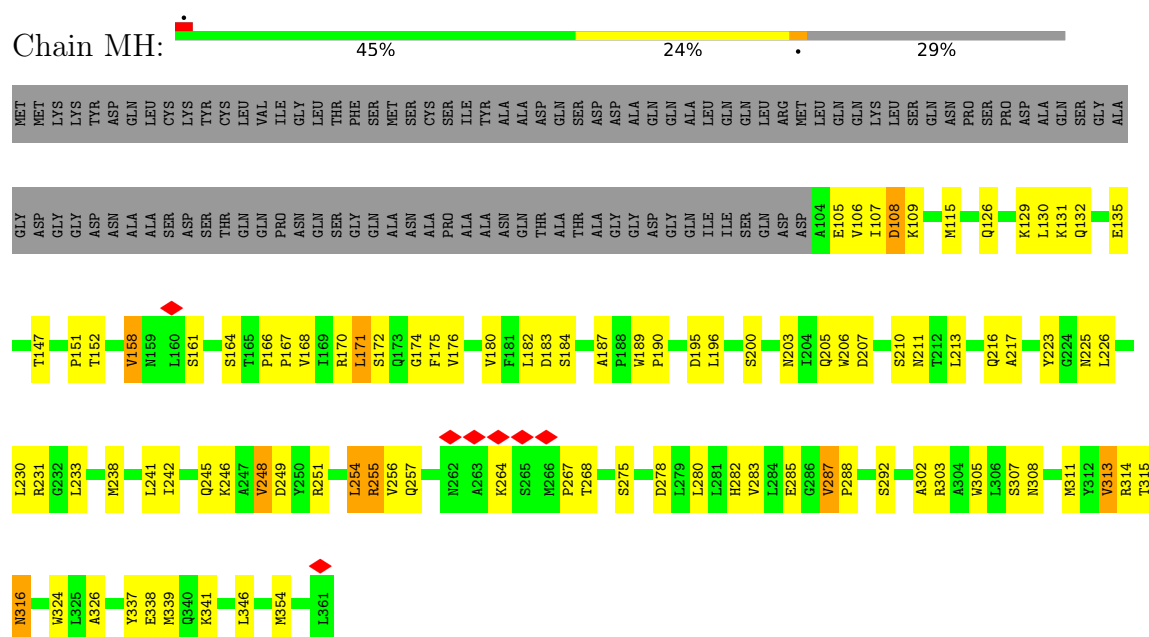
- Molecule 2: Type IV secretion protein IcmK



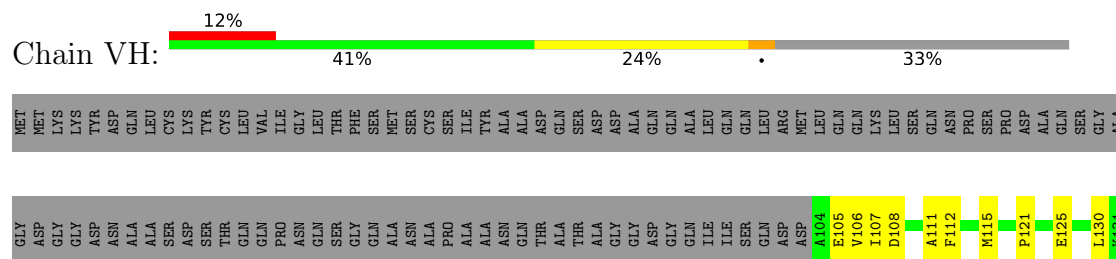
- Molecule 2: Type IV secretion protein IcmK

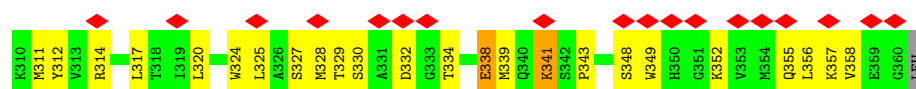


- Molecule 2: Type IV secretion protein IcmK

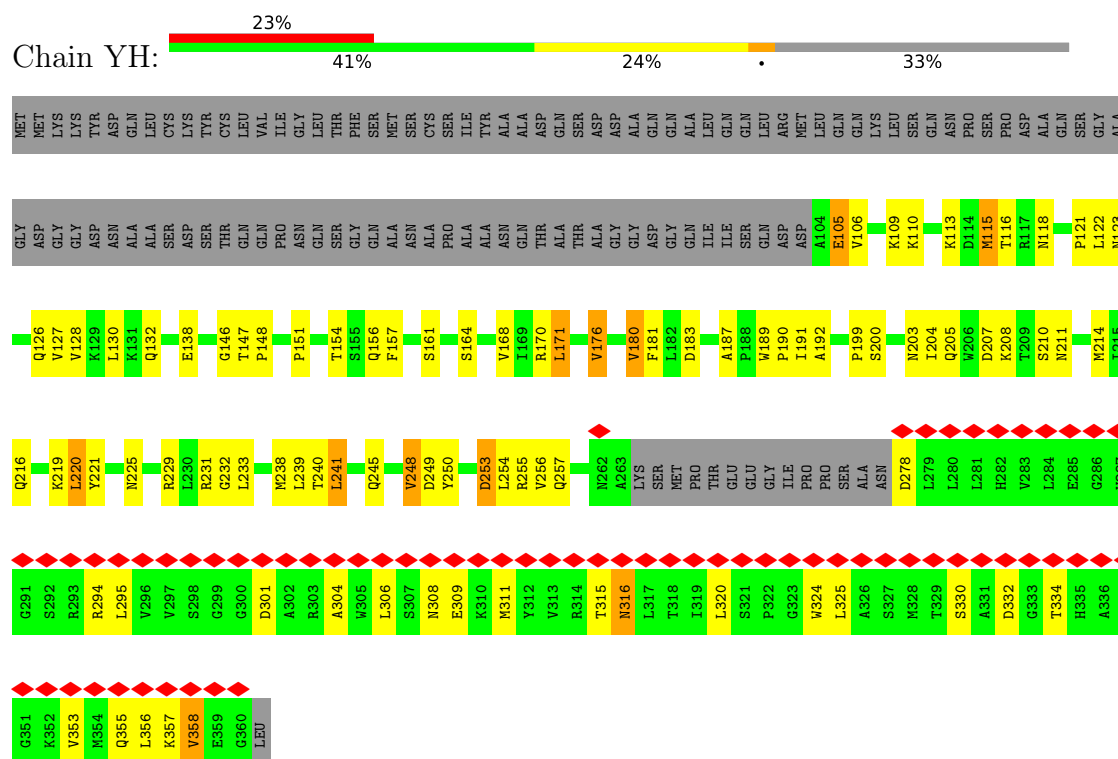


- Molecule 2: Type IV secretion protein IcmK

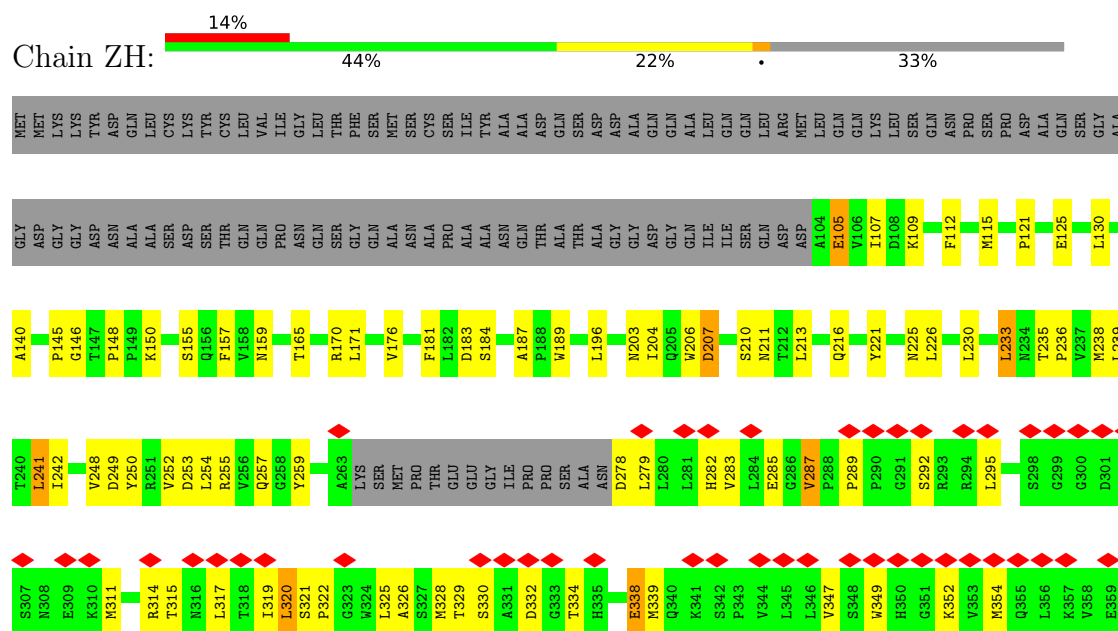




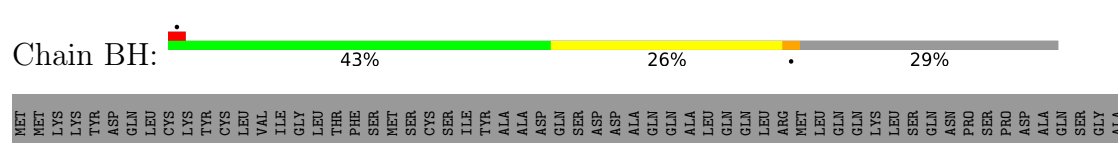
- Molecule 2: Type IV secretion protein IcmK

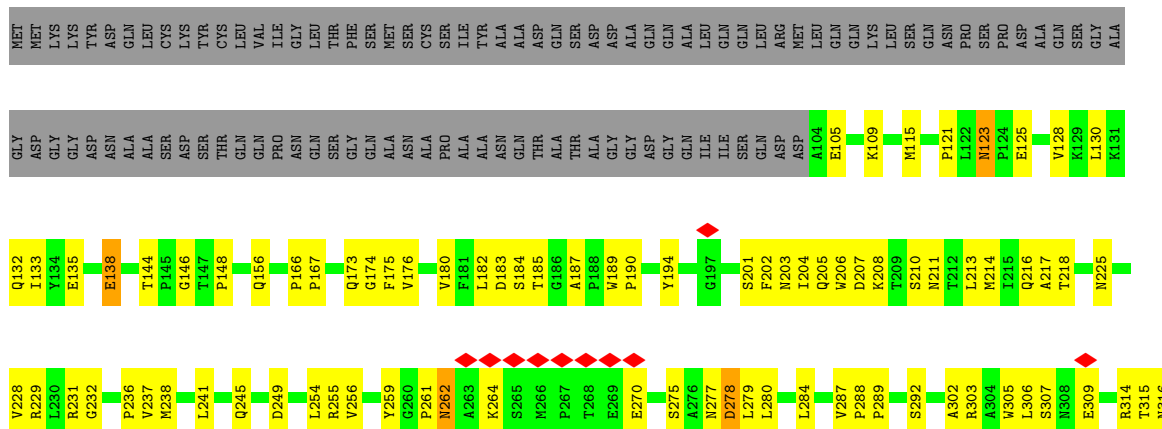


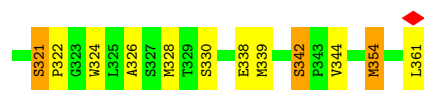
- Molecule 2: Type IV secretion protein IcmK



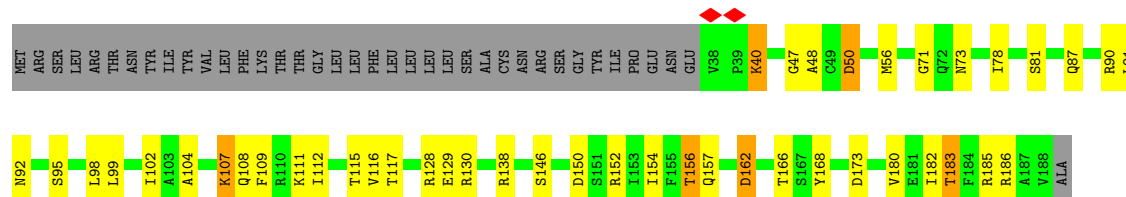
- Molecule 2: Type IV secretion protein IcmK



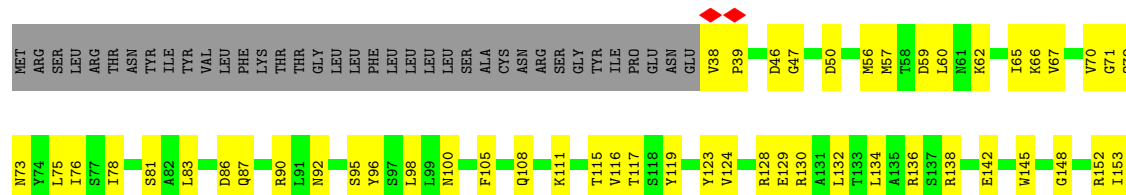




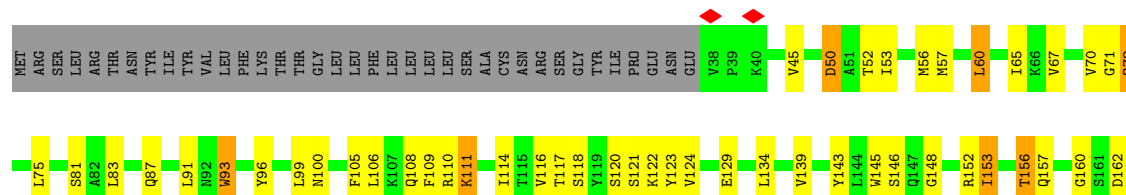
• Molecule 3: Inner membrane lipoprotein YiaD



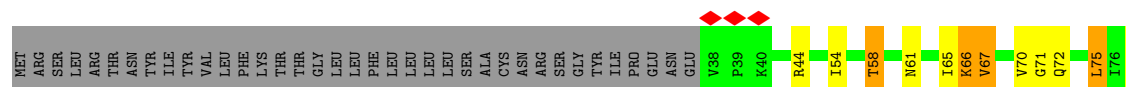
• Molecule 3: Inner membrane lipoprotein YiaD

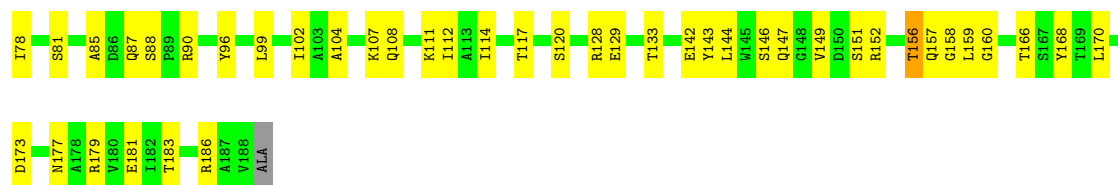


• Molecule 3: Inner membrane lipoprotein YiaD

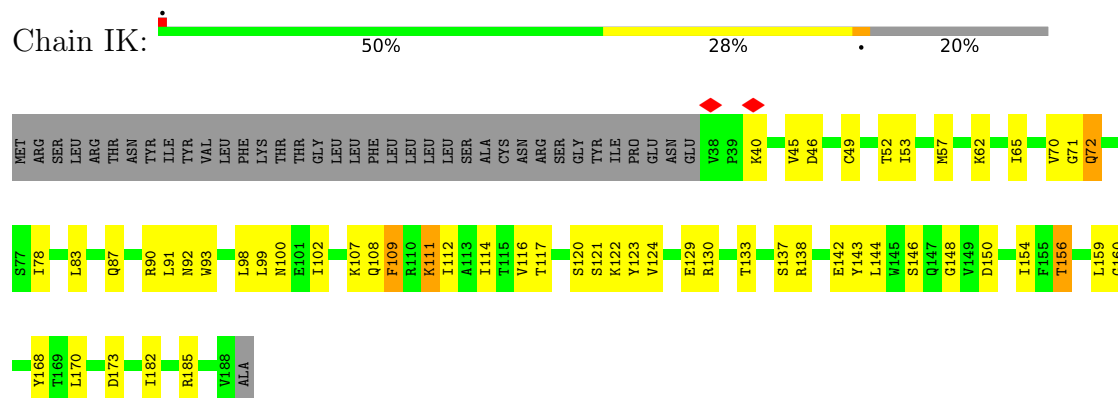


• Molecule 3: Inner membrane lipoprotein YiaD

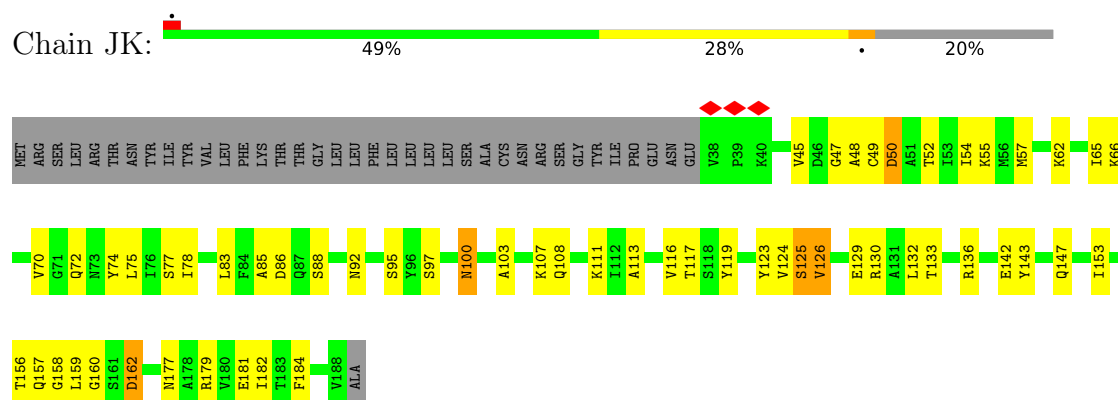




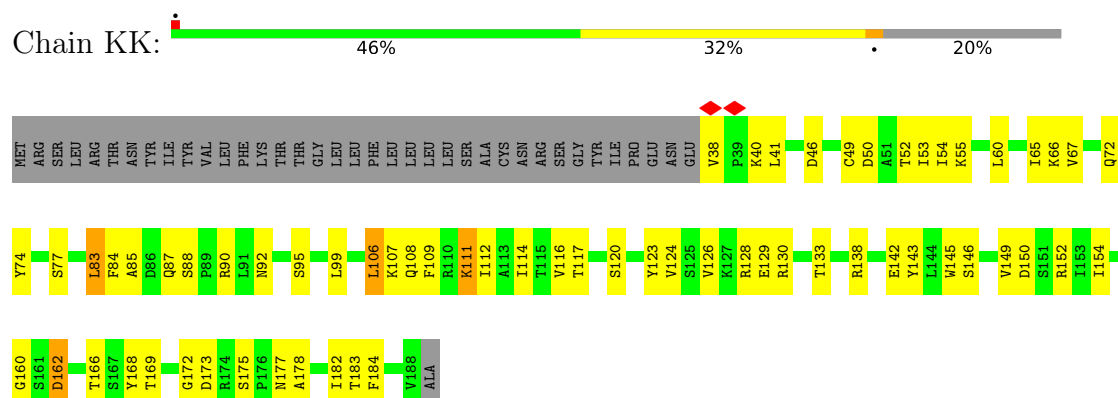
• Molecule 3: Inner membrane lipoprotein YiaD



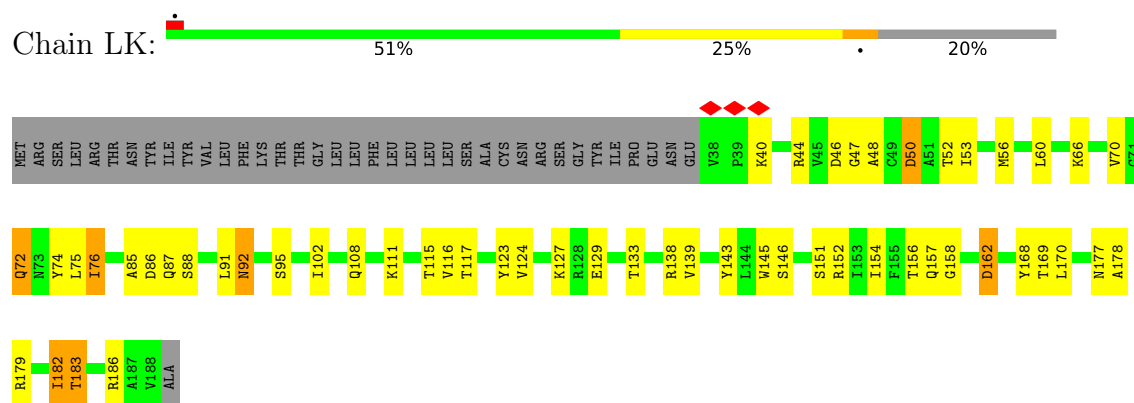
• Molecule 3: Inner membrane lipoprotein YiaD



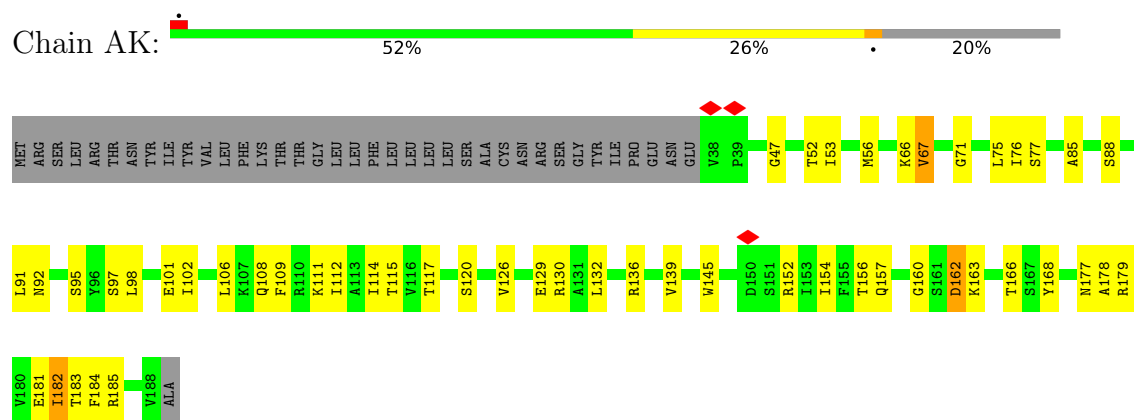
• Molecule 3: Inner membrane lipoprotein YiaD



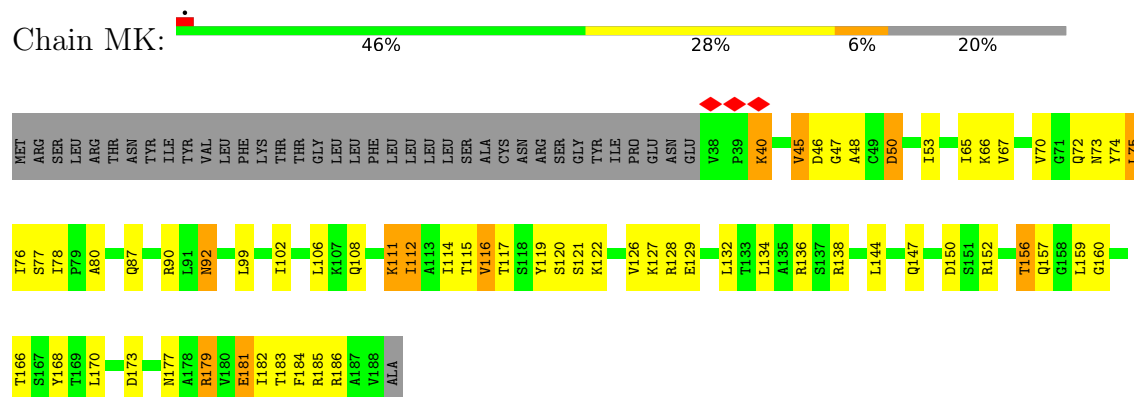
• Molecule 3: Inner membrane lipoprotein YiaD



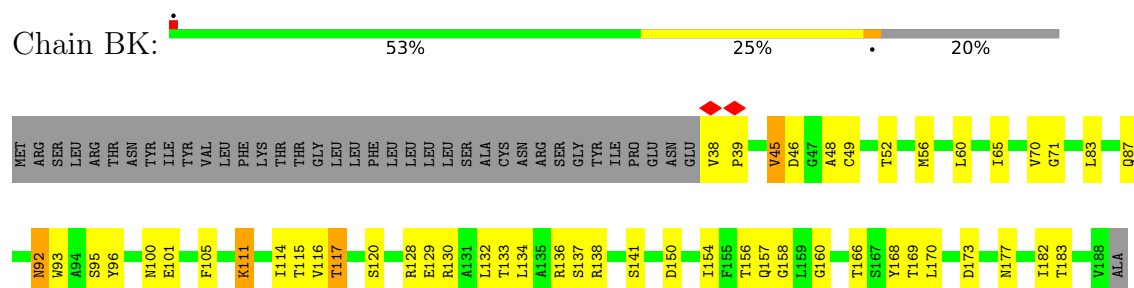
• Molecule 3: Inner membrane lipoprotein YiaD



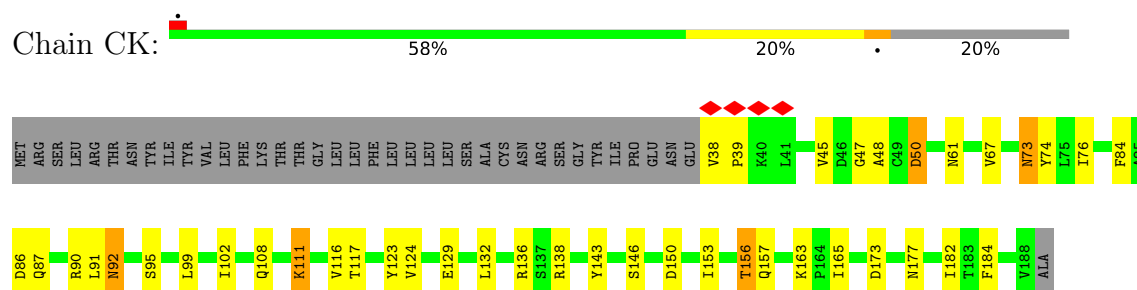
• Molecule 3: Inner membrane lipoprotein YiaD



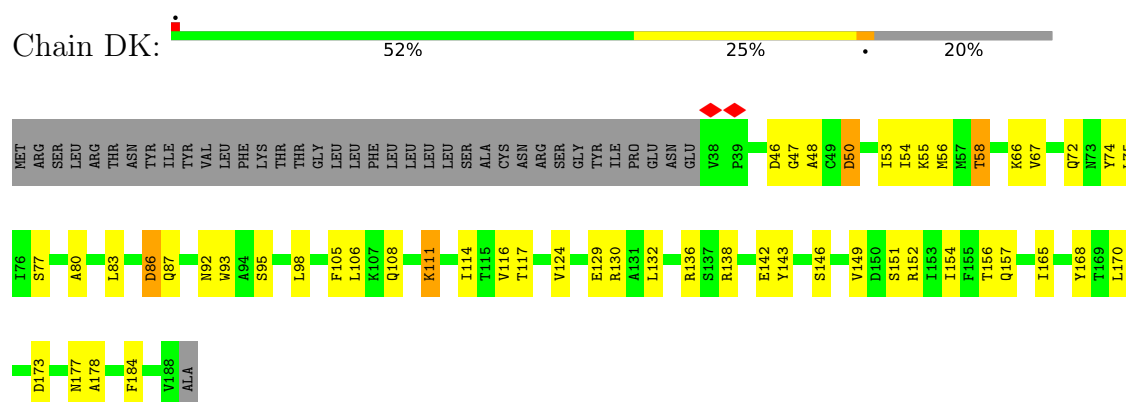
• Molecule 3: Inner membrane lipoprotein YiaD



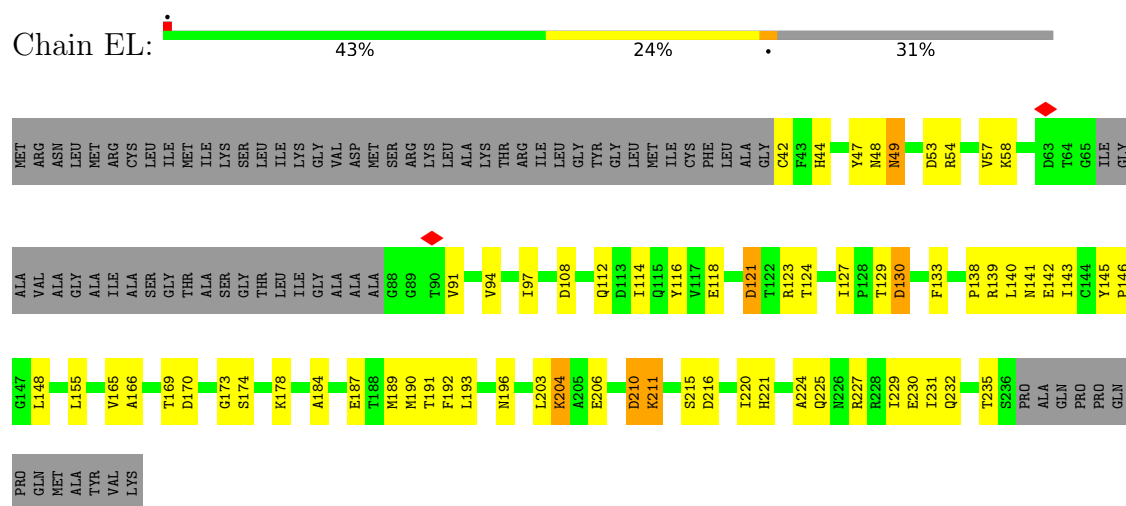
- Molecule 3: Inner membrane lipoprotein YiaD



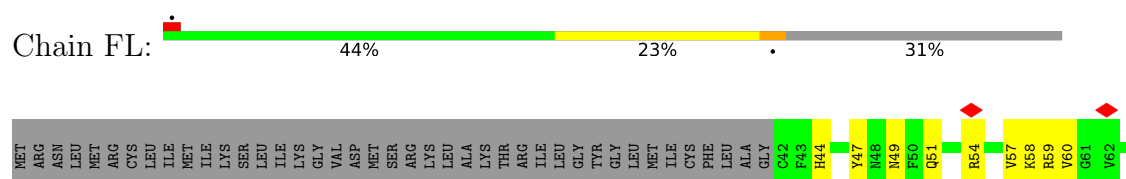
- Molecule 3: Inner membrane lipoprotein YiaD

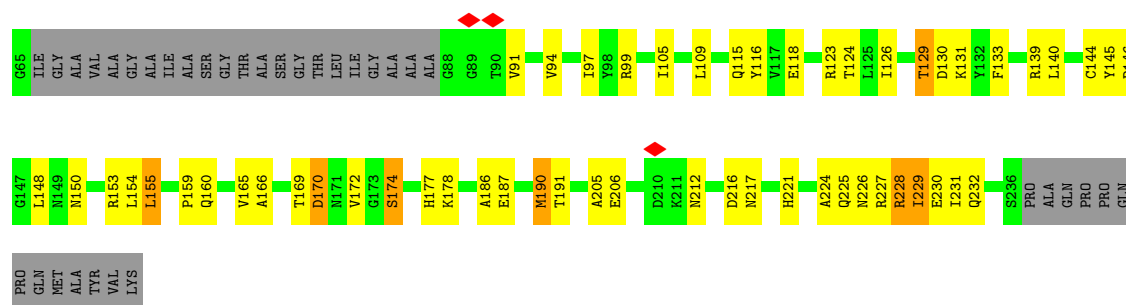


- Molecule 4: Outer membrane protein, OmpA family protein



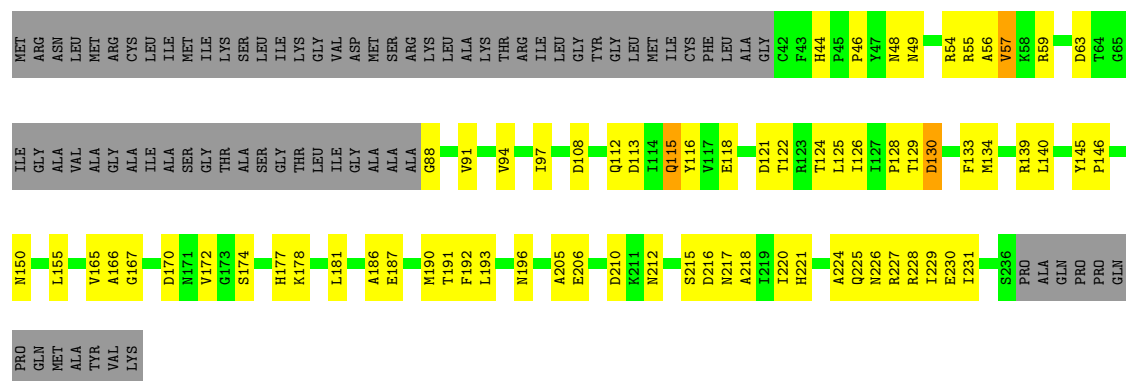
- Molecule 4: Outer membrane protein, OmpA family protein





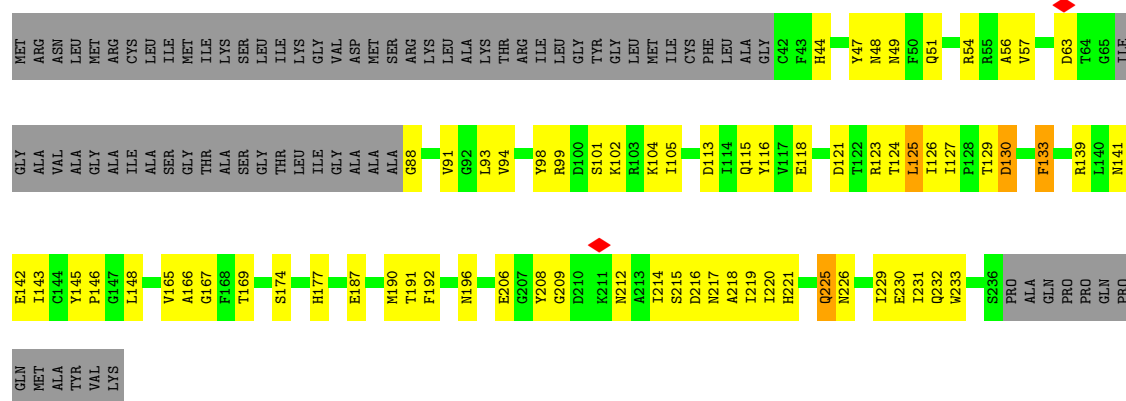
- Molecule 4: Outer membrane protein, OmpA family protein

Chain GL: 41% 27% • 31%



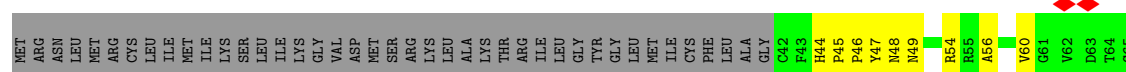
- Molecule 4: Outer membrane protein, OmpA family protein

Chain HL: 42% 26% • 31%



- Molecule 4: Outer membrane protein, OmpA family protein

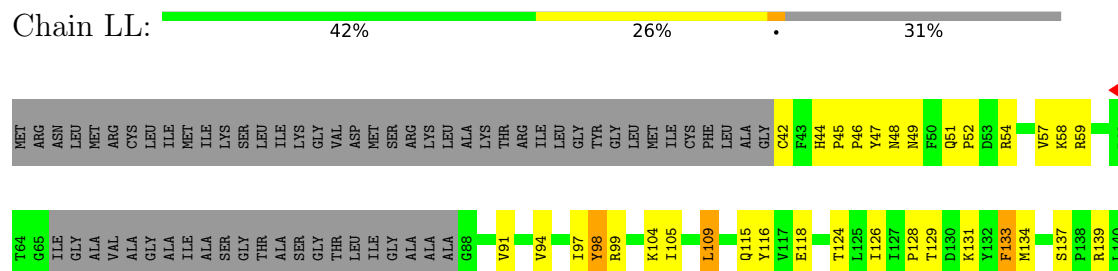
Chain IL: 43% 24% • 31%

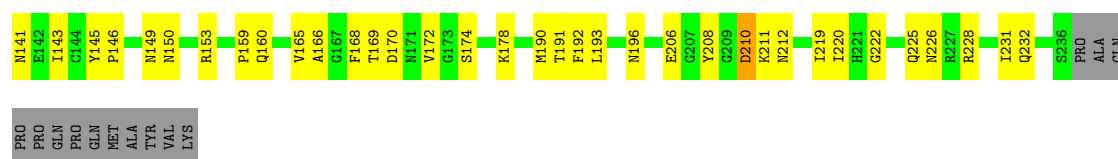


- Molecule 4: Outer membrane protein, OmpA family protein

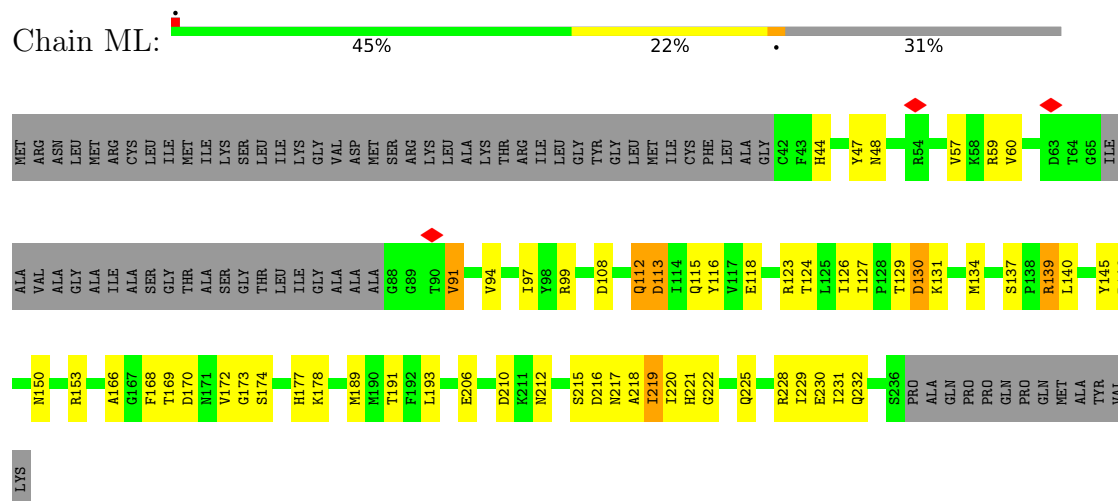
- Molecule 4: Outer membrane protein, OmpA family protein

- Molecule 4: Outer membrane protein, OmpA family protein

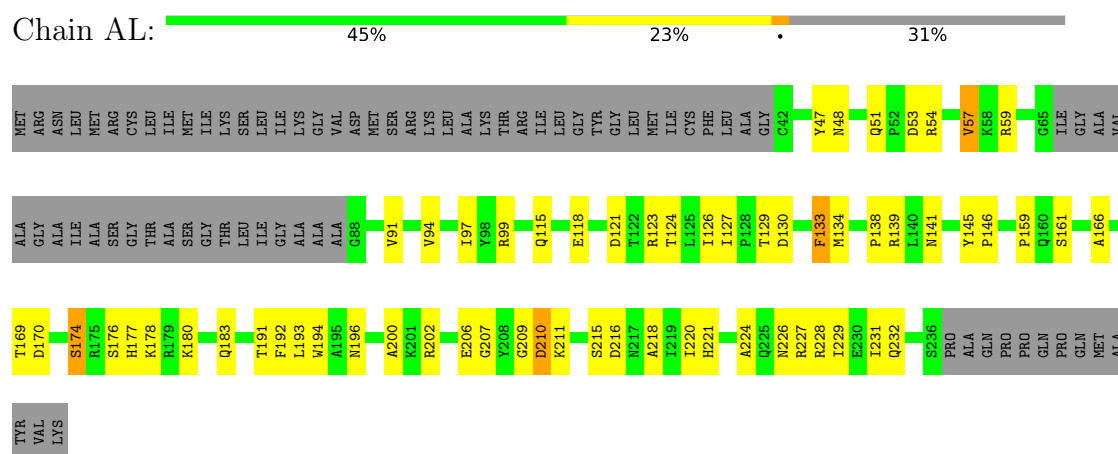




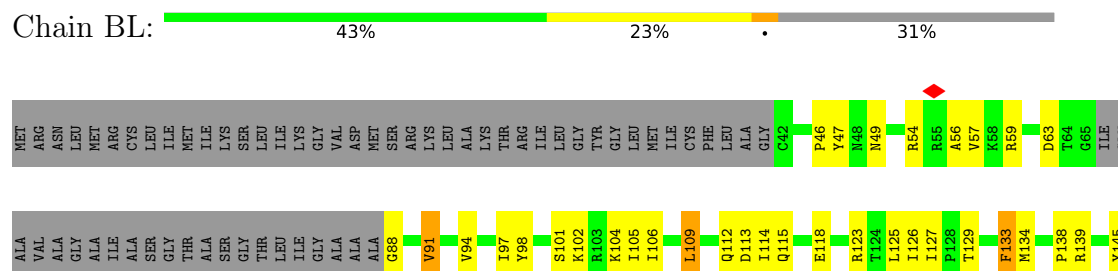
- Molecule 4: Outer membrane protein, OmpA family protein

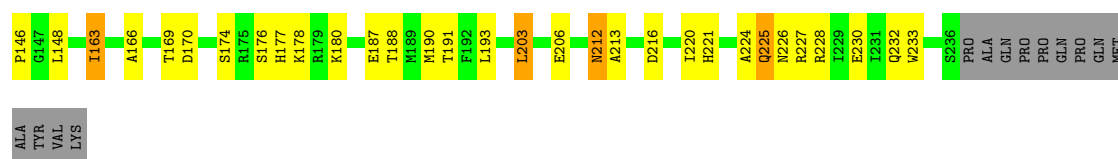


- Molecule 4: Outer membrane protein, OmpA family protein

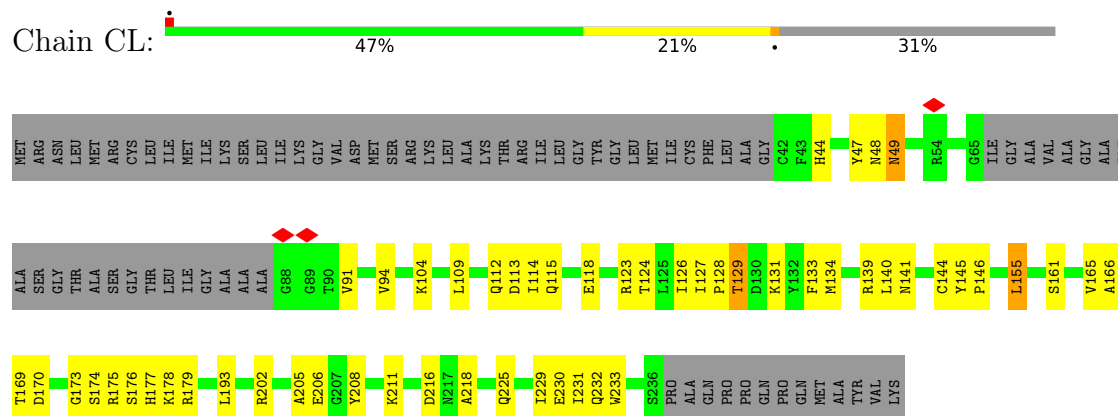


- Molecule 4: Outer membrane protein, OmpA family protein

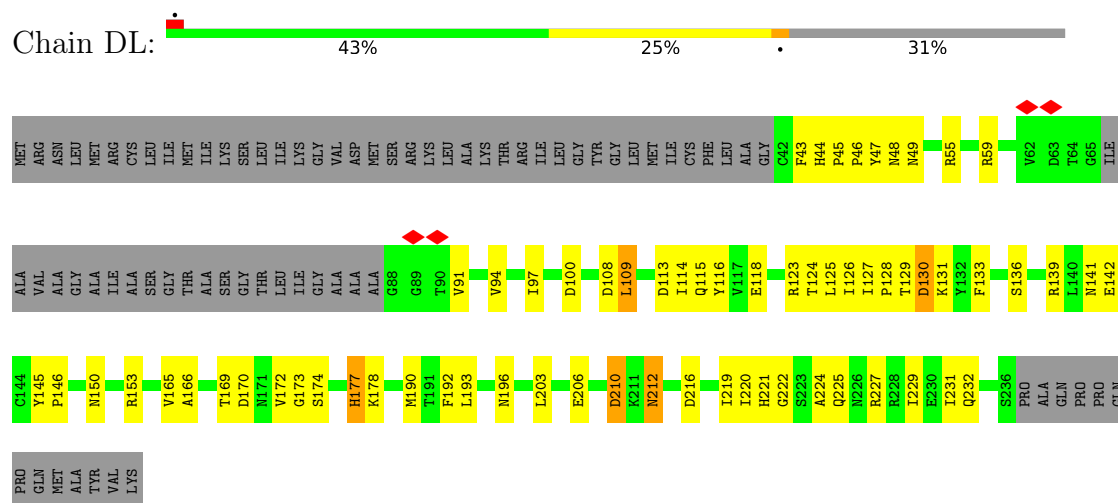




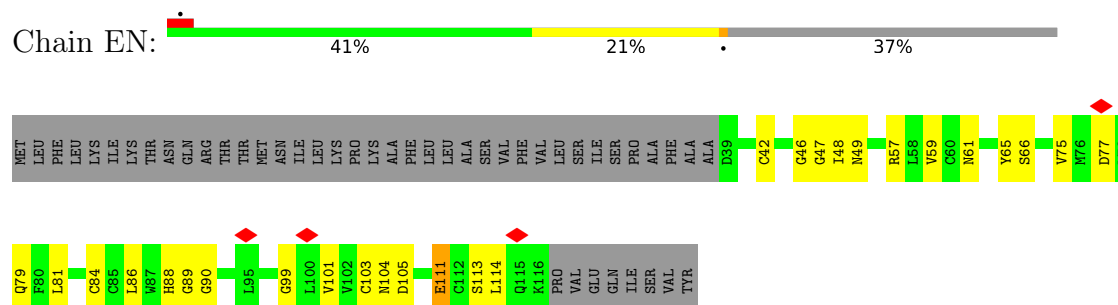
- Molecule 4: Outer membrane protein, OmpA family protein



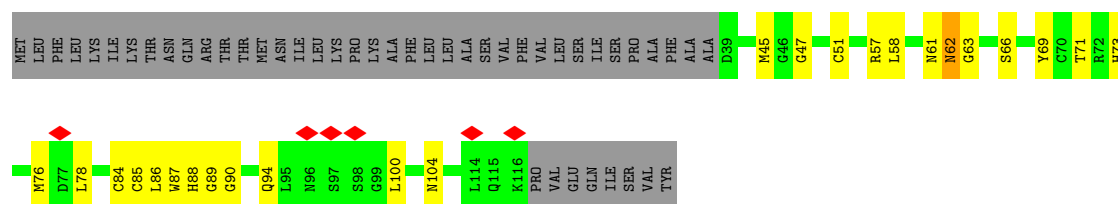
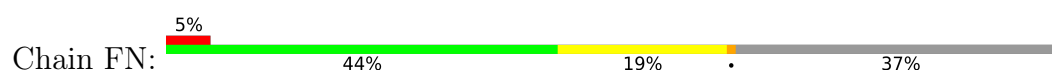
- Molecule 4: Outer membrane protein, OmpA family protein



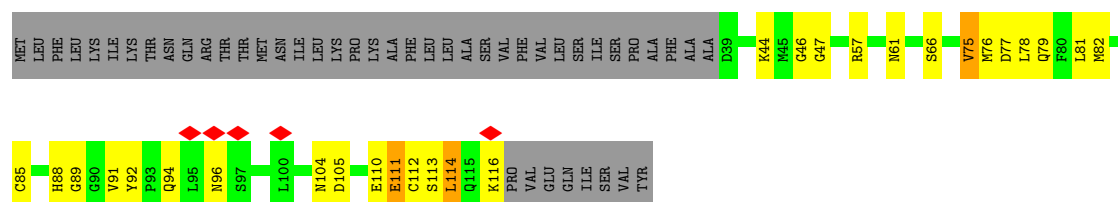
- Molecule 5: Neurogenic locus notch



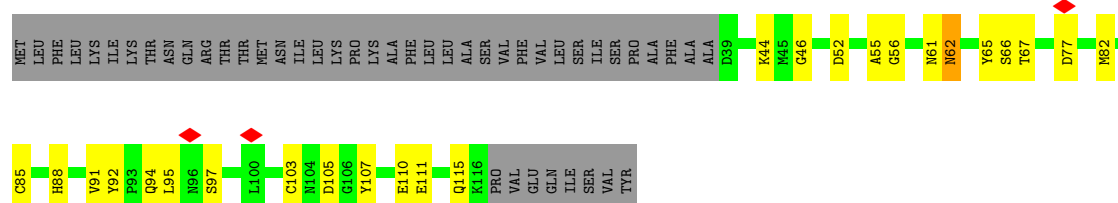
- Molecule 5: Neurogenic locus notch



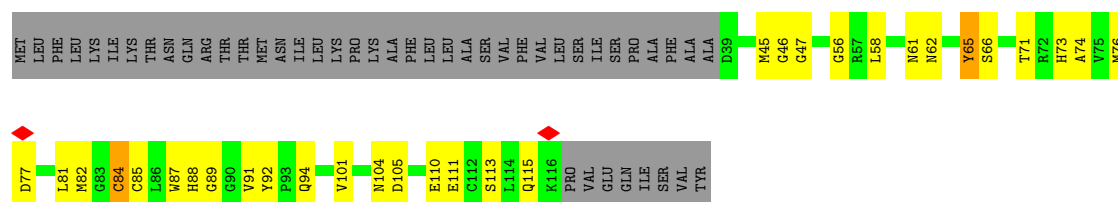
- Molecule 5: Neurogenic locus notch



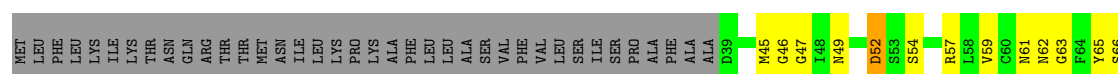
- Molecule 5: Neurogenic locus notch

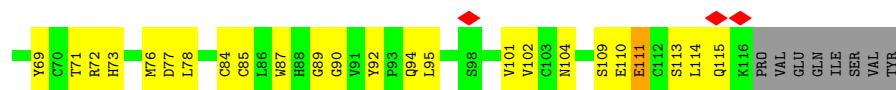


- Molecule 5: Neurogenic locus notch

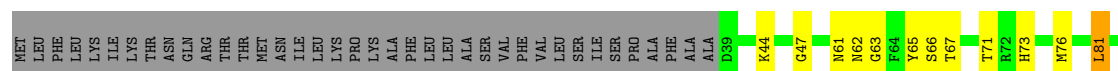


- Molecule 5: Neurogenic locus notch

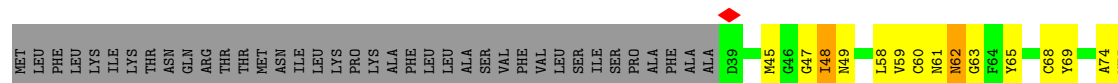




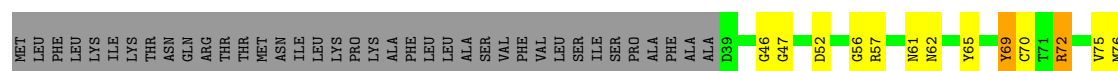
- Molecule 5: Neurogenic locus notch



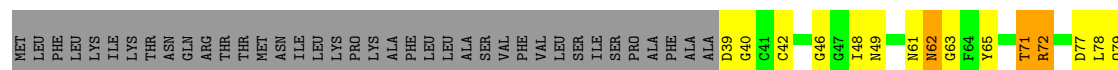
- Molecule 5: Neurogenic locus notch



- Molecule 5: Neurogenic locus notch

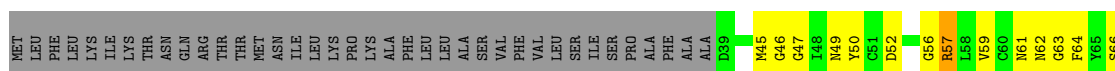


- Molecule 5: Neurogenic locus notch

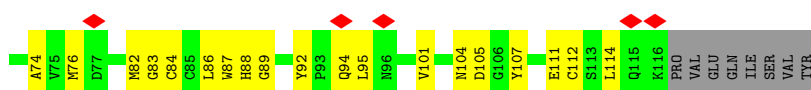
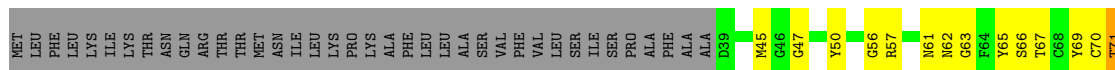


- Molecule 5: Neurogenic locus notch

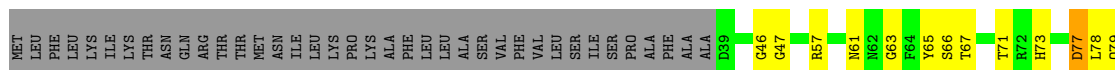




- Molecule 5: Neurogenic locus notch



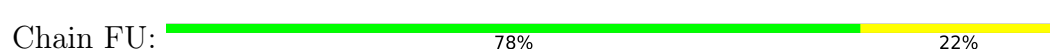
- Molecule 5: Neurogenic locus notch



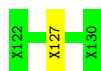
- Molecule 6: Unknown protein fragment



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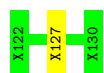


- Molecule 6: Unknown protein fragment



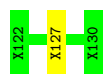
- Molecule 6: Unknown protein fragment

Chain HU:  89% 11%



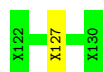
- Molecule 6: Unknown protein fragment

Chain IU:  89% 11%



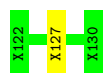
- Molecule 6: Unknown protein fragment

Chain JU:  89% 11%



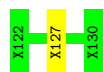
- Molecule 6: Unknown protein fragment

Chain KU:  89% 11%



- Molecule 6: Unknown protein fragment

Chain LU:  89% 11%



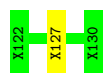
- Molecule 6: Unknown protein fragment

Chain MU:  100%

There are no outlier residues recorded for this chain.

- Molecule 6: Unknown protein fragment

Chain AU:  89% 11%



- Molecule 6: Unknown protein fragment

Chain BU:  100%

There are no outlier residues recorded for this chain.

- Molecule 6: Unknown protein fragment

Chain CU:  100%

There are no outlier residues recorded for this chain.

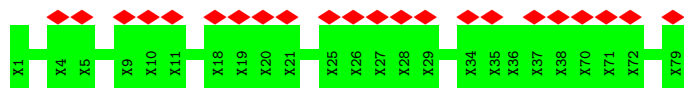
- Molecule 6: Unknown protein fragment

Chain DU:  89% 11%



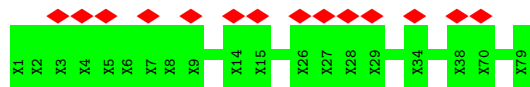
- Molecule 7: Unknown protein fragment

Chain EX:  46% 100%



- Molecule 7: Unknown protein fragment

Chain FX:  29% 100%



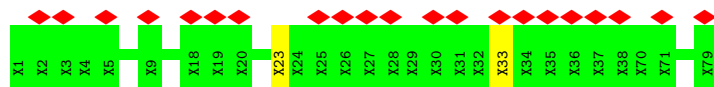
- Molecule 7: Unknown protein fragment

Chain GX:  33% 100%



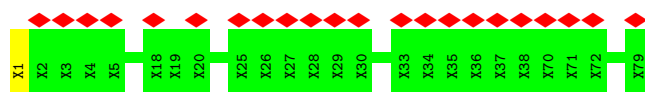
- Molecule 7: Unknown protein fragment

Chain HX:  44% 96%

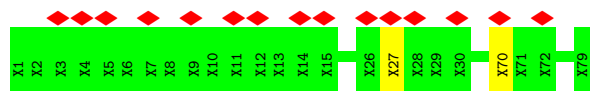


- Molecule 7: Unknown protein fragment

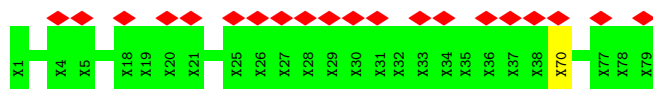
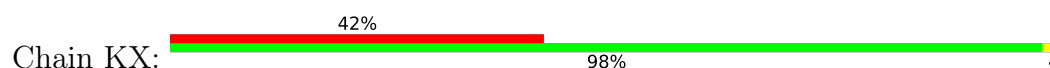
Chain IX:  46% 98%



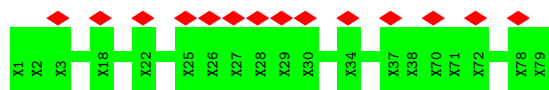
- Molecule 7: Unknown protein fragment



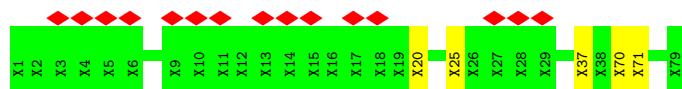
- Molecule 7: Unknown protein fragment



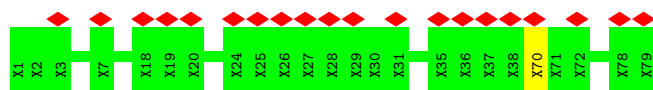
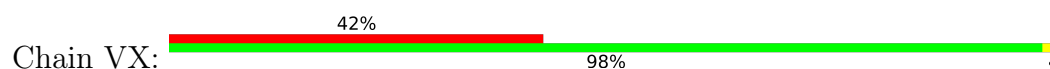
- Molecule 7: Unknown protein fragment



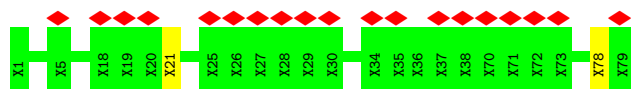
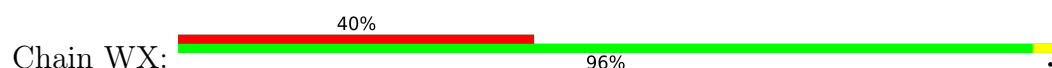
- Molecule 7: Unknown protein fragment



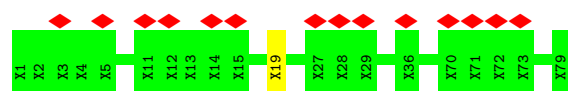
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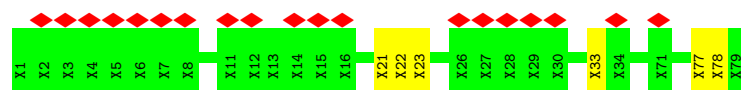
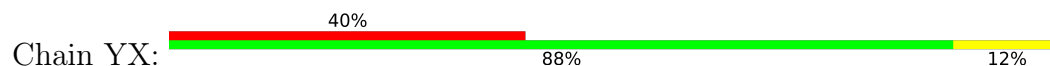
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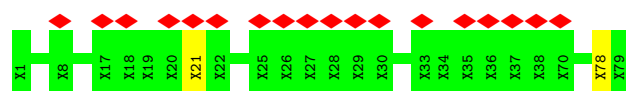
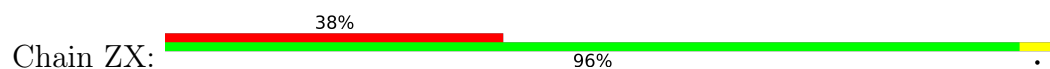
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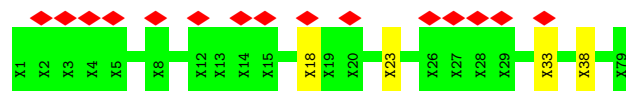
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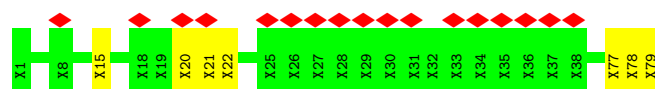
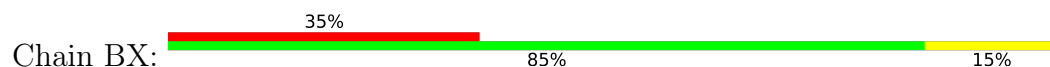
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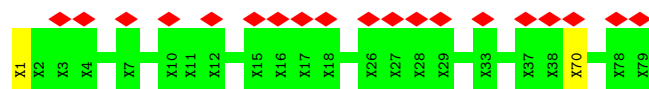
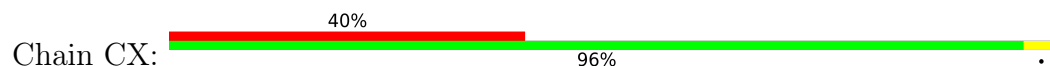
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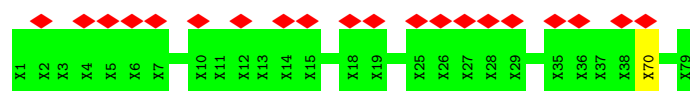
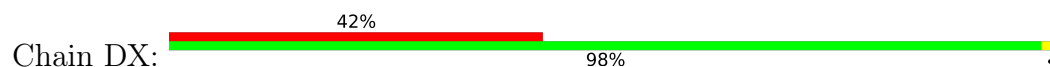
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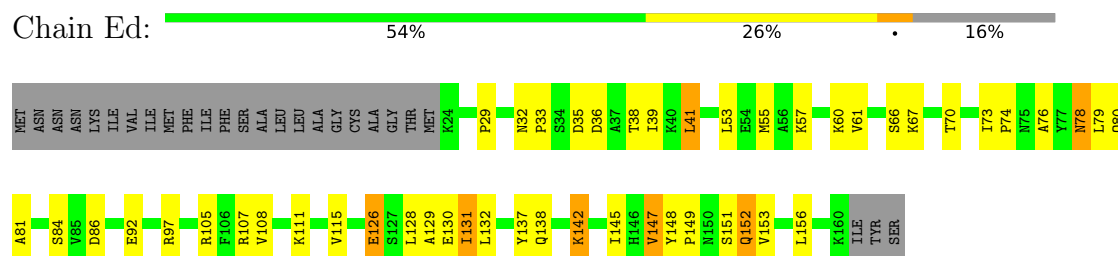
- Molecule 7: Unknown protein fragment



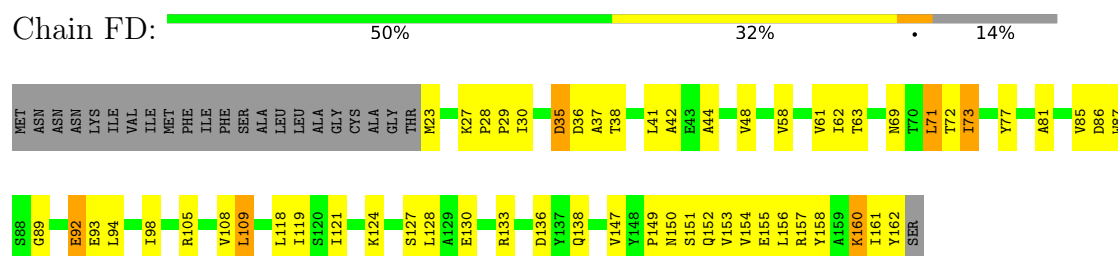
- Molecule 7: Unknown protein fragment



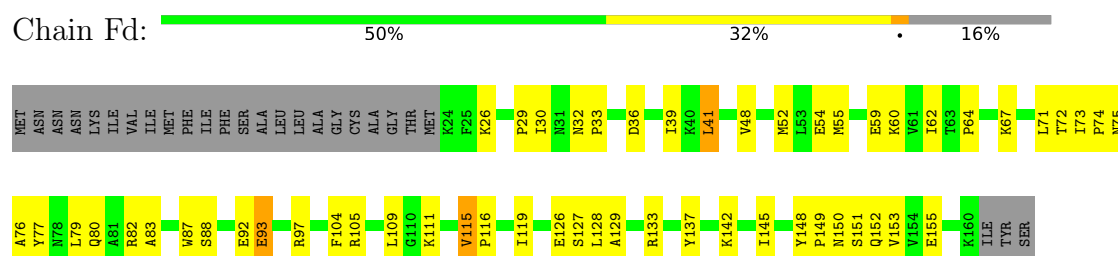
- Molecule 8: DotD



- Molecule 8: DotD



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- Molecule 8: DotD

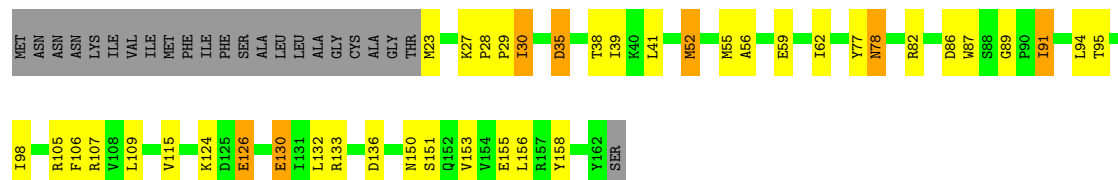


- Molecule 8: DotD



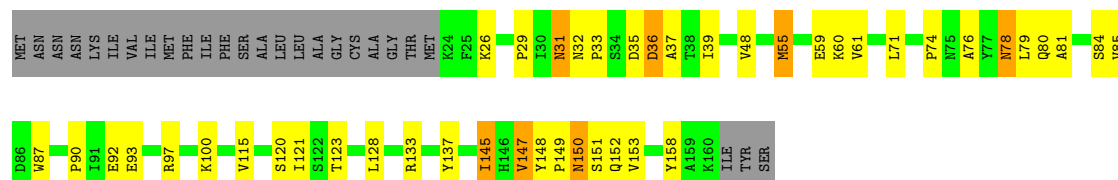
- Molecule 8: DotD

Chain HD: 



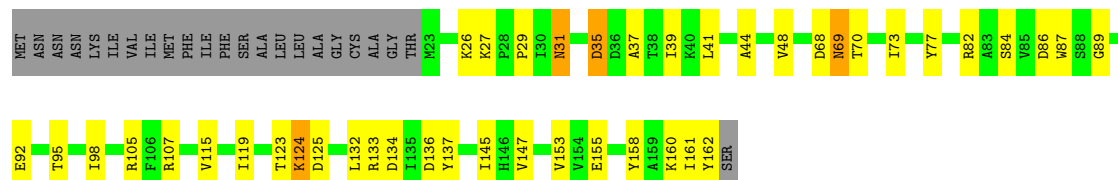
- Molecule 8: DotD

Chain Hd: 



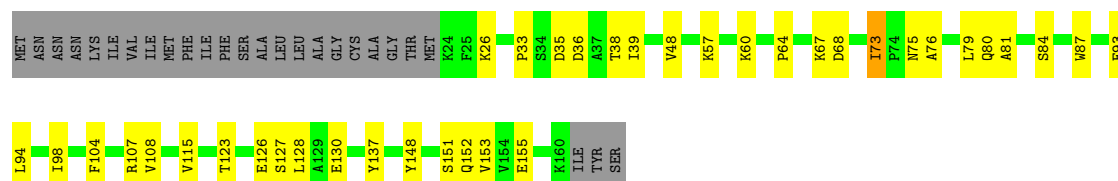
- Molecule 8: DotD

Chain ID: 



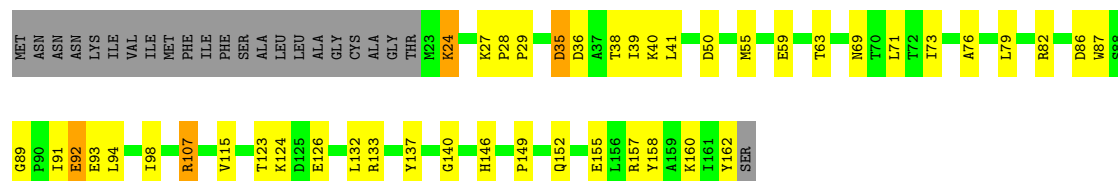
- Molecule 8: DotD

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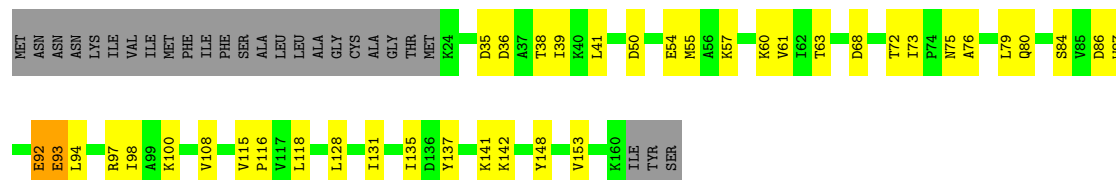
- Molecule 8: DotD

Chain JD: 



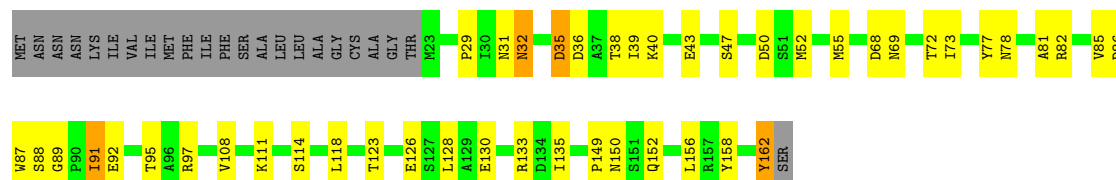
- Molecule 8: DotD

Chain Jd: 



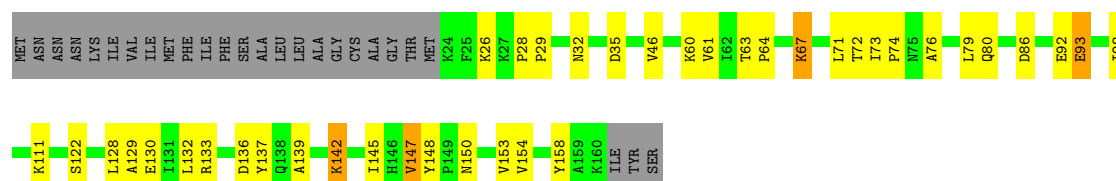
- Molecule 8: DotD

Chain KD: 



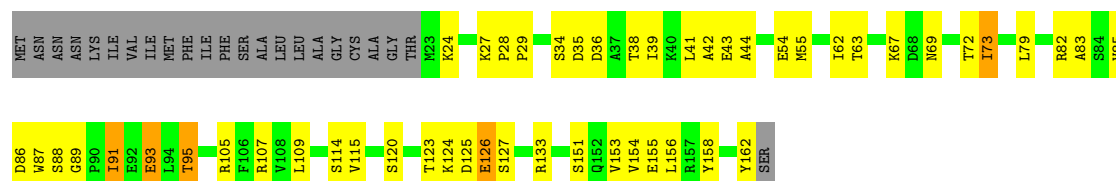
- Molecule 8: DotD

Chain Kd: 



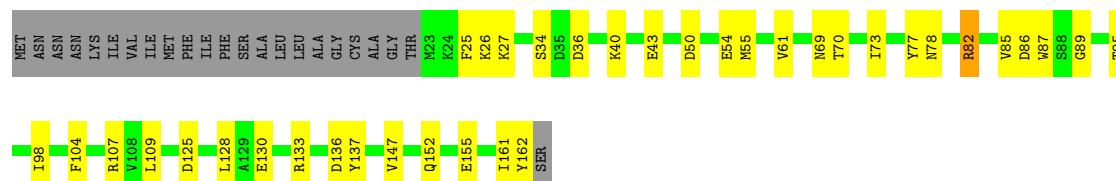
- Molecule 8: DotD

Chain LD: 

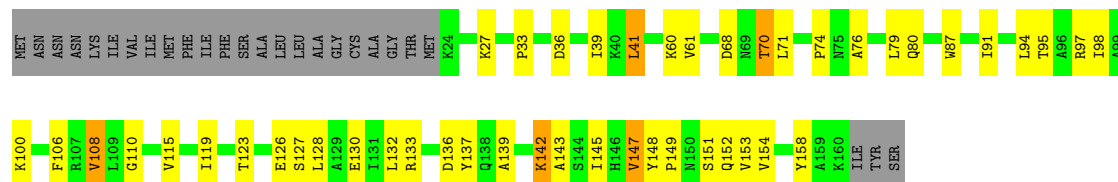


- Molecule 8: DotD

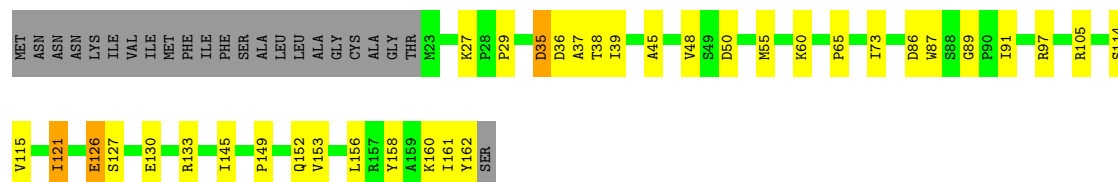
Chain CD: 



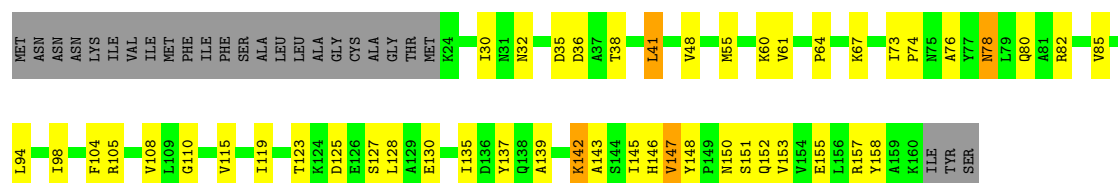
● Molecule 8: DotD

Chain Ld: 

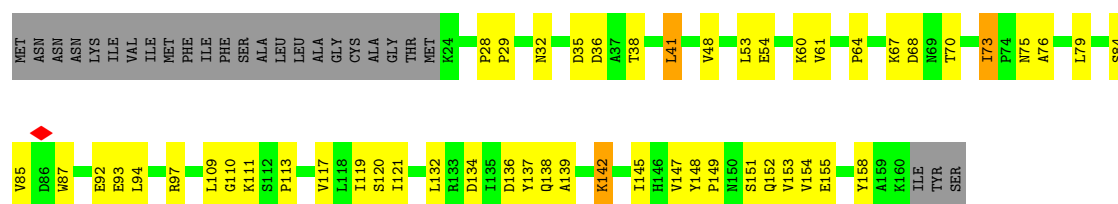
● Molecule 8: DotD

Chain MD: 

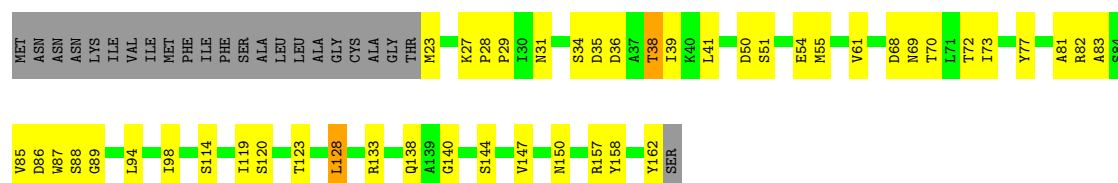
● Molecule 8: DotD

Chain Md: 

● Molecule 8: DotD

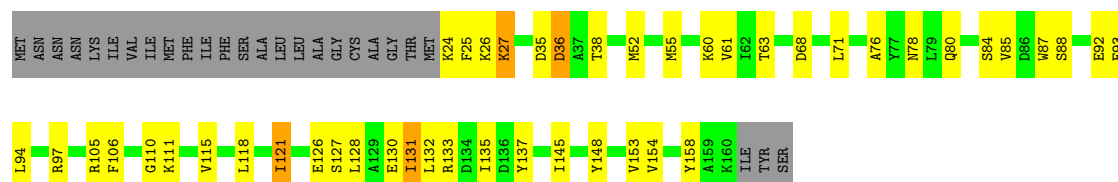
Chain Ad: 

● Molecule 8: DotD

Chain BD: 

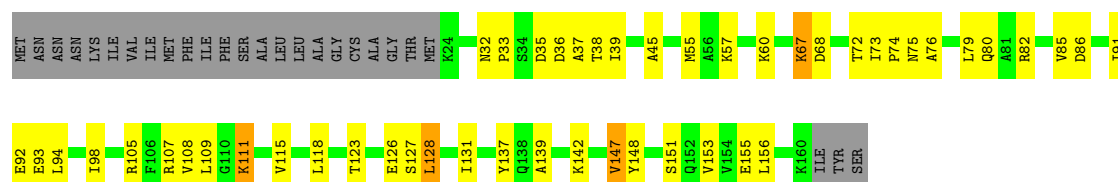
- Molecule 8: DotD

Chain Bd:  56% 26% 16%



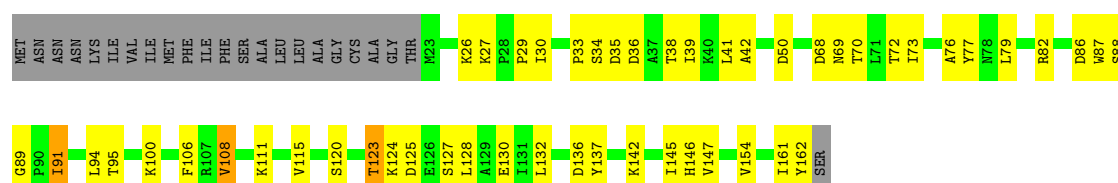
- Molecule 8: DotD

Chain Cd:  54% 28% 16%



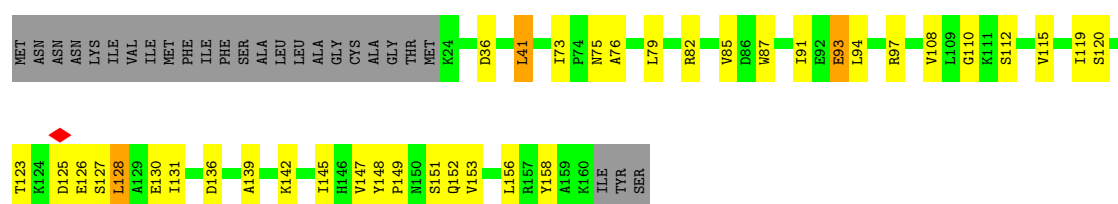
- Molecule 8: DotD

Chain DD:  55% 29% 14%



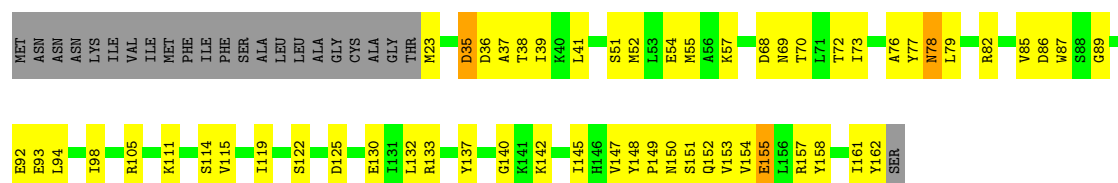
- Molecule 8: DotD

Chain Dd:  61% 21% 16%

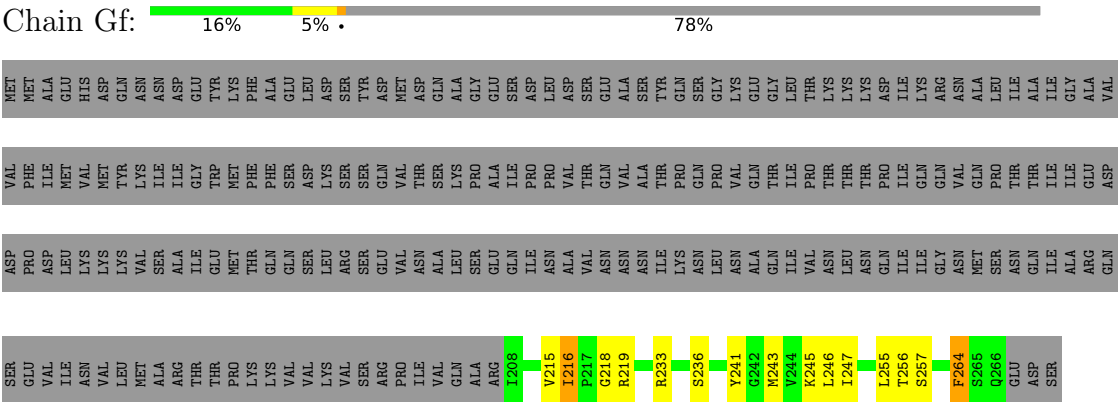


- Molecule 8: DotD

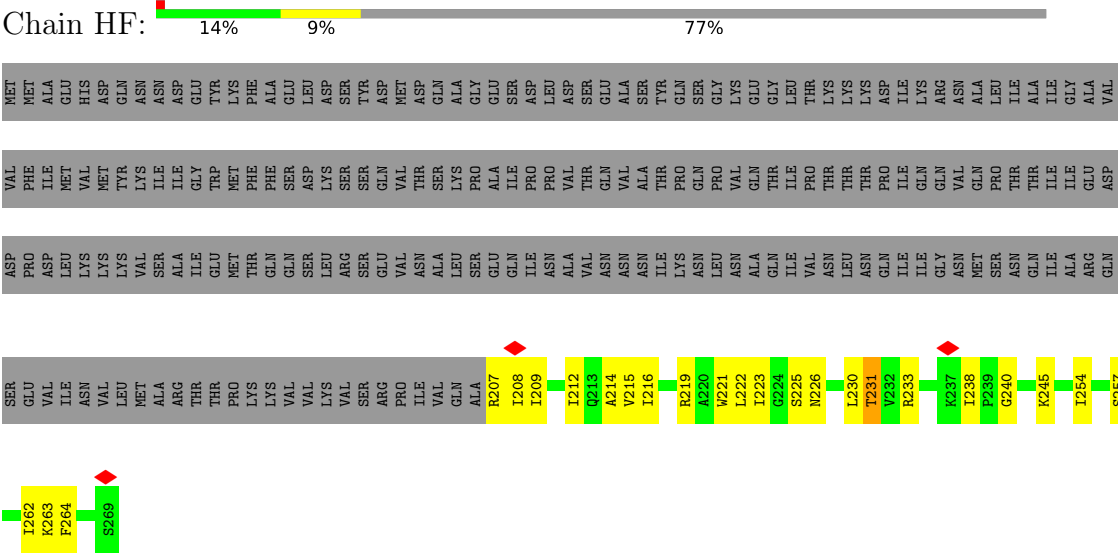
Chain AD:  51% 33% 14%



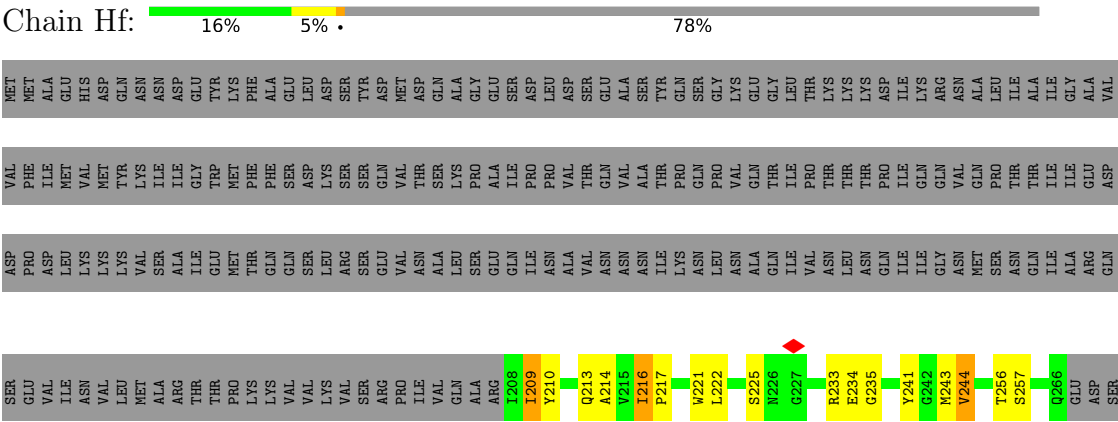
● Molecule 9: DotF



● Molecule 9: DotF

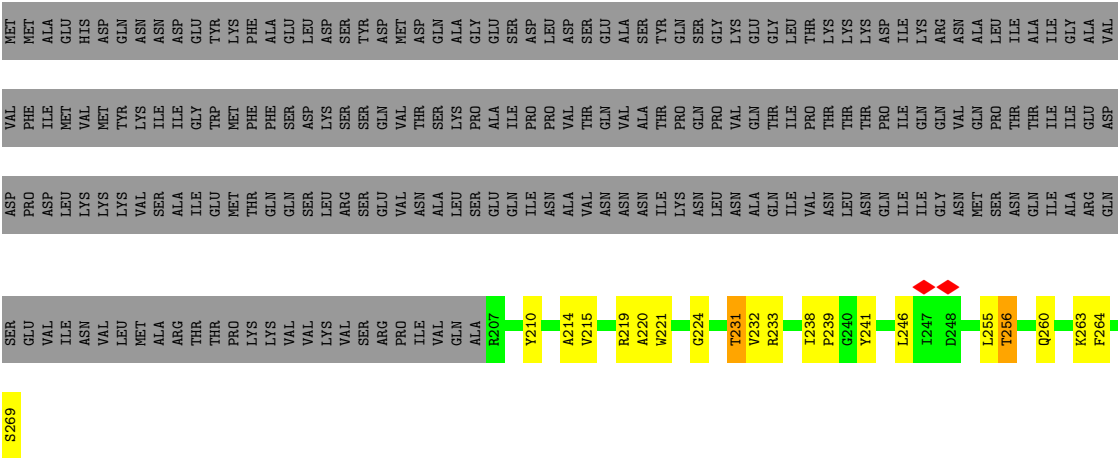


● Molecule 9: DotF

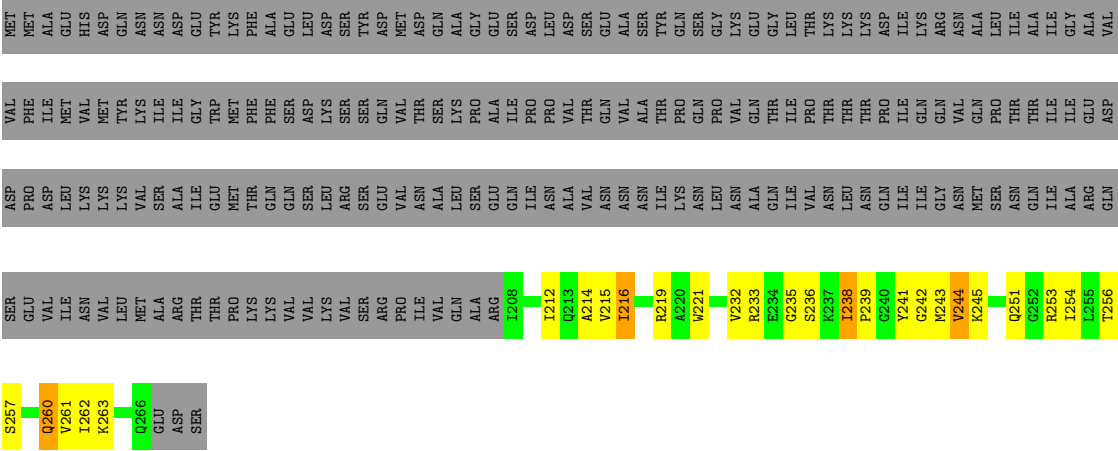


● Molecule 9: DotF

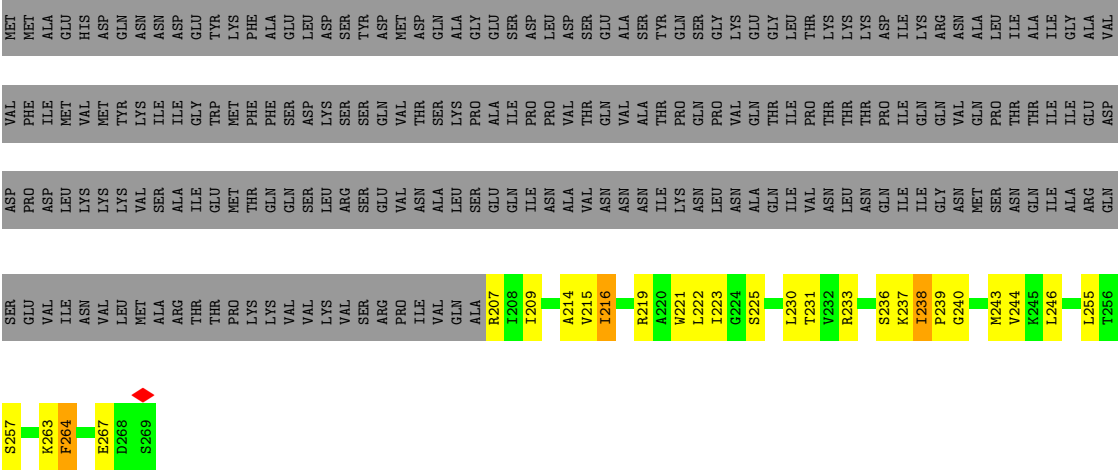




• Molecule 9: DotF



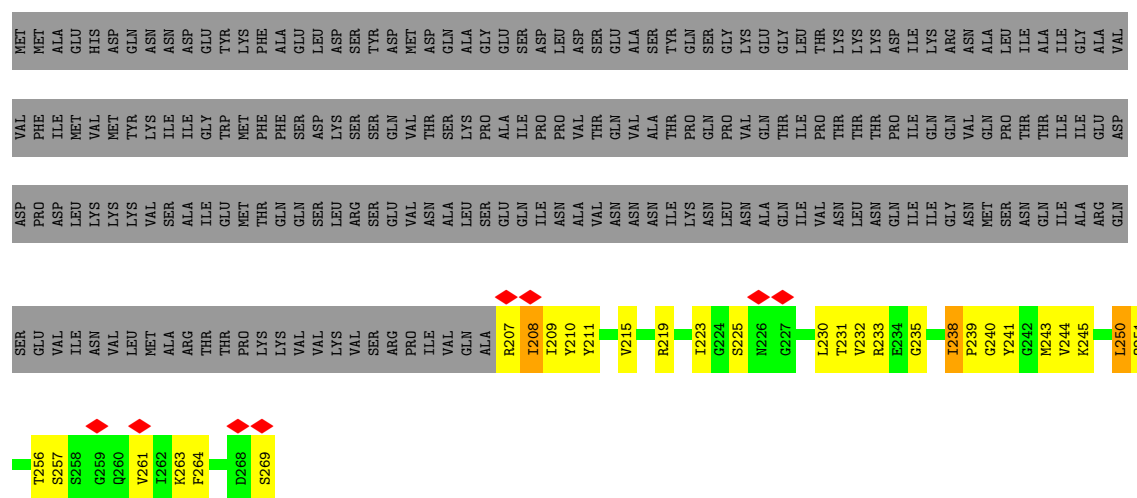
• Molecule 9: DotF



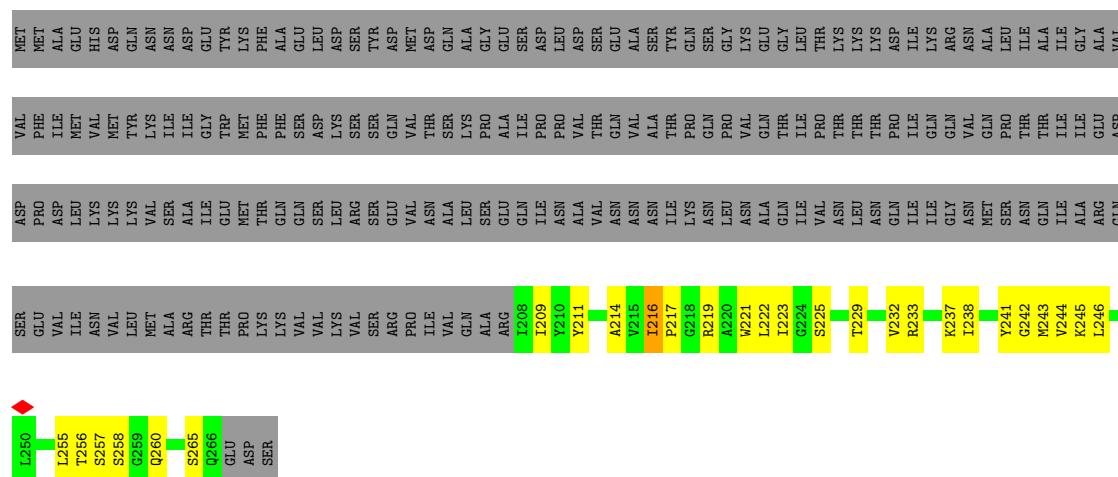
• Molecule 9: DotF

GLU	SER	ASP	MET
ASP	GLU	PRO	VAL
SER	VAL	ILE	PHE
	ILE	LEU	ILE
	ASN	LYS	MET
	VAL	LYS	MET
	LEU	VAL	TYR
	ALA	SER	LYS
	ARG	ALA	ILE
	THR	ILE	GLY
	THR	GLU	TRP
	PRO	THR	MET
	LYS	THR	LYS
	LYS	GLN	PHE
	VAL	GLM	ALA
	VAL	GLN	SER
	LYS	LEU	ASP
	VAL	ARG	LYS
	SER	SER	SER
	ARG	GLU	TYR
	PRO	VAL	GLN
	ILE	ASN	MET
	VAL	ALA	ASP
	GLN	LEU	GLN
	ALA	SER	ALA
	ARG	GLU	GLY
	I208	GLM	GLY
	A214	ILE	SER
	V215	ASN	ASP
	T216	ALA	LEU
	P217	VAL	ASP
		ASN	GLN
	A220	ASN	ALA
	V221	ILE	SER
	L222	LYS	TYR
	I223	ASN	GLN
		LEU	SER
	L230	ASN	GLY
	T231	ALA	LYS
	V232	GLN	GLU
	G235	ILE	GLY
	I238	VAL	LEU
		ASN	THR
	Y241	THR	LYS
	G242	GLN	LYS
	M243	ILE	ASP
	V244	GLY	LYS
	K245	GLN	ARG
	L246	MET	ASN
		SER	ALA
	L255	THR	GLN
	T256	GLN	LEU
		THR	ILE
	K263	ILE	ILE
		ALA	GLY
	V266	ARG	ILE
		GLN	VAL

Chain KF: 13% 10% 77%

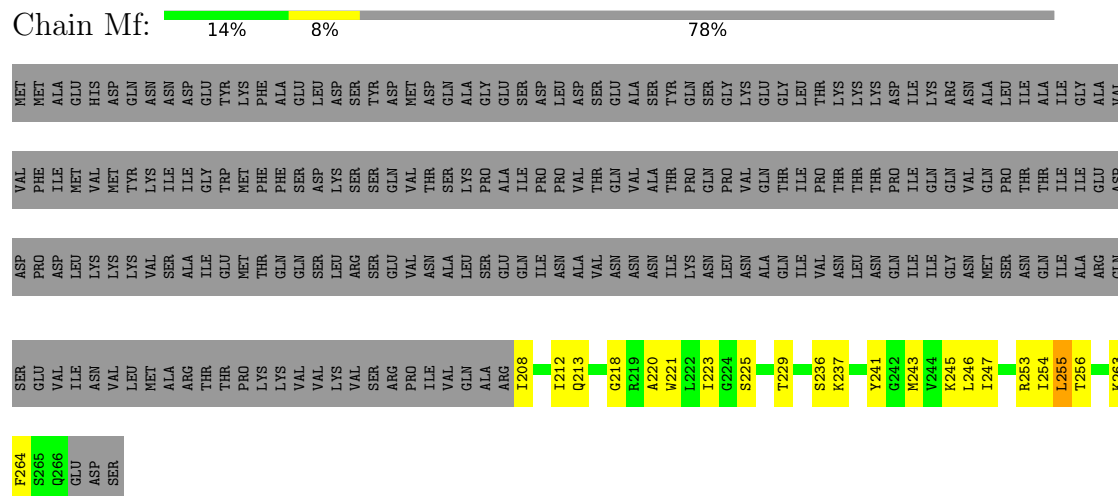


Chain Kf:

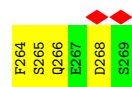
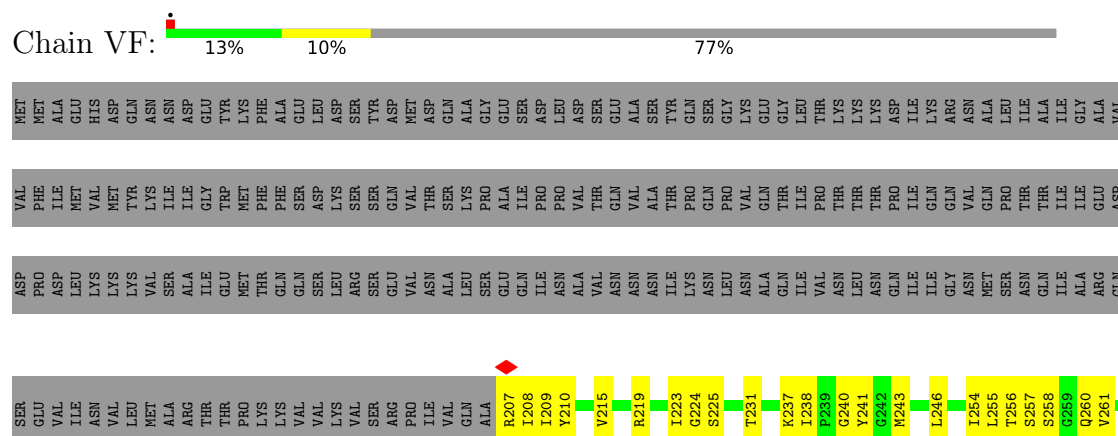




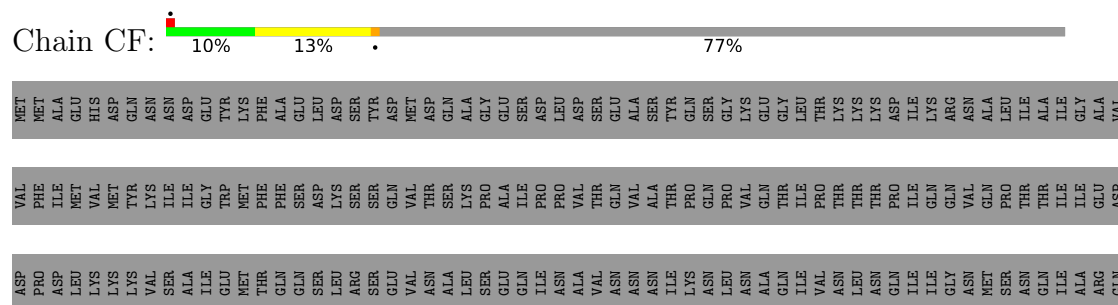
- Molecule 9: DotF

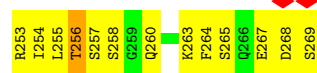


- Molecule 9: DotF

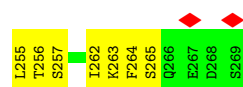
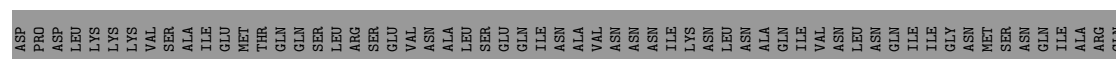
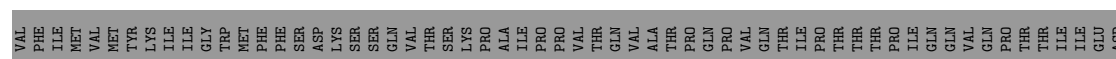
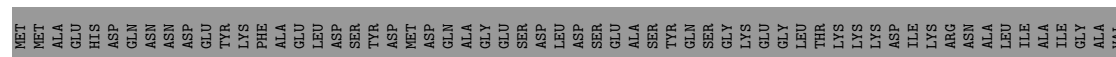


- Molecule 9: DotF

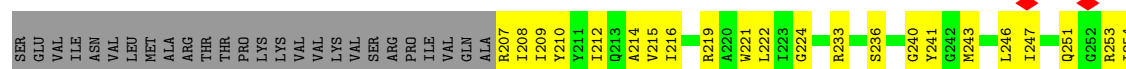
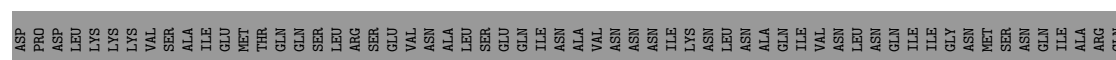
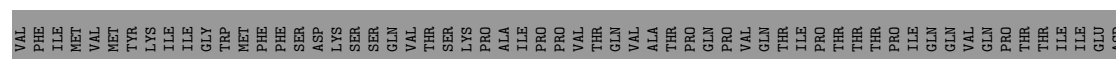
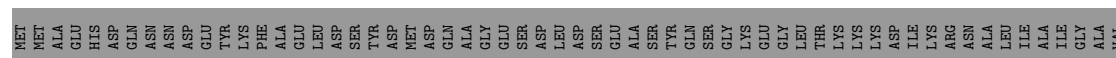




- Molecule 9: DotF



- Molecule 9: DotF



- Molecule 9: DotF



S258	V261	K263	F264	S265	Q266	E267	D268	S269
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Chain ZF:

SER	GLU	VAL	ILE	ASN	ASN	VAL	LEU	MET	ALA	ARG	THR	THR	PRO	PRO	LYS	LYS	VAL	VAL	VAL	LYS	VAL	SER	ARG	PRO	ILE	VAL	VAL	GLN	R207	R208	R209	R210	R211	R212	R213	R214	R215	R216	R217	R218	R219	R220	R221	R222	R223	R224	R225	R226	R227	R228	R229	R230	R231	R232	R233	R234	R235	R236	R237	R238	R239	R240	R241	R242	R243	R244	R245	R246	R247	R248	R249	R250	R251	R252	R253	R254	R255	R256	R257	R258	R259	R260	R261	R262	R263	R264	R265	R266	R267	R268	R269	R270	R271	R272	R273	R274	R275	R276	R277	R278	R279	R280	R281	R282	R283	R284	R285	R286	R287	R288	R289	R290	R291	R292	R293	R294	R295	R296	R297	R298	R299	R300	R301	R302	R303	R304	R305	R306	R307	R308	R309	R310	R311	R312	R313	R314	R315	R316	R317	R318	R319	R320	R321	R322	R323	R324	R325	R326	R327	R328	R329	R330	R331	R332	R333	R334	R335	R336	R337	R338	R339	R340	R341	R342	R343	R344	R345	R346	R347	R348	R349	R350	R351	R352	R353	R354	R355	R356	R357	R358	R359	R360	R361	R362	R363	R364	R365	R366	R367	R368	R369	R370	R371	R372	R373	R374	R375	R376	R377	R378	R379	R380	R381	R382	R383	R384	R385	R386	R387	R388	R389	R390	R391	R392	R393	R394	R395	R396	R397	R398	R399	R400	R401	R402	R403	R404	R405	R406	R407	R408	R409	R410	R411	R412	R413	R414	R415	R416	R417	R418	R419	R420	R421	R422	R423	R424	R425	R426	R427	R428	R429	R430	R431	R432	R433	R434	R435	R436	R437	R438	R439	R440	R441	R442	R443	R444	R445	R446	R447	R448	R449	R450	R451	R452	R453	R454	R455	R456	R457	R458	R459	R460	R461	R462	R463	R464	R465	R466	R467	R468	R469	R470	R471	R472	R473	R474	R475	R476	R477	R478	R479	R480	R481	R482	R483	R484	R485	R486	R487	R488	R489	R490	R491	R492	R493	R494	R495	R496	R497	R498	R499	R500	R501	R502	R503	R504	R505	R506	R507	R508	R509	R510	R511	R512	R513	R514	R515	R516	R517	R518	R519	R520	R521	R522	R523	R524	R525	R526	R527	R528	R529	R530	R531	R532	R533	R534	R535	R536	R537	R538	R539	R540	R541	R542	R543	R544	R545	R546	R547	R548	R549	R550	R551	R552	R553	R554	R555	R556	R557	R558	R559	R560	R561	R562	R563	R564	R565	R566	R567	R568	R569	R570	R571	R572	R573	R574	R575	R576	R577	R578	R579	R580	R581	R582	R583	R584	R585	R586	R587	R588	R589	R590	R591	R592	R593	R594	R595	R596	R597	R598	R599	R600	R601	R602	R603	R604	R605	R606	R607	R608	R609	R610	R611	R612	R613	R614	R615	R616	R617	R618	R619	R620	R621	R622	R623	R624	R625	R626	R627	R628	R629	R630	R631	R632	R633	R634	R635	R636	R637	R638	R639	R640	R641	R642	R643	R644	R645	R646	R647	R648	R649	R650	R651	R652	R653	R654	R655	R656	R657	R658	R659	R660	R661	R662	R663	R664	R665	R666	R667	R668	R669	R670	R671	R672	R673	R674	R675	R676	R677	R678	R679	R680	R681	R682	R683	R684	R685	R686	R687	R688	R689	R690	R691	R692	R693	R694	R695	R696	R697	R698	R699	R700	R701	R702	R703	R704	R705	R706	R707	R708	R709	R710	R711	R712	R713	R714	R715	R716	R717	R718	R719	R720	R721	R722	R723	R724	R725	R726	R727	R728	R729	R730	R731	R732	R733	R734	R735	R736	R737	R738	R739	R740	R741	R742	R743	R744	R745	R746	R747	R748	R749	R750	R751	R752	R753	R754	R755	R756	R757	R758	R759	R760	R761	R762	R763	R764	R765	R766	R767	R768	R769	R770	R771	R772	R773	R774	R775	R776	R777	R778	R779	R780	R781	R782	R783	R784	R785	R786	R787	R788	R789	R790	R791	R792	R793	R794	R795	R796	R797	R798	R799	R800	R801	R802	R803	R804	R805	R806	R807	R808	R809	R810	R811	R812	R813	R814	R815	R816	R817	R818	R819	R820	R821	R822	R823	R824	R825	R826	R827	R828	R829	R830	R831	R832	R833	R834	R835	R836	R837	R838	R839	R840	R841	R842	R843	R844	R845	R846	R847	R848	R849	R850	R851	R852	R853	R854	R855	R856	R857	R858	R859	R860	R861	R862	R863	R864	R865	R866	R867	R868	R869	R870	R871	R872	R873	R874	R875	R876	R877	R878	R879	R880	R881	R882	R883	R884	R885	R886	R887	R888	R889	R890	R891	R892	R893	R894	R895	R896	R897	R898	R899	R900	R901	R902	R903	R904	R905	R906	R907	R908	R909	R910	R911	R912	R913	R914	R915	R916	R917	R918	R919	R920	R921	R922	R923	R924	R925	R926	R927	R928	R929	R930	R931	R932	R933	R934	R935	R936	R937	R938	R939	R940	R941	R942	R943	R944	R945	R946	R947	R948	R949	R950	R951	R952	R953	R954	R955	R956	R957	R958	R959	R960	R961	R962	R963	R964	R965	R966	R967	R968	R969	R970	R971	R972	R973	R974	R975	R976	R977	R978	R979	R980	R981	R982	R983	R984	R985	R986	R987	R988	R989	R990	R991	R992	R993	R994	R995	R996	R997	R998	R999	R1000
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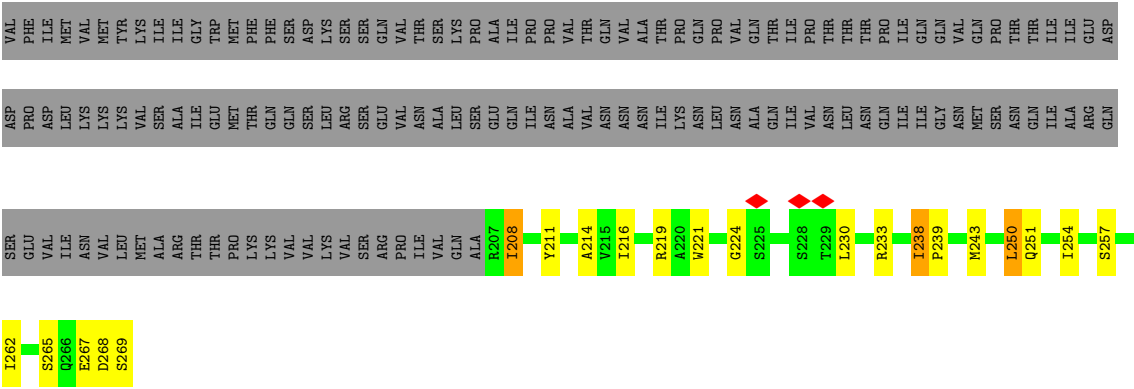
Chain Af: 15% 7% 78%

SER	GLU	VAL	ILE	ASN	VAL	LEU	MET	ALA	ARG	THR	THR	PRO	LYS	LYS	VAL	VAL	LYS	VAL	SER	ARG	PRO	ILE	VAL	GLN	ALA	ALA	ARG	I208	I210	I212	I213	I214	I215	I216	I221	I222	I223	I229	I238	P239	M243	M244	K245	D248	R253	I254	I256	T256	S257	P260	Q261	I262	I263
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F264	S265	Q266	GLU	ASP	SER
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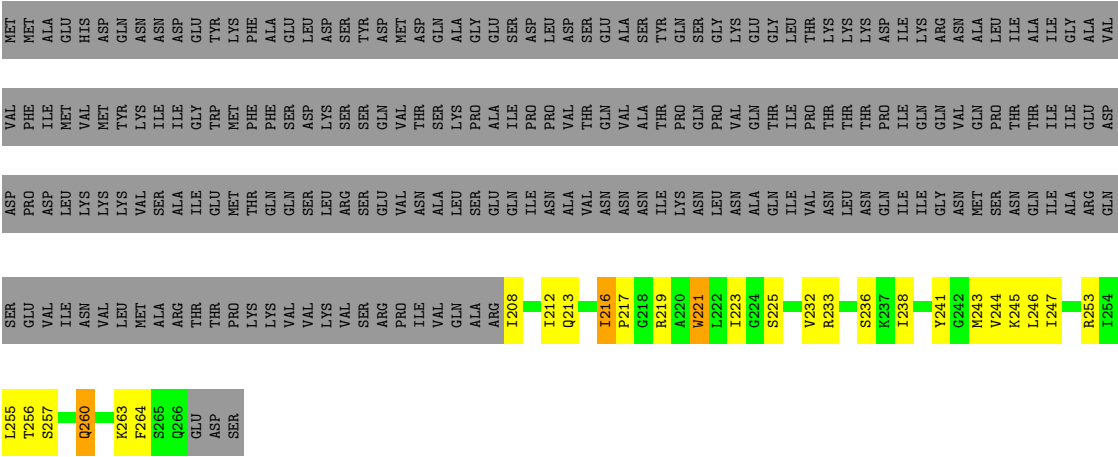
Chain BF: 16% 7% 77%

MET	MET	ALA	ALA	GLU	HIS	GLN	ASP	ASN	ASN	ASP	GLU	TYR	LYS	PHE	ALA	GLU	LEU	ASP	SER	SER	TYR	ASP	MET	ASP	GLN	ALA	GLY	GLU	SER	SER	ASP	LEU	ASP	SER	GLU	ALA	ALA	SER	TYR	GLN	LEU	THR	LEU	LYS	LYS	LYS	LYS	ASP	ASP	ILE	LYS	ARG	ASN	ALA	LEU	ILE	ILE	GLY	ALA	ASP
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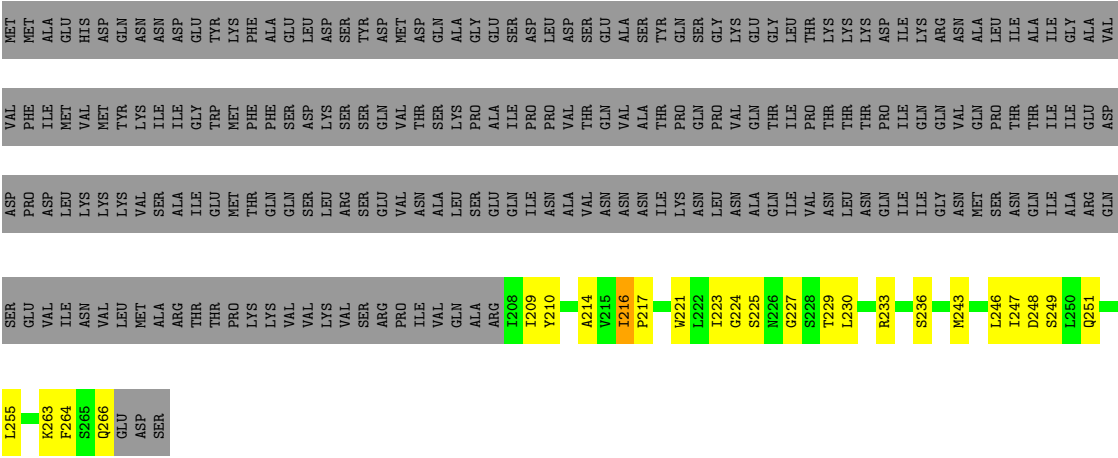
• Molecule 9: DotF

Chain Bf: 12% 9% 78%



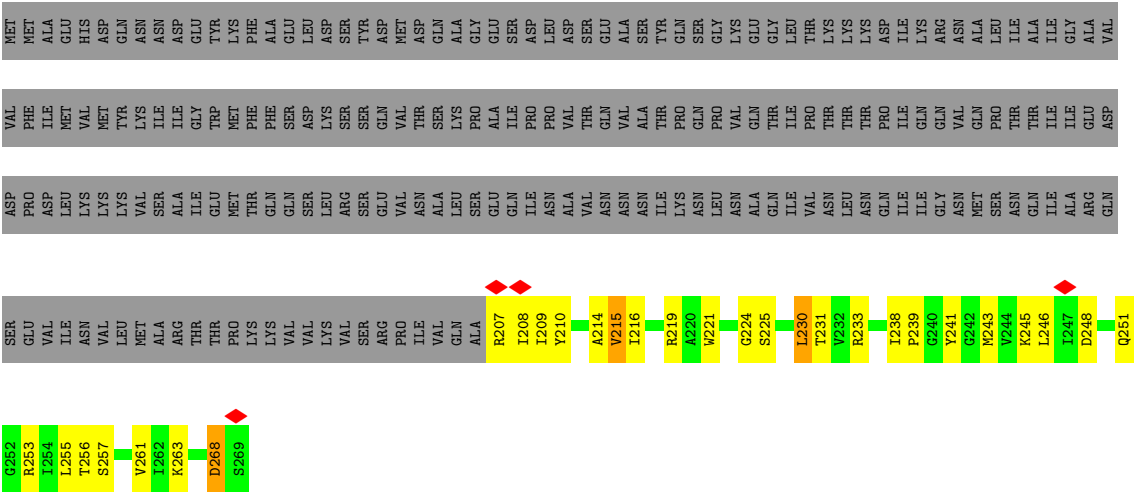
• Molecule 9: DotF

Chain Cf: 13% 9% 78%

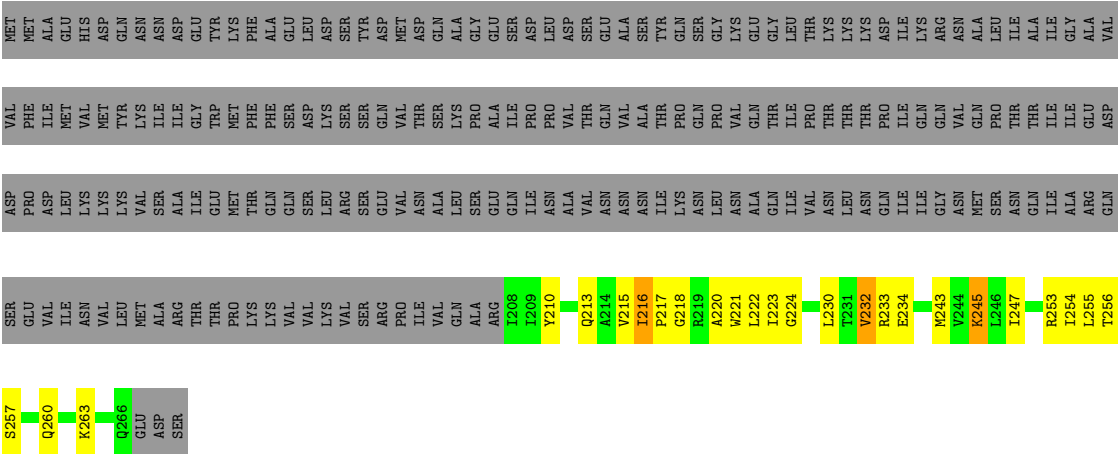


• Molecule 9: DotF

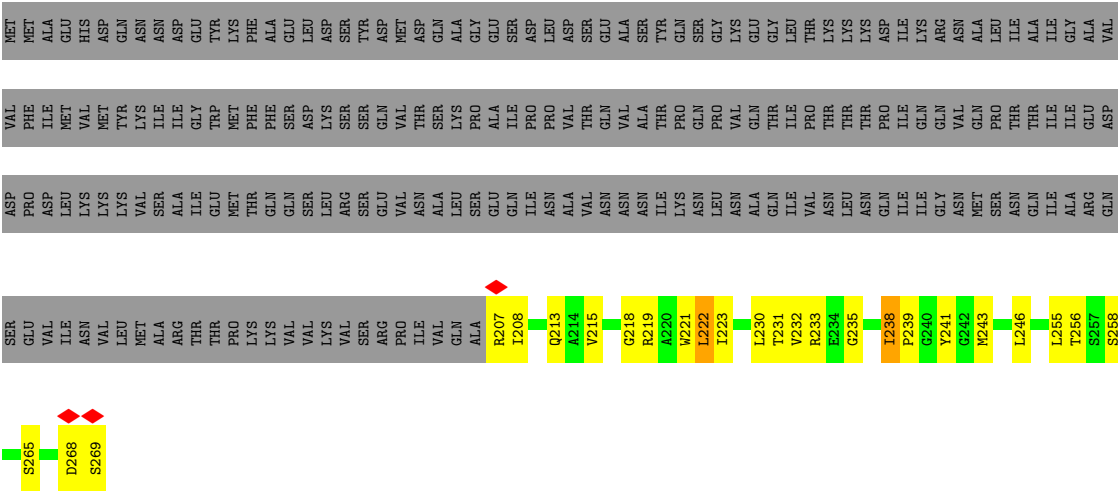
Chain DF: 13% 10% 77%



● Molecule 9: DotF

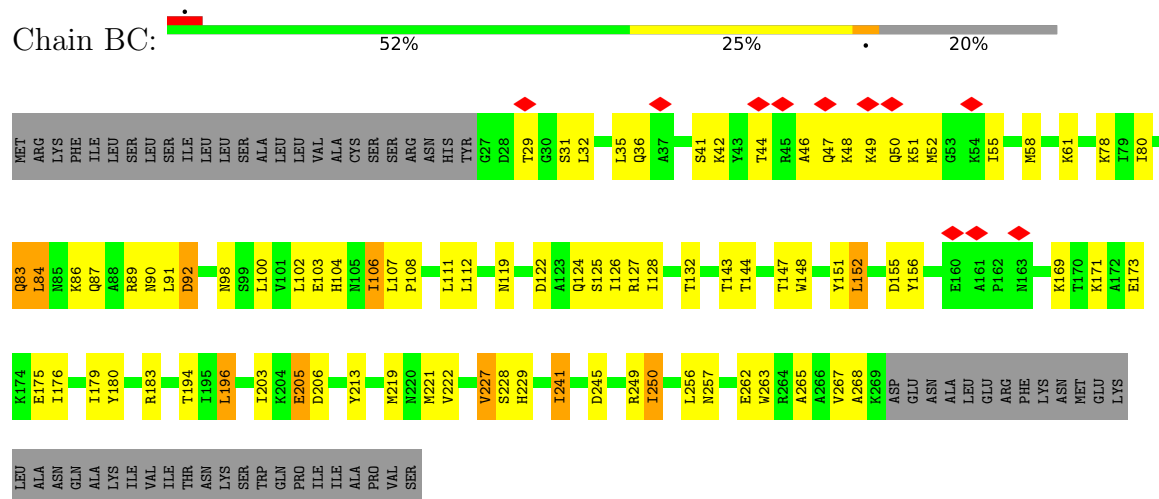


● Molecule 9: DotF



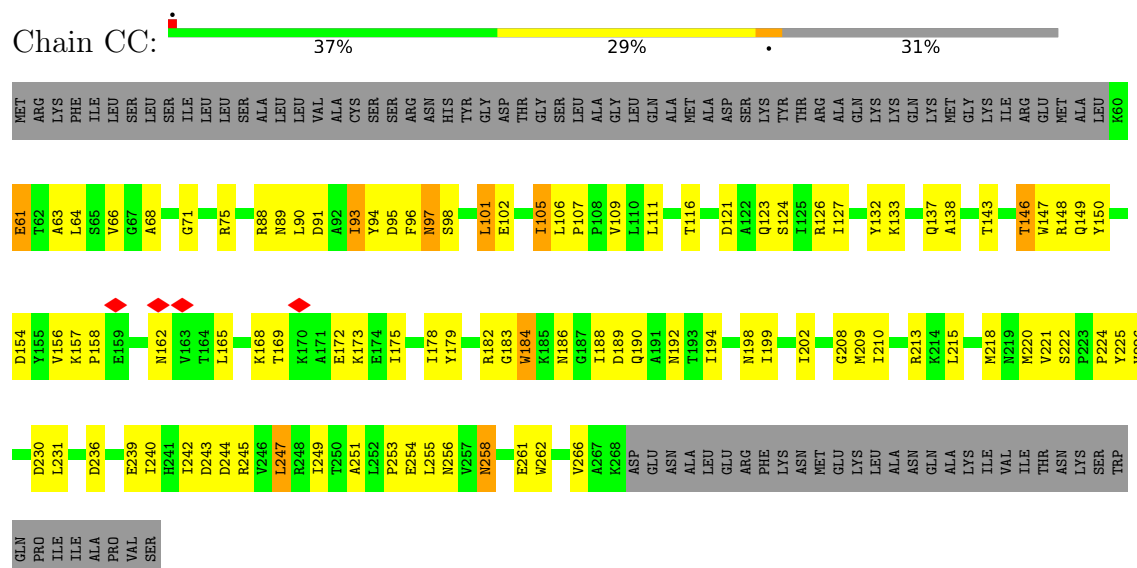
● Molecule 10: DotC

Chain BC:



● Molecule 10: DotC

Chain CC:

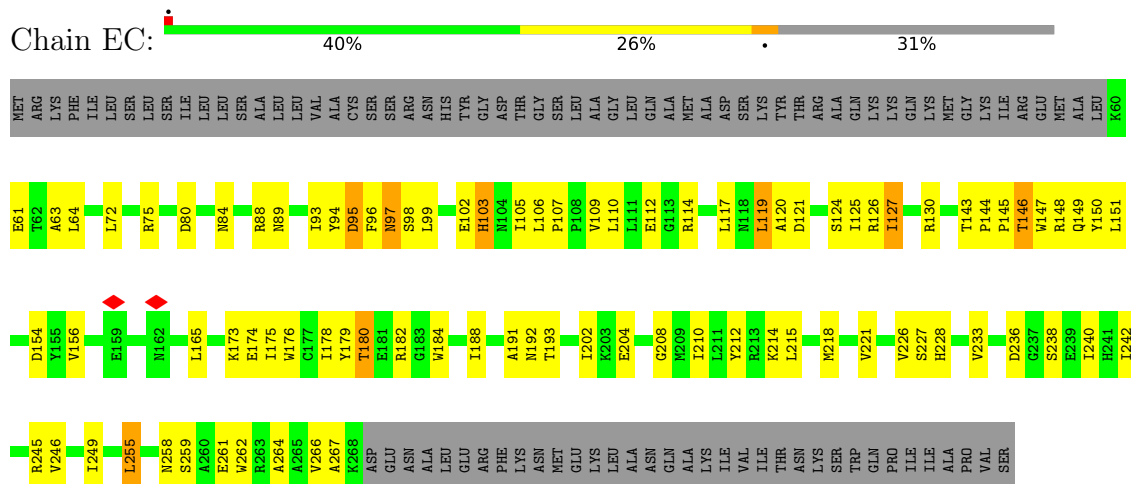


● Molecule 10: DotC

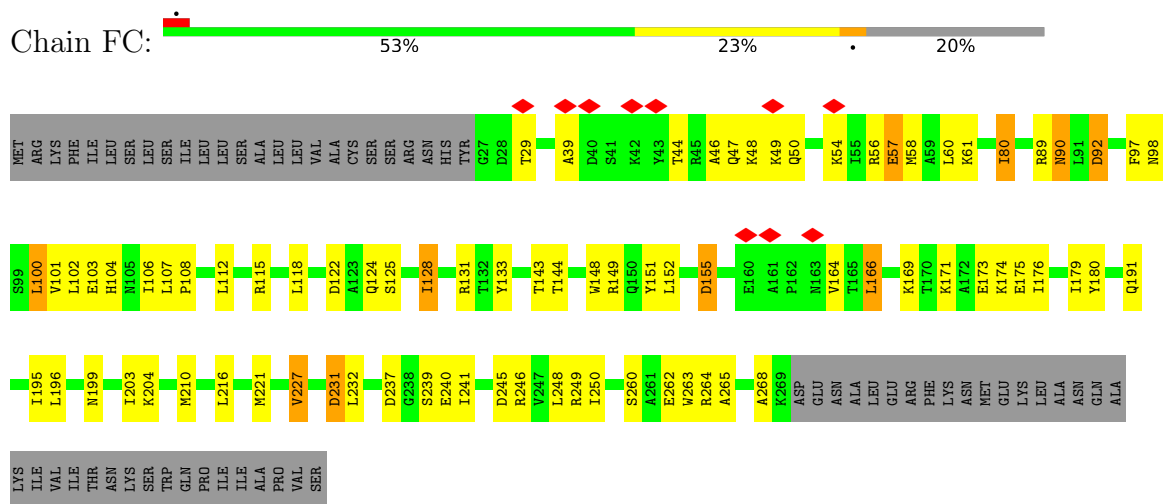
Chain DC:



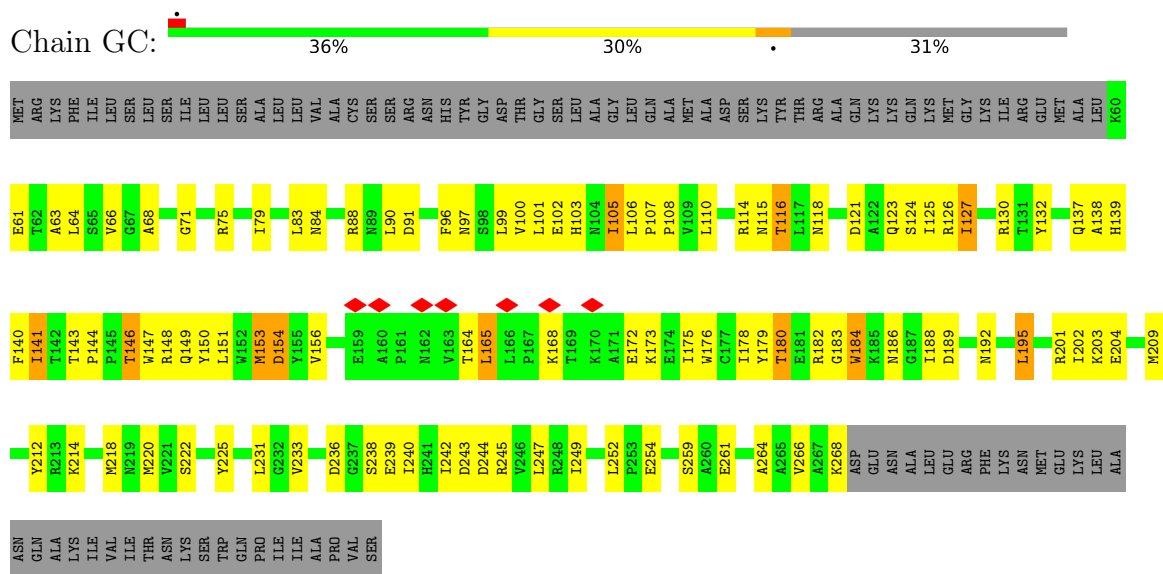
- Molecule 10: DotC



- Molecule 10: DotC



- Molecule 10: DotC



Chain HC:

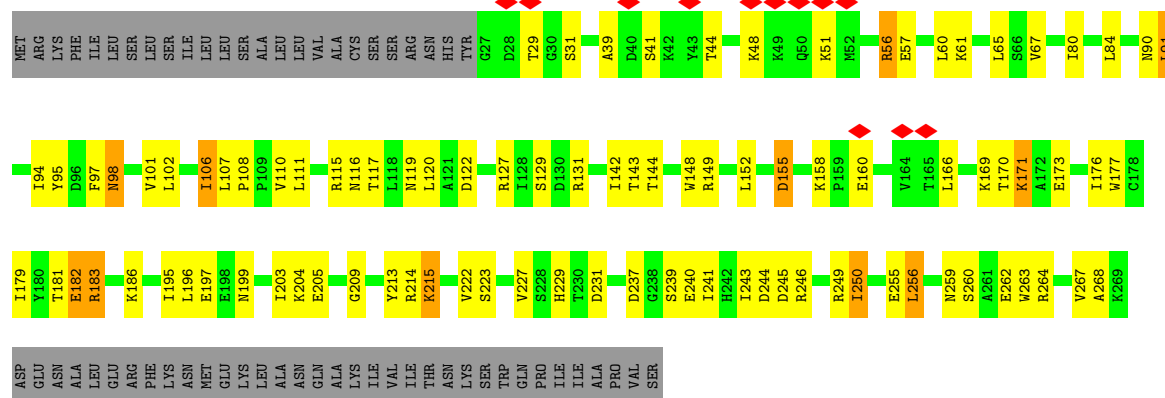
Category	Percentage
MET	43%
ARG	23%
LYS	31%

Chain IC:

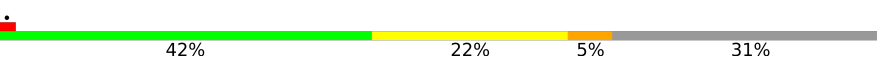
Chain JC:

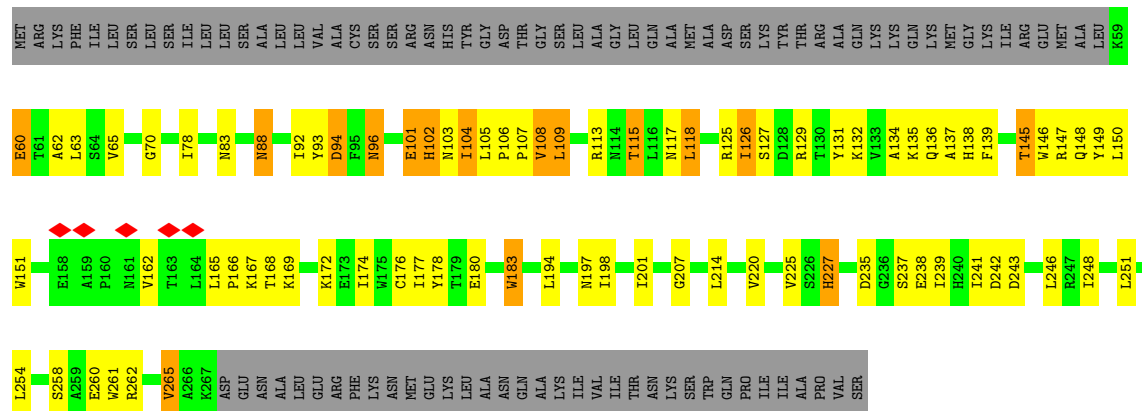
Amino Acid	Category
MET	Grey
ARG	Grey
LYS	Grey
PHE	Grey
ILE	Grey
LEU	Grey
LEU	Grey
SER	Grey
ILE	Grey
LEU	Grey
LEU	Grey
SER	Grey
ALA	Green
LEU	Green
VAL	Green
ALA	Green
CYS	Green
SER	Green
SER	Green
ASN	Green
HIS	Green
TYR	Green
G27	Green
D28	Green
T29	Green
G30	Green
S31	Green
L32	Green
Q36	Green
A39	Green
D40	Green
S41	Green
T44	Green
R45	Green
A46	Green
Q47	Green
K48	Green
K49	Green
Q50	Green
K54	Green
E57	Green
K61	Green
A64	Green
L65	Green
Q70	Green
R76	Green
A77	Green
K78	Green
I79	Yellow
I80	Yellow
N90	Yellow
I94	Yellow
Y95	Yellow
N98	Yellow
S99	Yellow
E103	Yellow
H104	Yellow
H105	Yellow
I106	Yellow
L107	Yellow
P108	Yellow
P109	Yellow
V110	Yellow
L111	Yellow
L112	Yellow
N116	Yellow
T117	Yellow
L118	Yellow
D122	Yellow
A123	Yellow
Q124	Yellow
S125	Yellow
I126	Yellow
R127	Yellow
D130	Yellow
A139	Yellow
H140	Yellow
F141	Yellow
I142	Yellow
T143	Yellow
T144	Yellow
P145	Yellow
P146	Yellow
T147	Yellow
Q150	Yellow
Y151	Yellow
L152	Yellow
D155	Yellow
Y156	Yellow
E160	Yellow
A161	Yellow
L166	Yellow
K171	Yellow
A172	Yellow
E173	Yellow
K174	Yellow
E175	Yellow
I176	Yellow
G177	Yellow
C178	Yellow
I179	Yellow
Y180	Yellow
R183	Yellow
G184	Yellow
W185	Yellow
D190	Yellow
T194	Yellow
L195	Yellow
L196	Yellow
THR	Yellow
ASN	Yellow
N199	Yellow
E205	Yellow
G209	Yellow
M210	Yellow
I211	Yellow
L216	Yellow
M221	Yellow
V222	Yellow
V227	Yellow
S228	Yellow
D231	Yellow
L243	Yellow
D244	Yellow
D245	Yellow
R246	Yellow
L250	Yellow
L256	Yellow
N259	Yellow
S260	Yellow
W263	Yellow
R264	Yellow
A265	Yellow
A266	Yellow
V267	Yellow
A268	Yellow
K269	Yellow
ASP	Grey
GLU	Grey
ASN	Grey
ALA	Grey
LEU	Grey

Chain KC: 

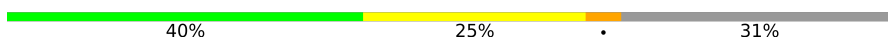


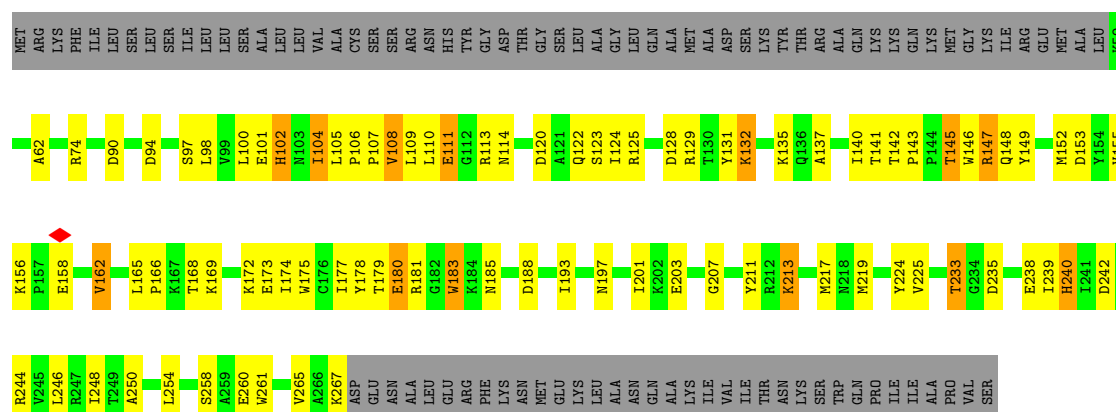
• Molecule 10: DotC

Chain LC: 



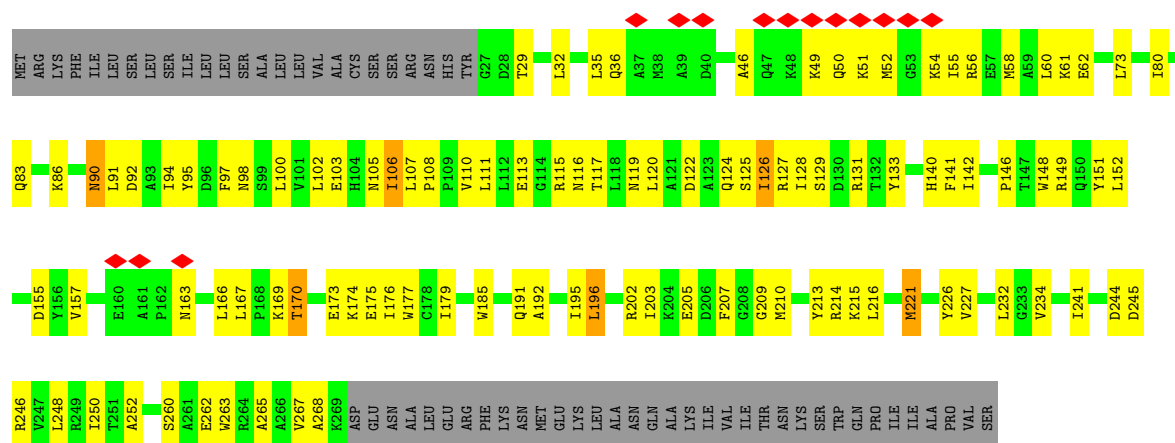
• Molecule 10: DotC

Chain MC: 

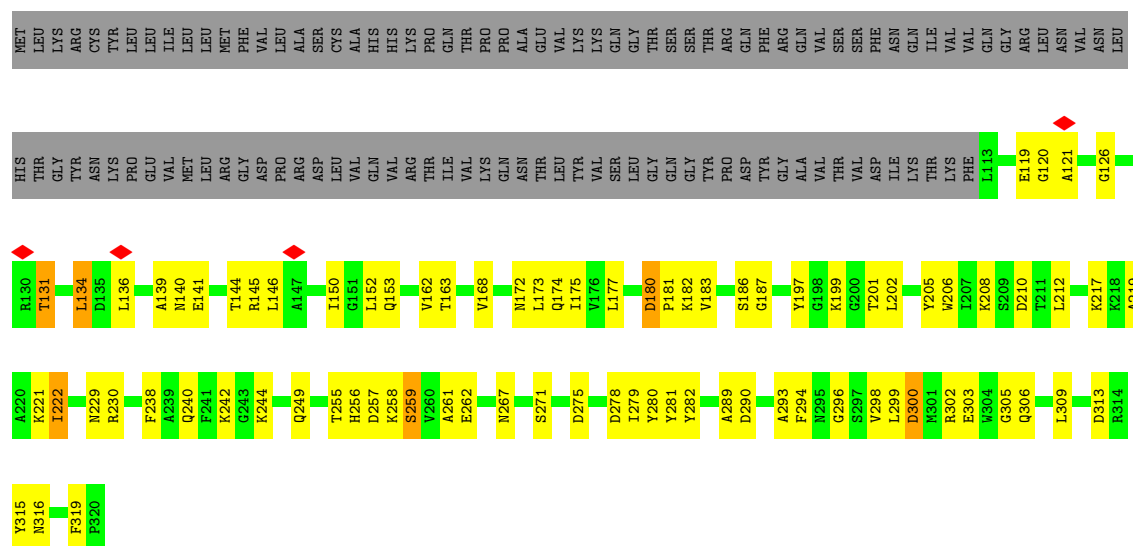


• Molecule 10: DotC

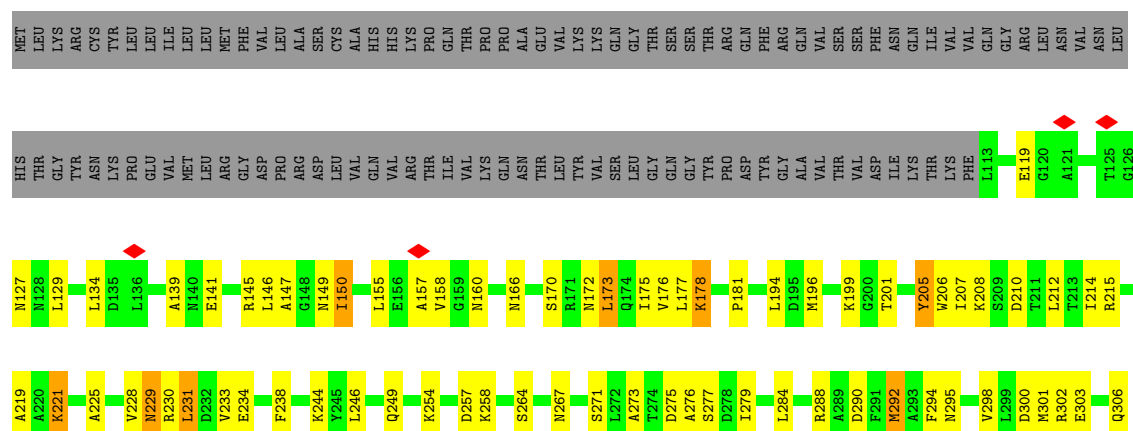
Chain AC: 



- Molecule 11: DUF2807 domain-containing protein

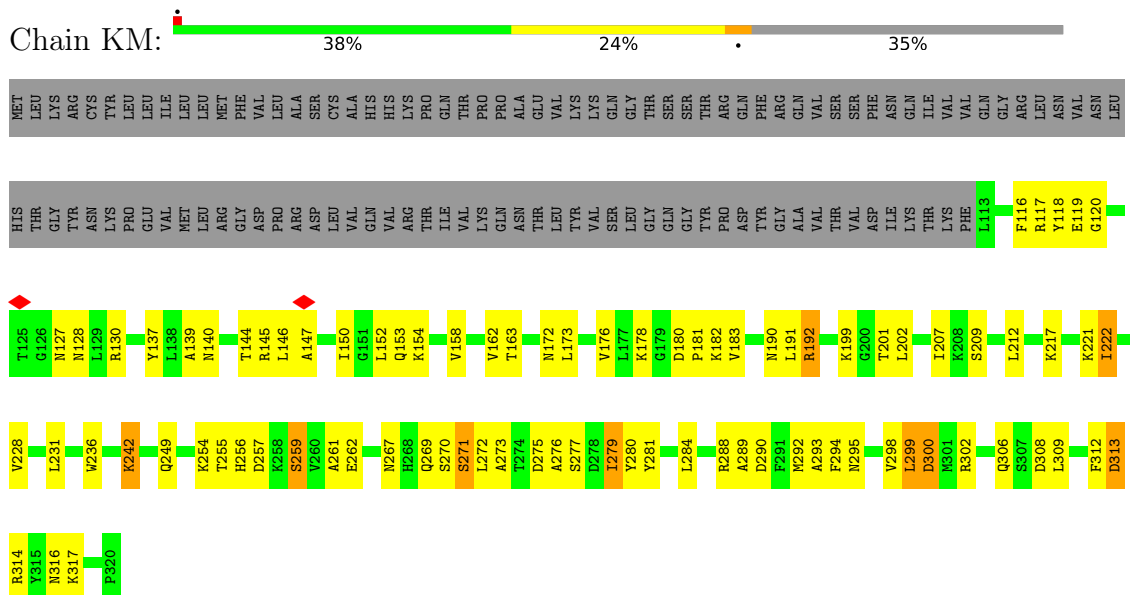


- Molecule 11: DUF2807 domain-containing protein

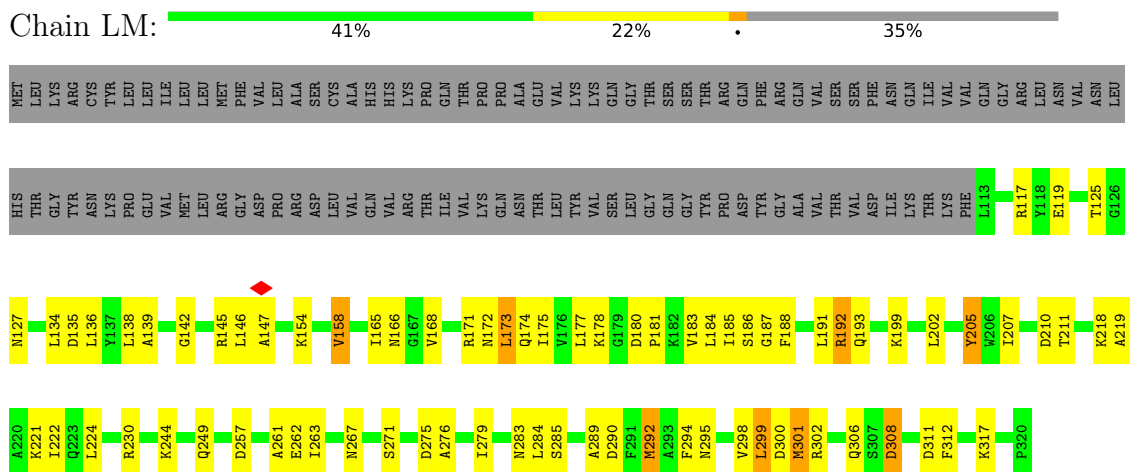




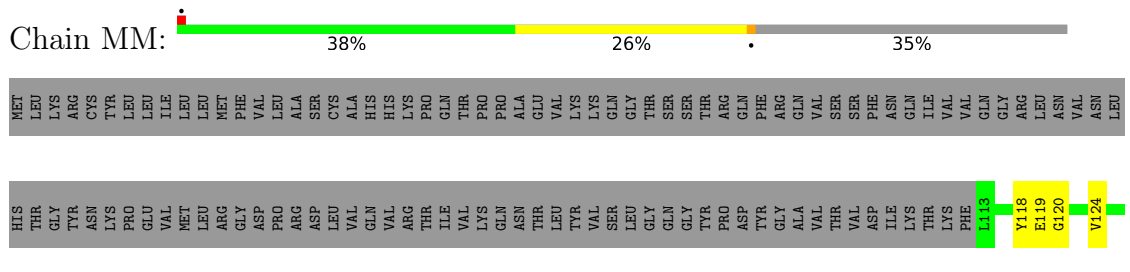
- Molecule 11: DUF2807 domain-containing protein

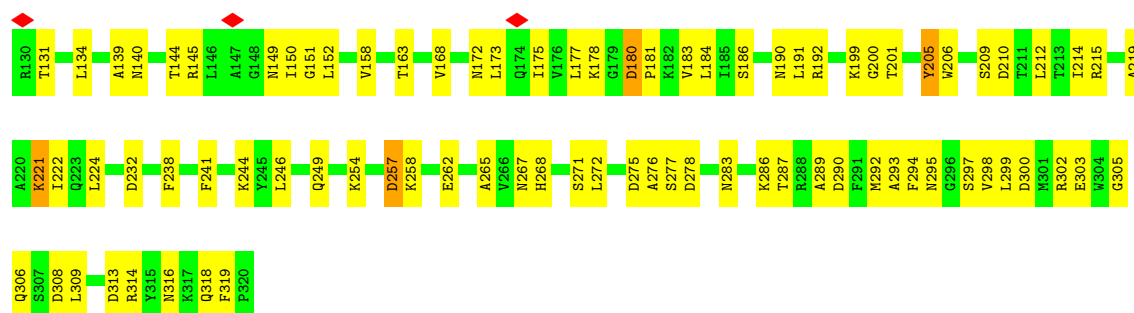


- Molecule 11: DUF2807 domain-containing protein

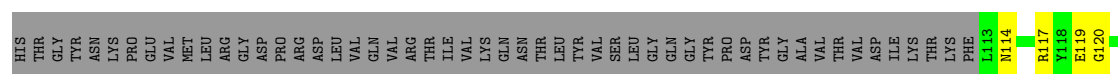
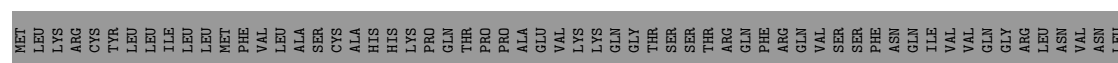
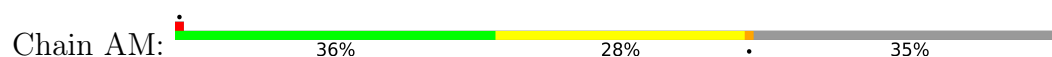


- Molecule 11: DUF2807 domain-containing protein

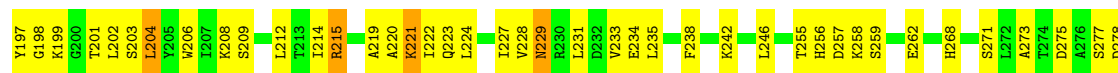
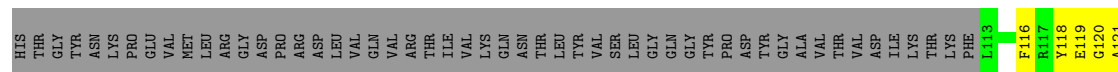
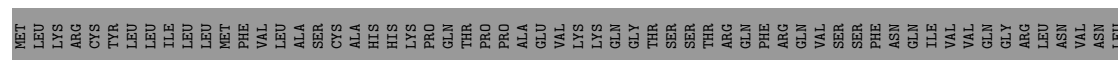




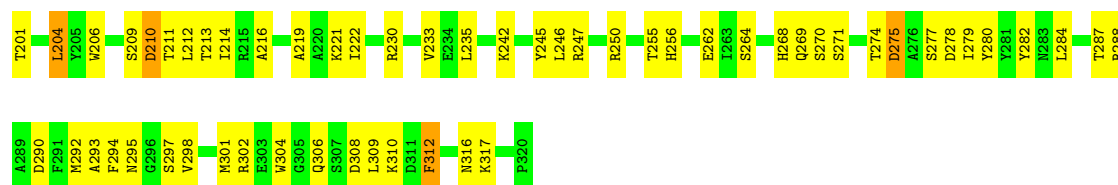
- Molecule 11: DUF2807 domain-containing protein



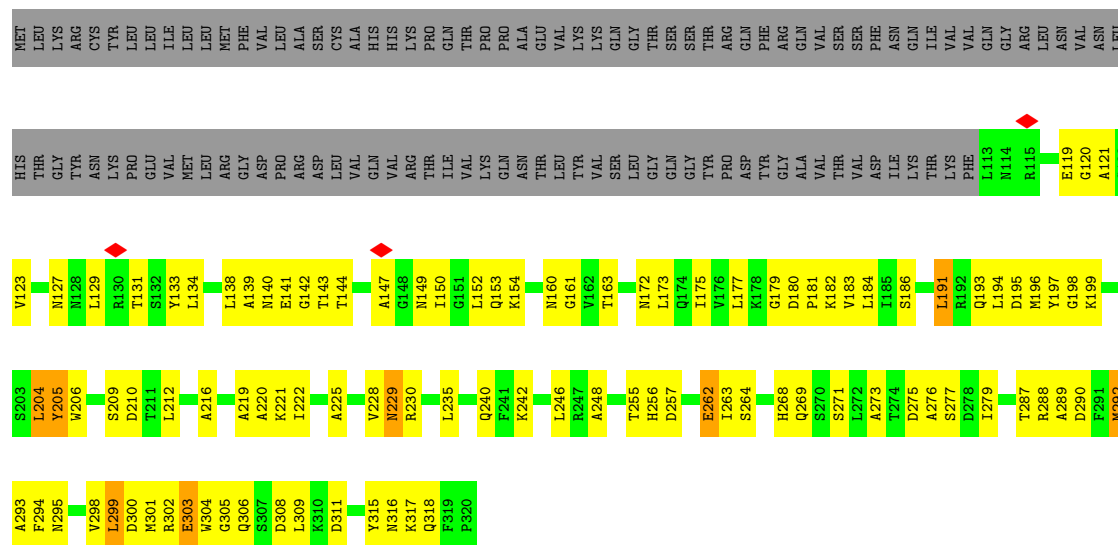
- Molecule 11: DUF2807 domain-containing protein



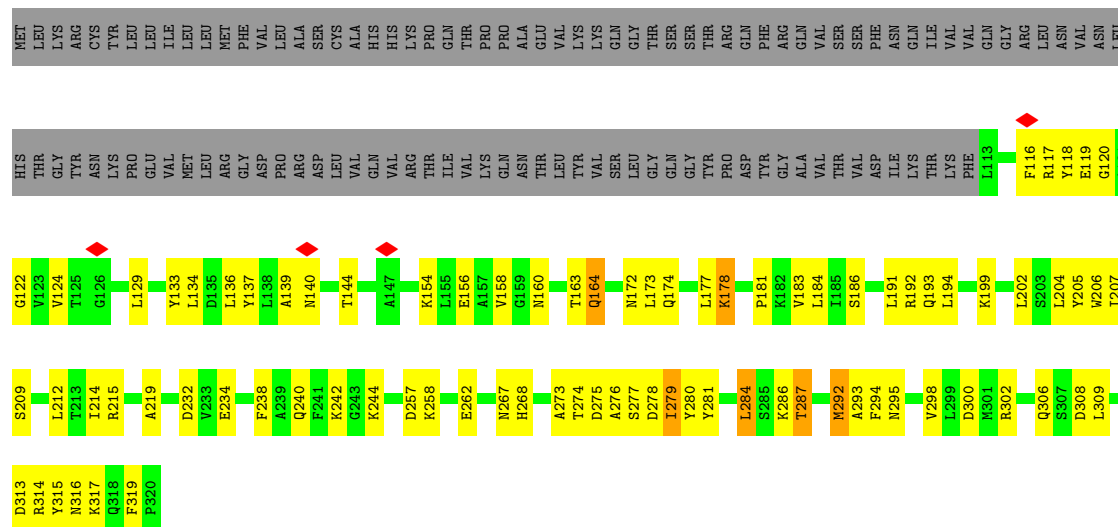
- Molecule 11: DUF2807 domain-containing protein



- Molecule 11: DUF2807 domain-containing protein



- Molecule 11: DUF2807 domain-containing protein



- Molecule 11: DUF2807 domain-containing protein



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	64698	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	9.229	Depositor
Minimum map value	-3.621	Depositor
Average map value	0.091	Depositor
Map value standard deviation	0.546	Depositor
Recommended contour level	2.25	Depositor
Map size ($\text{\AA}$)	561.0, 561.0, 561.0	wwPDB
Map dimensions	250, 250, 250	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.244, 2.244, 2.244	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AG	0.15	0/1250	0.38	0/1699
1	Ag	0.12	0/278	0.23	0/377
1	BG	0.16	0/1250	0.40	0/1699
1	Bg	0.12	0/278	0.23	0/377
1	CG	0.16	0/1250	0.40	0/1699
1	Cg	0.11	0/278	0.24	0/377
1	DG	0.16	0/1250	0.40	0/1699
1	Dg	0.12	0/278	0.28	0/377
1	EG	0.16	0/1250	0.39	0/1699
1	Eg	0.12	0/278	0.25	0/377
1	FG	0.17	0/1250	0.43	0/1699
1	Fg	0.11	0/278	0.24	0/377
1	GG	0.17	0/1250	0.42	0/1699
1	Gg	0.11	0/278	0.26	0/377
1	HG	0.16	0/1250	0.40	0/1699
1	Hg	0.11	0/278	0.24	0/377
1	IG	0.16	0/1250	0.42	0/1699
1	Ig	0.11	0/278	0.26	0/377
1	JG	0.16	0/1250	0.40	0/1699
1	Jg	0.11	0/278	0.24	0/377
1	KG	0.16	0/1250	0.39	0/1699
1	Kg	0.11	0/278	0.27	0/377
1	LG	0.16	0/1250	0.42	0/1699
1	Lg	0.11	0/278	0.26	0/377
1	MG	0.17	0/1250	0.38	0/1699
1	Mg	0.11	0/278	0.26	0/377
1	NG	0.16	0/1250	0.39	0/1699
1	OG	0.16	0/1250	0.39	0/1699
1	PG	0.16	0/1250	0.39	0/1699
1	VG	0.12	0/278	0.32	0/377
1	WG	0.13	0/278	0.31	0/377
1	XG	0.15	0/278	0.36	0/377
1	YG	0.13	0/278	0.32	0/377
1	ZG	0.14	0/278	0.29	0/377

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	AH	0.15	0/2033	0.33	0/2775
2	BH	0.15	0/2033	0.32	0/2775
2	CH	0.14	0/2033	0.30	0/2775
2	DH	0.14	0/2033	0.30	0/2775
2	EH	0.15	0/2033	0.31	0/2775
2	FH	0.15	0/2033	0.31	0/2775
2	GH	0.14	0/2033	0.30	0/2775
2	HH	0.13	0/2033	0.27	0/2775
2	IH	0.14	0/2033	0.31	0/2775
2	JH	0.14	0/2033	0.29	0/2775
2	KH	0.14	0/2033	0.29	0/2775
2	LH	0.14	0/2033	0.33	0/2775
2	MH	0.14	0/2033	0.30	0/2775
2	VH	0.11	0/1921	0.29	0/2620
2	WH	0.11	0/1921	0.29	0/2620
2	XH	0.11	0/1921	0.29	0/2620
2	YH	0.11	0/1921	0.29	0/2620
2	ZH	0.12	0/1921	0.30	0/2620
3	AK	0.18	0/1195	0.31	0/1616
3	BK	0.18	0/1195	0.30	0/1616
3	CK	0.16	0/1195	0.32	0/1616
3	DK	0.16	0/1195	0.29	0/1616
3	EK	0.15	0/1195	0.29	0/1616
3	FK	0.16	0/1195	0.30	0/1616
3	GK	0.16	0/1195	0.32	0/1616
3	HK	0.16	0/1195	0.31	0/1616
3	IK	0.15	0/1195	0.30	0/1616
3	JK	0.16	0/1195	0.29	0/1616
3	KK	0.16	0/1195	0.30	0/1616
3	LK	0.16	0/1195	0.30	0/1616
3	MK	0.16	0/1195	0.30	0/1616
4	AL	0.14	0/1417	0.30	0/1912
4	BL	0.16	0/1417	0.34	0/1912
4	CL	0.15	0/1417	0.32	0/1912
4	DL	0.15	0/1417	0.32	0/1912
4	EL	0.15	0/1417	0.36	0/1912
4	FL	0.15	0/1417	0.32	0/1912
4	GL	0.15	0/1417	0.34	0/1912
4	HL	0.15	0/1417	0.34	0/1912
4	IL	0.15	0/1417	0.33	0/1912
4	JL	0.15	0/1417	0.33	0/1912
4	KL	0.15	0/1417	0.31	0/1912
4	LL	0.15	0/1417	0.31	0/1912

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
4	ML	0.15	0/1417	0.32	0/1912
5	AN	0.15	0/593	0.31	0/799
5	BN	0.13	0/593	0.27	0/799
5	CN	0.14	0/593	0.30	0/799
5	DN	0.15	0/593	0.29	0/799
5	EN	0.14	0/593	0.29	0/799
5	FN	0.15	0/593	0.27	0/799
5	GN	0.15	0/593	0.28	0/799
5	HN	0.13	0/593	0.26	0/799
5	IN	0.15	0/593	0.29	0/799
5	JN	0.13	0/593	0.27	0/799
5	KN	0.13	0/593	0.29	0/799
5	LN	0.14	0/593	0.29	0/799
5	MN	0.13	0/593	0.27	0/799
8	AD	0.16	0/1107	0.32	0/1502
8	Ad	0.15	0/1078	0.31	0/1463
8	BD	0.17	0/1107	0.33	0/1502
8	Bd	0.15	0/1078	0.27	0/1463
8	CD	0.15	0/1107	0.34	0/1502
8	Cd	0.14	0/1078	0.30	0/1463
8	DD	0.15	0/1107	0.32	0/1502
8	Dd	0.15	0/1078	0.30	0/1463
8	ED	0.16	0/1107	0.35	0/1502
8	Ed	0.14	0/1078	0.27	0/1463
8	FD	0.16	0/1107	0.36	0/1502
8	Fd	0.14	0/1078	0.28	0/1463
8	GD	0.16	0/1107	0.35	0/1502
8	Gd	0.16	0/1078	0.30	0/1463
8	HD	0.17	0/1107	0.34	0/1502
8	Hd	0.14	0/1078	0.27	0/1463
8	ID	0.16	0/1107	0.34	0/1502
8	Id	0.15	0/1078	0.28	0/1463
8	JD	0.15	0/1107	0.33	0/1502
8	Jd	0.14	0/1078	0.27	0/1463
8	KD	0.15	0/1107	0.34	0/1502
8	Kd	0.14	0/1078	0.27	0/1463
8	LD	0.16	0/1107	0.32	0/1502
8	Ld	0.15	0/1078	0.28	0/1463
8	MD	0.16	0/1107	0.33	0/1502
8	Md	0.14	0/1078	0.30	0/1463
9	AF	0.11	0/490	0.26	0/660
9	Af	0.11	0/456	0.31	0/615
9	BF	0.11	0/490	0.23	0/660

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
9	Bf	0.12	0/456	0.30	0/615
9	CF	0.11	0/490	0.30	0/660
9	Cf	0.11	0/456	0.24	0/615
9	DF	0.12	0/490	0.23	0/660
9	Df	0.13	0/456	0.28	0/615
9	EF	0.10	0/490	0.24	0/660
9	Ef	0.10	0/456	0.25	0/615
9	FF	0.10	0/490	0.25	0/660
9	Ff	0.12	0/456	0.30	0/615
9	GF	0.10	0/490	0.26	0/660
9	Gf	0.11	0/456	0.25	0/615
9	HF	0.11	0/490	0.28	0/660
9	Hf	0.12	0/456	0.32	0/615
9	IF	0.10	0/490	0.28	0/660
9	If	0.10	0/456	0.26	0/615
9	JF	0.10	0/490	0.27	0/660
9	Jf	0.11	0/456	0.26	0/615
9	KF	0.09	0/490	0.26	0/660
9	Kf	0.11	0/456	0.29	0/615
9	LF	0.10	0/490	0.30	0/660
9	Lf	0.12	0/456	0.25	0/615
9	MF	0.10	0/490	0.30	0/660
9	Mf	0.13	0/456	0.32	0/615
9	VF	0.12	0/490	0.26	0/660
9	WF	0.09	0/490	0.25	0/660
9	XF	0.11	0/490	0.26	0/660
9	YF	0.10	0/490	0.29	0/660
9	ZF	0.10	0/490	0.25	0/660
10	AC	0.15	0/1957	0.30	0/2651
10	BC	0.16	0/1957	0.31	0/2651
10	CC	0.17	0/1702	0.30	0/2315
10	DC	0.17	0/1702	0.32	0/2315
10	EC	0.17	0/1702	0.32	0/2315
10	FC	0.16	0/1957	0.30	0/2651
10	GC	0.16	0/1702	0.31	0/2315
10	HC	0.16	0/1702	0.30	0/2315
10	IC	0.16	0/1702	0.29	0/2315
10	JC	0.16	0/1957	0.32	0/2651
10	KC	0.16	0/1957	0.31	0/2651
10	LC	0.16	0/1702	0.30	0/2315
10	MC	0.17	0/1702	0.30	0/2315
11	AM	0.14	0/1678	0.32	0/2262
11	BM	0.13	0/1678	0.34	0/2262

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
11	CM	0.14	0/1678	0.32	0/2262
11	DM	0.14	0/1678	0.32	0/2262
11	EM	0.14	0/1678	0.32	0/2262
11	FM	0.13	0/1678	0.35	0/2262
11	GM	0.14	0/1678	0.33	0/2262
11	HM	0.14	0/1678	0.31	0/2262
11	IM	0.14	0/1678	0.33	0/2262
11	JM	0.14	0/1678	0.32	0/2262
11	KM	0.13	0/1678	0.31	0/2262
11	LM	0.14	0/1678	0.33	0/2262
11	MM	0.13	0/1678	0.32	0/2262
All	All	0.15	0/191071	0.32	0/258997

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AG	1229	0	1231	65	0
1	Ag	276	0	263	12	0
1	BG	1229	0	1231	59	0
1	Bg	276	0	263	18	0
1	CG	1229	0	1231	66	0
1	Cg	276	0	263	19	0
1	DG	1229	0	1231	65	0
1	Dg	276	0	263	18	0
1	EG	1229	0	1231	55	0
1	Eg	276	0	263	21	0
1	FG	1229	0	1231	55	0
1	Fg	276	0	263	15	0
1	GG	1229	0	1231	66	0
1	Gg	276	0	263	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	HG	1229	0	1231	64	0
1	Hg	276	0	263	12	0
1	IG	1229	0	1231	67	0
1	Ig	276	0	263	23	0
1	JG	1229	0	1231	60	0
1	Jg	276	0	263	17	0
1	KG	1229	0	1231	64	0
1	Kg	276	0	263	22	0
1	LG	1229	0	1231	50	0
1	Lg	276	0	263	18	0
1	MG	1229	0	1231	56	0
1	Mg	276	0	263	18	0
1	NG	1229	0	1231	72	0
1	OG	1229	0	1231	76	0
1	PG	1229	0	1231	63	0
1	VG	276	0	263	16	0
1	WG	276	0	263	17	0
1	XG	276	0	263	16	0
1	YG	276	0	263	16	0
1	ZG	276	0	263	17	0
2	AH	1983	0	2009	78	0
2	BH	1983	0	2009	82	0
2	CH	1983	0	2009	65	0
2	DH	1983	0	2009	80	0
2	EH	1983	0	2009	85	0
2	FH	1983	0	2009	74	0
2	GH	1983	0	2009	56	0
2	HH	1983	0	2009	72	0
2	IH	1983	0	2009	70	0
2	JH	1983	0	2009	65	0
2	KH	1983	0	2009	69	0
2	LH	1983	0	2009	73	0
2	MH	1983	0	2009	66	0
2	VH	1875	0	1900	70	0
2	WH	1875	0	1900	51	0
2	XH	1875	0	1900	68	0
2	YH	1875	0	1900	72	0
2	ZH	1875	0	1900	63	0
3	AK	1175	0	1221	29	0
3	BK	1175	0	1221	35	0
3	CK	1175	0	1221	27	0
3	DK	1175	0	1221	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	EK	1175	0	1221	34	0
3	FK	1175	0	1221	47	0
3	GK	1175	0	1221	40	0
3	HK	1175	0	1221	38	0
3	IK	1175	0	1221	39	0
3	JK	1175	0	1221	35	0
3	KK	1175	0	1221	43	0
3	LK	1175	0	1221	39	0
3	MK	1175	0	1221	42	0
4	AL	1388	0	1378	41	0
4	BL	1388	0	1378	48	0
4	CL	1388	0	1378	33	0
4	DL	1388	0	1378	51	0
4	EL	1388	0	1378	47	0
4	FL	1388	0	1378	40	0
4	GL	1388	0	1378	56	0
4	HL	1388	0	1378	52	0
4	IL	1388	0	1378	46	0
4	JL	1388	0	1378	48	0
4	KL	1388	0	1378	57	0
4	LL	1388	0	1378	49	0
4	ML	1388	0	1378	39	0
5	AN	582	0	530	21	0
5	BN	582	0	530	27	0
5	CN	582	0	530	19	0
5	DN	582	0	530	20	0
5	EN	582	0	530	19	0
5	FN	582	0	530	17	0
5	GN	582	0	530	17	0
5	HN	582	0	530	19	0
5	IN	582	0	530	24	0
5	JN	582	0	530	25	0
5	KN	582	0	530	16	0
5	LN	582	0	530	25	0
5	MN	582	0	530	20	0
6	AU	45	0	12	1	0
6	BU	45	0	12	0	0
6	CU	45	0	12	0	0
6	DU	45	0	12	1	0
6	EU	45	0	12	1	0
6	FU	45	0	12	1	0
6	GU	45	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	HU	45	0	12	1	0
6	IU	45	0	12	1	0
6	JU	45	0	13	1	0
6	KU	45	0	13	1	0
6	LU	45	0	12	1	0
6	MU	45	0	12	0	0
7	AX	240	0	56	2	0
7	BX	240	0	57	5	0
7	CX	240	0	57	2	0
7	DX	240	0	56	2	0
7	EX	240	0	55	0	0
7	FX	240	0	54	0	0
7	GX	240	0	54	0	0
7	HX	240	0	55	1	0
7	IX	240	0	55	1	0
7	JX	240	0	57	2	0
7	KX	240	0	55	1	0
7	LX	240	0	55	0	0
7	MX	240	0	58	3	0
7	VX	240	0	54	1	0
7	WX	240	0	52	1	0
7	XX	240	0	54	1	0
7	YX	240	0	55	4	0
7	ZX	240	0	54	1	0
8	AD	1086	0	1121	44	0
8	Ad	1058	0	1092	36	0
8	BD	1086	0	1121	37	0
8	Bd	1058	0	1092	36	0
8	CD	1086	0	1121	34	0
8	Cd	1058	0	1092	40	0
8	DD	1086	0	1121	42	0
8	Dd	1058	0	1092	23	0
8	ED	1086	0	1121	38	0
8	Ed	1058	0	1092	38	0
8	FD	1086	0	1121	44	0
8	Fd	1058	0	1092	46	0
8	GD	1086	0	1121	41	0
8	Gd	1058	0	1092	31	0
8	HD	1086	0	1121	37	0
8	Hd	1058	0	1092	33	0
8	ID	1086	0	1121	34	0
8	Id	1058	0	1092	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	JD	1086	0	1121	32	0
8	Jd	1058	0	1092	30	0
8	KD	1086	0	1121	36	0
8	Kd	1058	0	1092	28	0
8	LD	1086	0	1121	33	0
8	Ld	1058	0	1092	34	0
8	MD	1086	0	1121	25	0
8	Md	1058	0	1092	28	0
9	AF	483	0	502	23	0
9	Af	449	0	474	11	0
9	BF	483	0	502	15	0
9	Bf	449	0	474	15	0
9	CF	483	0	502	23	0
9	Cf	449	0	474	14	0
9	DF	483	0	502	22	0
9	Df	449	0	474	18	0
9	EF	483	0	502	17	0
9	Ef	449	0	474	17	0
9	FF	483	0	502	17	0
9	Ff	449	0	474	19	0
9	GF	483	0	502	20	0
9	Gf	449	0	474	12	0
9	HF	483	0	502	18	0
9	Hf	449	0	474	12	0
9	IF	483	0	502	15	0
9	If	449	0	474	26	0
9	JF	483	0	502	16	0
9	Jf	449	0	474	11	0
9	KF	483	0	502	18	0
9	Kf	449	0	474	19	0
9	LF	483	0	502	13	0
9	Lf	449	0	474	15	0
9	MF	483	0	502	18	0
9	Mf	449	0	474	11	0
9	VF	483	0	502	22	0
9	WF	483	0	502	20	0
9	XF	483	0	502	22	0
9	YF	483	0	502	21	0
9	ZF	483	0	502	10	0
10	AC	1921	0	1952	84	0
10	BC	1921	0	1952	63	0
10	CC	1667	0	1682	68	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	DC	1667	0	1682	70	0
10	EC	1667	0	1682	56	0
10	FC	1921	0	1952	65	0
10	GC	1667	0	1682	74	0
10	HC	1667	0	1682	53	0
10	IC	1667	0	1682	74	0
10	JC	1921	0	1952	65	0
10	KC	1921	0	1952	77	0
10	LC	1667	0	1682	67	0
10	MC	1667	0	1682	66	0
11	AM	1650	0	1658	65	0
11	BM	1650	0	1658	72	0
11	CM	1650	0	1658	57	0
11	DM	1650	0	1658	46	0
11	EM	1650	0	1658	68	0
11	FM	1650	0	1658	73	0
11	GM	1650	0	1658	67	0
11	HM	1650	0	1658	59	0
11	IM	1650	0	1658	51	0
11	JM	1650	0	1658	72	0
11	KM	1650	0	1658	64	0
11	LM	1650	0	1658	45	0
11	MM	1650	0	1658	54	0
All	All	192370	0	190612	6122	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 16.

All (6122) 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)
11:EM:198:GLY:O	11:EM:219:ALA:HB3	1.66	0.96
1:ZG:798:THR:HA	2:BH:115:MET:HE1	1.50	0.92
11:JM:275:ASP:HB3	11:JM:294:PHE:HB2	1.50	0.91
5:LN:78:LEU:H	2:MH:354:MET:HE1	1.43	0.83
4:DL:166:ALA:HA	4:DL:206:GLU:O	1.77	0.83
2:EH:176:VAL:H	2:DH:225:ASN:HD21	1.24	0.82
8:HD:105:ARG:HB2	8:HD:153:VAL:HG12	1.62	0.81
8:LD:55:MET:HB3	10:GC:214:LYS:HG3	1.61	0.81
1:EG:969:GLY:HA3	1:EG:1009:ALA:HB2	1.62	0.81
10:AC:226:TYR:HB3	10:AC:252:ALA:HB3	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:ZH:203:ASN:HB3	2:ZH:216:GLN:HB3	1.63	0.81
11:JM:120:GLY:H	11:JM:140:ASN:HB2	1.45	0.81
10:MC:108:VAL:HG23	10:MC:207:GLY:HA3	1.63	0.80
11:GM:275:ASP:HB3	11:GM:294:PHE:HB2	1.61	0.80
2:BH:189:TRP:HE1	2:BH:232:GLY:H	1.30	0.80
10:BC:124:GLN:HG3	10:AC:250:ILE:HG13	1.63	0.79
11:LM:306:GLN:HG2	11:LM:308:ASP:H	1.47	0.79
11:FM:275:ASP:HB3	11:FM:294:PHE:HB2	1.64	0.79
9:CF:241:TYR:HB3	9:CF:256:THR:HG21	1.65	0.79
8:Ad:121:ILE:HD11	8:Ad:138:GLN:HE22	1.46	0.78
2:CH:202:PHE:HB3	2:CH:215:ILE:HD11	1.64	0.78
9:GF:241:TYR:HB3	9:GF:256:THR:HG21	1.66	0.78
9:XF:210:TYR:HA	9:XF:224:GLY:HA2	1.66	0.78
11:EM:275:ASP:HB3	11:EM:294:PHE:HB2	1.65	0.78
10:BC:51:LYS:HB3	1:BG:938:ASN:HD21	1.48	0.78
9:WF:210:TYR:HA	9:WF:224:GLY:HA2	1.66	0.78
11:EM:120:GLY:H	11:EM:140:ASN:HB2	1.49	0.78
1:IG:875:THR:HA	1:JG:940:ALA:HB1	1.66	0.77
4:FL:170:ASP:OD1	4:FL:170:ASP:N	2.17	0.77
2:IH:176:VAL:H	2:XH:225:ASN:HD21	1.32	0.77
10:CC:245:ARG:HB3	10:DC:126:ILE:HG23	1.65	0.77
1:GG:899:LEU:HD13	1:GG:919:MET:HG2	1.67	0.77
8:Ed:84:SER:H	10:AC:268:ALA:HB3	1.49	0.76
1:CG:871:ALA:HB2	1:CG:889:ILE:HD13	1.67	0.76
4:CL:166:ALA:HA	4:CL:206:GLU:O	1.86	0.76
1:KG:972:PHE:HB3	1:KG:1005:VAL:HG22	1.65	0.76
11:CM:119:GLU:HG3	11:CM:139:ALA:HB3	1.66	0.76
1:DG:899:LEU:HD13	1:DG:919:MET:HG2	1.65	0.76
1:YG:818:GLN:NE2	2:YH:203:ASN:OD1	2.19	0.76
11:AM:120:GLY:H	11:AM:140:ASN:HB2	1.50	0.76
8:CD:125:ASP:OD1	3:CK:138:ARG:NH1	2.19	0.76
9:MF:219:ARG:HH22	2:ZH:150:LYS:HG3	1.50	0.76
10:DC:145:THR:H	10:DC:148:GLN:HE22	1.33	0.76
11:BM:275:ASP:HB3	11:BM:294:PHE:HB2	1.67	0.76
10:AC:117:THR:HG1	10:AC:129:SER:HG	1.30	0.76
1:AG:900:ILE:HD11	1:BG:866:GLY:HA3	1.68	0.75
2:EH:326:ALA:HB3	2:EH:338:GLU:HB3	1.68	0.75
9:Hf:235:GLY:HA2	9:Hf:243:MET:HE1	1.69	0.75
2:AH:275:SER:HA	10:IC:125:ARG:HD3	1.67	0.75
4:LL:166:ALA:HA	4:LL:206:GLU:O	1.87	0.75
3:BK:166:THR:HB	3:BK:177:ASN:HD21	1.52	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:HM:121:ALA:HA	11:HM:141:GLU:HG2	1.69	0.75
4:GL:192:PHE:O	4:GL:196:ASN:ND2	2.20	0.75
1:HG:899:LEU:HD13	1:HG:919:MET:HG2	1.68	0.75
8:FD:105:ARG:HB2	8:FD:153:VAL:HG12	1.67	0.75
11:EM:138:LEU:HD11	11:EM:142:GLY:HA3	1.69	0.75
4:GL:166:ALA:HA	4:GL:206:GLU:O	1.87	0.75
10:JC:57:GLU:O	10:JC:61:LYS:NZ	2.19	0.75
4:CL:115:GLN:HB3	4:CL:126:ILE:HB	1.69	0.75
9:Gf:219:ARG:HG3	9:Gf:233:ARG:HH11	1.52	0.75
10:FC:246:ARG:HB2	10:GC:127:ILE:HG12	1.69	0.75
1:JG:1003:ASN:HA	1:JG:1006:ILE:HD12	1.69	0.75
1:AG:912:MET:HB3	1:AG:944:LEU:HB2	1.69	0.74
10:MC:166:PRO:HB2	10:MC:172:LYS:HG2	1.69	0.74
1:OG:899:LEU:HD13	1:OG:919:MET:HG2	1.69	0.74
1:OG:972:PHE:HB3	1:OG:1005:VAL:HG22	1.69	0.74
11:EM:306:GLN:HB3	11:EM:309:LEU:HB2	1.69	0.74
11:IM:275:ASP:HB3	11:IM:294:PHE:HB2	1.67	0.74
2:DH:183:ASP:HA	2:DH:256:VAL:HG12	1.70	0.74
1:LG:1003:ASN:HA	1:LG:1006:ILE:HD12	1.68	0.74
9:HF:254:ILE:HB	9:HF:262:ILE:HB	1.69	0.74
1:NG:899:LEU:HD13	1:NG:919:MET:HG2	1.68	0.74
8:Kd:64:PRO:HG2	8:Kd:67:LYS:HE2	1.70	0.74
2:EH:344:VAL:HG11	5:DN:87:TRP:HE1	1.53	0.74
4:ML:130:ASP:N	4:ML:130:ASP:OD1	2.21	0.74
1:HG:900:ILE:HG13	1:HG:918:THR:HB	1.70	0.74
2:JH:171:LEU:HD11	2:JH:241:LEU:HB2	1.70	0.74
11:MM:306:GLN:HG2	11:MM:308:ASP:H	1.53	0.73
1:Cg:798:THR:HA	2:DH:115:MET:HE1	1.70	0.73
2:LH:230:LEU:HB2	2:LH:233:LEU:HB2	1.70	0.73
4:KL:44:HIS:HB2	4:KL:48:ASN:HA	1.69	0.73
10:KC:143:THR:HG22	10:KC:144:THR:HG23	1.70	0.73
3:EK:150:ASP:OD1	3:EK:152:ARG:NH2	2.21	0.73
3:GK:148:GLY:H	8:Gd:30:ILE:HD13	1.52	0.73
2:MH:183:ASP:HA	2:MH:256:VAL:HG22	1.69	0.73
1:XG:797:ARG:HH12	1:XG:801:MET:HE2	1.53	0.73
8:AD:105:ARG:HB2	8:AD:153:VAL:HG12	1.69	0.73
4:IL:130:ASP:OD1	4:IL:130:ASP:N	2.21	0.73
10:KC:110:VAL:HG13	10:KC:209:GLY:HA3	1.71	0.73
11:MM:276:ALA:H	11:MM:295:ASN:HB2	1.53	0.73
10:IC:145:THR:H	10:IC:148:GLN:HE22	1.37	0.73
4:EL:108:ASP:O	4:EL:112:GLN:NE2	2.21	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:HL:129:THR:O	4:HL:133:PHE:HB2	1.88	0.73
9:MF:235:GLY:HA2	9:MF:243:MET:HE1	1.70	0.73
10:AC:102:LEU:HB2	10:AC:106:ILE:HG23	1.71	0.73
8:KD:91:ILE:HD11	8:KD:156:LEU:HD11	1.71	0.73
11:BM:120:GLY:H	11:BM:140:ASN:HB2	1.53	0.73
1:Ig:801:MET:HB3	2:JH:121:PRO:HB2	1.71	0.73
2:AH:176:VAL:H	2:ZH:225:ASN:HD21	1.36	0.73
4:AL:166:ALA:HA	4:AL:206:GLU:O	1.88	0.73
2:GH:324:TRP:HB3	2:GH:339:MET:HE2	1.70	0.72
11:HM:240:GLN:HB3	11:HM:242:LYS:HE3	1.71	0.72
8:BD:114:SER:HA	10:KC:116:ASN:HD21	1.54	0.72
1:Dg:807:GLN:O	1:Dg:810:GLN:NE2	2.22	0.72
9:Df:213:GLN:HB2	9:Df:221:TRP:HD1	1.51	0.72
2:EH:107:ILE:HB	1:VG:794:ILE:HD11	1.70	0.72
11:MM:173:LEU:O	11:MM:192:ARG:NH2	2.23	0.72
4:GL:54:ARG:HH21	4:GL:57:VAL:HG13	1.53	0.72
1:Ig:797:ARG:NH1	1:Ig:801:MET:SD	2.62	0.72
2:LH:278:ASP:OD1	2:LH:278:ASP:N	2.19	0.72
2:BH:230:LEU:HB2	2:BH:233:LEU:HB2	1.70	0.72
2:DH:208:LYS:HD3	1:Eg:824:THR:H	1.53	0.72
1:MG:969:GLY:HA3	1:MG:1009:ALA:HB2	1.70	0.72
9:Ff:253:ARG:HH12	11:FM:306:GLN:HE22	1.38	0.72
10:CC:258:ASN:N	10:CC:258:ASN:OD1	2.22	0.72
11:KM:275:ASP:HB3	11:KM:294:PHE:HB2	1.70	0.72
4:LL:219:ILE:HG22	4:LL:222:GLY:H	1.52	0.72
2:MH:108:ASP:N	2:MH:108:ASP:OD1	2.21	0.72
4:AL:115:GLN:HB3	4:AL:126:ILE:HB	1.71	0.72
10:DC:243:ASP:OD1	10:DC:243:ASP:N	2.20	0.72
2:KH:279:LEU:HD11	2:KH:289:PRO:HB3	1.72	0.72
9:GF:230:LEU:HA	2:GH:165:THR:HG21	1.71	0.72
11:AM:174:GLN:HE22	11:AM:193:GLN:HB3	1.52	0.72
5:EN:89:GLY:HA3	5:EN:104:ASN:HB2	1.71	0.72
8:ID:29:PRO:HG2	4:IL:225:GLN:HA	1.72	0.72
1:Mg:811:ASP:O	1:Mg:814:GLN:NE2	2.23	0.72
4:ML:166:ALA:HA	4:ML:206:GLU:O	1.89	0.72
10:FC:232:LEU:HB2	10:FC:245:ASP:HB3	1.72	0.72
11:AM:284:LEU:HB3	11:AM:310:LYS:HE3	1.72	0.71
8:Kd:71:LEU:O	8:Kd:133:ARG:NH1	2.23	0.71
4:FL:115:GLN:HB3	4:FL:126:ILE:HB	1.71	0.71
11:DM:275:ASP:HB3	11:DM:294:PHE:HB2	1.72	0.71
1:MG:899:LEU:HD13	1:MG:919:MET:HG2	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:HL:192:PHE:O	4:HL:196:ASN:ND2	2.23	0.71
10:CC:258:ASN:O	10:CC:262:TRP:NE1	2.22	0.71
11:LM:119:GLU:HG3	11:LM:139:ALA:HB3	1.70	0.71
2:YH:154:THR:HB	2:YH:156:GLN:HE22	1.54	0.71
1:AG:938:ASN:ND2	10:AC:52:MET:O	2.24	0.71
10:CC:188:ILE:O	10:CC:192:ASN:ND2	2.22	0.71
11:GM:306:GLN:NE2	11:GM:308:ASP:OD1	2.23	0.71
2:VH:208:LYS:HD2	1:Dg:824:THR:H	1.54	0.71
10:EC:110:LEU:HD23	10:EC:212:TYR:HB2	1.72	0.71
2:JH:208:LYS:HD2	1:Kg:823:GLY:HA3	1.70	0.71
11:EM:306:GLN:HG3	11:EM:308:ASP:H	1.54	0.71
5:KN:71:THR:HG22	5:KN:73:HIS:H	1.56	0.71
8:CD:77:TYR:O	8:CD:78:ASN:ND2	2.23	0.71
2:XH:341:LYS:H	2:XH:341:LYS:HZ3	1.38	0.71
1:PG:951:HIS:H	1:PG:1027:THR:HG22	1.56	0.71
2:JH:143:ALA:O	2:KH:131:LYS:NZ	2.24	0.71
2:EH:171:LEU:HD11	2:EH:241:LEU:HB2	1.71	0.71
2:AH:187:ALA:HB1	2:AH:262:ASN:HB2	1.73	0.71
11:FM:120:GLY:H	11:FM:140:ASN:HB2	1.56	0.71
1:Jg:807:GLN:O	1:Jg:810:GLN:NE2	2.24	0.70
8:Jd:97:ARG:HD3	10:FC:264:ARG:HH12	1.56	0.70
10:LC:227:HIS:HB3	10:LC:246:LEU:HD13	1.71	0.70
8:CD:107:ARG:HE	8:CD:155:GLU:HG3	1.56	0.70
1:AG:924:ALA:HB3	1:AG:926:LYS:HE3	1.74	0.70
11:BM:214:ILE:O	11:BM:215:ARG:NH1	2.24	0.70
1:LG:899:LEU:HD13	1:LG:919:MET:HG2	1.73	0.70
10:BC:111:LEU:HD23	10:BC:213:TYR:HB2	1.72	0.70
8:GD:39:ILE:HD12	4:GL:220:ILE:HG13	1.73	0.70
11:HM:120:GLY:H	11:HM:140:ASN:HB2	1.55	0.70
11:EM:284:LEU:HB3	11:EM:310:LYS:HE3	1.74	0.70
3:BK:141:SER:HB3	3:BK:156:THR:HG21	1.73	0.70
10:KC:246:ARG:HB2	10:LC:126:ILE:HG23	1.74	0.70
8:HD:55:MET:HE2	10:CC:210:ILE:HD11	1.73	0.70
2:AH:189:TRP:HE1	2:AH:232:GLY:H	1.37	0.70
4:ML:113:ASP:OD1	4:ML:113:ASP:N	2.24	0.70
11:BM:306:GLN:NE2	11:BM:308:ASP:OD1	2.24	0.70
2:VH:225:ASN:HD21	2:DH:176:VAL:H	1.40	0.70
4:DL:192:PHE:O	4:DL:196:ASN:ND2	2.20	0.70
3:EK:47:GLY:O	3:EK:108:GLN:NE2	2.24	0.70
2:FH:171:LEU:HD11	2:FH:241:LEU:HB2	1.73	0.70
4:FL:166:ALA:HA	4:FL:206:GLU:O	1.90	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EG:899:LEU:HD13	1:EG:919:MET:HG2	1.74	0.70
10:LC:94:ASP:OD1	10:LC:96:ASN:ND2	2.25	0.70
4:EL:165:VAL:HG12	4:EL:231:ILE:HG12	1.74	0.70
10:IC:120:ASP:N	10:IC:123:SER:OG	2.25	0.70
4:EL:108:ASP:OD1	4:EL:112:GLN:NE2	2.25	0.70
2:WH:320:LEU:HD11	10:MC:250:ALA:HB2	1.74	0.70
4:DL:212:ASN:OD1	4:DL:212:ASN:N	2.23	0.70
10:CC:75:ARG:HG3	10:CC:188:ILE:HA	1.72	0.69
9:IF:241:TYR:HB3	9:IF:256:THR:HG21	1.72	0.69
9:MF:241:TYR:HB3	9:MF:256:THR:HG21	1.74	0.69
1:EG:924:ALA:HB3	1:EG:926:LYS:HE3	1.74	0.69
2:GH:176:VAL:HG13	2:GH:216:GLN:HE21	1.57	0.69
1:DG:1024:ASN:N	1:DG:1024:ASN:OD1	2.24	0.69
9:DF:210:TYR:HA	9:DF:224:GLY:HA2	1.75	0.69
1:AG:969:GLY:HA3	1:AG:1009:ALA:HB2	1.74	0.69
8:Ed:108:VAL:HG12	8:Ed:156:LEU:HB3	1.75	0.69
10:BC:241:ILE:HG12	10:CC:132:TYR:HB2	1.74	0.69
2:HH:238:MET:HG3	2:XH:250:TYR:HB3	1.75	0.69
8:JD:76:ALA:H	8:JD:79:LEU:HD12	1.56	0.69
8:LD:39:ILE:HD12	4:LL:220:ILE:HG13	1.75	0.69
1:GG:944:LEU:HD11	1:GG:1031:VAL:HA	1.74	0.69
4:EL:192:PHE:O	4:EL:196:ASN:ND2	2.25	0.69
1:GG:881:GLU:HG3	1:HG:911:LYS:HE2	1.73	0.69
10:HC:100:LEU:HB2	10:HC:104:ILE:HG13	1.75	0.69
8:HD:52:MET:HE1	8:Hd:48:VAL:HA	1.74	0.69
4:KL:146:PRO:O	4:KL:150:ASN:ND2	2.25	0.69
1:HG:900:ILE:HD11	1:IG:865:THR:HG22	1.75	0.69
1:LG:969:GLY:HA3	1:LG:1009:ALA:HB2	1.75	0.69
10:AC:92:ASP:OD1	10:AC:148:TRP:NE1	2.24	0.69
4:EL:54:ARG:HE	4:EL:57:VAL:HG13	1.58	0.69
10:BC:92:ASP:OD1	10:BC:148:TRP:NE1	2.26	0.69
1:Bg:797:ARG:HH11	2:VH:111:ALA:HB3	1.57	0.69
1:Ig:792:GLN:O	1:Ig:795:GLN:NE2	2.25	0.69
11:KM:120:GLY:H	11:KM:140:ASN:HB2	1.58	0.69
2:LH:236:PRO:HG2	2:MH:251:ARG:HH12	1.56	0.69
8:Md:64:PRO:HD2	8:Md:67:LYS:HE3	1.74	0.69
9:CF:214:ALA:H	9:CF:221:TRP:HB2	1.57	0.69
11:CM:276:ALA:H	11:CM:295:ASN:HB2	1.58	0.69
4:HL:44:HIS:HB2	4:HL:48:ASN:HA	1.75	0.69
8:LD:107:ARG:HB3	8:LD:155:GLU:HG2	1.73	0.69
11:EM:145:ARG:HH22	11:EM:162:VAL:HG23	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:IL:210:ASP:OD1	4:IL:210:ASP:N	2.26	0.69
9:Lf:251:GLN:HB3	9:Lf:253:ARG:HE	1.58	0.69
8:Md:76:ALA:O	8:Md:80:GLN:NE2	2.26	0.69
4:AL:177:HIS:ND1	11:AM:315:TYR:OH	2.25	0.69
9:BF:265:SER:HB3	9:BF:268:ASP:HB3	1.74	0.69
4:BL:230:GLU:OE2	4:BL:232:GLN:NE2	2.26	0.69
4:DL:129:THR:O	4:DL:133:PHE:HB2	1.93	0.69
5:DN:77:ASP:N	5:DN:77:ASP:OD1	2.25	0.69
2:EH:251:ARG:NH2	2:DH:236:PRO:O	2.25	0.68
8:KD:118:LEU:O	10:FC:98:ASN:ND2	2.25	0.68
4:LL:115:GLN:HB3	4:LL:126:ILE:HB	1.73	0.68
11:MM:163:THR:HB	11:MM:183:VAL:HG12	1.76	0.68
1:EG:886:LEU:HB3	1:EG:900:ILE:HG22	1.73	0.68
3:BK:111:LYS:NZ	3:BK:150:ASP:O	2.22	0.68
8:Bd:84:SER:H	10:KC:268:ALA:HB3	1.59	0.68
10:FC:92:ASP:OD1	10:FC:148:TRP:NE1	2.26	0.68
2:VH:292:SER:HB3	2:VH:307:SER:HB2	1.75	0.68
1:Gg:810:GLN:NE2	1:Gg:811:ASP:OD1	2.26	0.68
1:CG:900:ILE:HG13	1:CG:918:THR:HB	1.74	0.68
4:JL:114:ILE:HD12	4:JL:127:ILE:HG12	1.74	0.68
10:CC:101:LEU:HB3	10:CC:105:ILE:HG23	1.74	0.68
5:AN:46:GLY:HA3	5:AN:61:ASN:HB2	1.76	0.68
8:Ad:29:PRO:O	8:Ad:32:ASN:ND2	2.26	0.68
5:BN:57:ARG:NH1	5:BN:66:SER:O	2.27	0.68
9:JF:214:ALA:HB3	9:JF:221:TRP:HB2	1.75	0.68
4:JL:166:ALA:HA	4:JL:206:GLU:O	1.91	0.68
2:HH:197:GLY:HA2	1:XG:818:GLN:HB3	1.76	0.68
11:LM:138:LEU:HD11	11:LM:142:GLY:HA3	1.75	0.68
4:AL:54:ARG:HB3	4:AL:57:VAL:HB	1.75	0.68
8:DD:77:TYR:OH	3:DK:130:ARG:NH1	2.27	0.68
4:DL:44:HIS:HB2	4:DL:48:ASN:HA	1.75	0.68
3:FK:116:VAL:HG22	3:FK:182:ILE:HG22	1.76	0.68
9:GF:246:LEU:HB3	9:GF:255:LEU:HB2	1.74	0.68
2:HH:238:MET:N	2:HH:238:MET:SD	2.66	0.68
2:BH:184:SER:N	2:BH:256:VAL:O	2.25	0.68
11:CM:275:ASP:HB3	11:CM:294:PHE:HB2	1.75	0.68
1:HG:1024:ASN:OD1	1:HG:1024:ASN:N	2.26	0.68
10:AC:32:LEU:O	10:AC:36:GLN:NE2	2.26	0.68
3:GK:116:VAL:HG22	3:GK:182:ILE:HG22	1.75	0.68
3:HK:117:THR:HA	3:HK:157:GLN:O	1.94	0.68
9:If:245:LYS:NZ	9:If:256:THR:O	2.23	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:EC:146:THR:OG1	10:EC:147:TRP:N	2.26	0.68
1:NG:1042:THR:OG1	1:NG:1043:GLN:OE1	2.12	0.68
9:JF:233:ARG:NH2	9:KF:269:SER:OG	2.26	0.68
4:JL:44:HIS:HB2	4:JL:48:ASN:HA	1.75	0.68
8:LD:29:PRO:HG2	4:LL:225:GLN:HA	1.74	0.68
11:MM:275:ASP:HB3	11:MM:294:PHE:HB2	1.75	0.68
2:ZH:171:LEU:HD11	2:ZH:241:LEU:HB2	1.76	0.68
10:GC:249:ILE:HB	10:HC:122:GLN:HG2	1.76	0.68
8:Dd:108:VAL:HG12	8:Dd:156:LEU:HB3	1.75	0.68
2:FH:108:ASP:N	2:FH:108:ASP:OD1	2.25	0.68
3:KK:162:ASP:N	3:KK:162:ASP:OD1	2.27	0.68
2:WH:171:LEU:HD11	2:WH:241:LEU:HB2	1.76	0.68
2:WH:174:GLY:HA2	2:WH:216:GLN:HE21	1.58	0.68
1:Kg:811:ASP:O	1:Kg:814:GLN:NE2	2.26	0.68
11:BM:319:PHE:H	4:BL:139:ARG:HE	1.42	0.68
8:Kd:60:LYS:NZ	8:Kd:61:VAL:O	2.27	0.67
4:BL:166:ALA:HA	4:BL:206:GLU:O	1.94	0.67
8:HD:158:TYR:O	8:Hd:137:TYR:OH	2.12	0.67
2:HH:108:ASP:O	1:WG:797:ARG:NH1	2.27	0.67
11:IM:201:THR:HG22	11:IM:221:LYS:HB2	1.75	0.67
1:CG:969:GLY:HA3	1:CG:1009:ALA:HB2	1.76	0.67
10:DC:109:LEU:HD23	10:DC:211:TYR:HB2	1.75	0.67
1:JG:900:ILE:HG13	1:JG:918:THR:HB	1.74	0.67
1:KG:899:LEU:HD13	1:KG:919:MET:HG2	1.76	0.67
1:NG:871:ALA:HB2	1:NG:889:ILE:HD13	1.76	0.67
8:Hd:36:ASP:N	8:Hd:36:ASP:OD1	2.27	0.67
1:FG:1006:ILE:O	1:FG:1010:THR:OG1	2.12	0.67
11:AM:186:SER:HA	11:AM:205:TYR:HB2	1.77	0.67
11:JM:306:GLN:NE2	11:JM:308:ASP:OD1	2.27	0.67
10:FC:143:THR:HG22	10:FC:144:THR:HG23	1.77	0.67
1:Ag:807:GLN:O	1:Ag:810:GLN:NE2	2.28	0.67
4:HL:54:ARG:HH21	4:HL:57:VAL:HG13	1.60	0.67
1:Jg:802:LEU:HD22	2:YH:115:MET:HE3	1.76	0.67
8:CD:87:TRP:CD1	8:CD:89:GLY:H	2.12	0.67
10:DC:145:THR:OG1	10:DC:146:TRP:N	2.27	0.67
4:CL:230:GLU:OE2	4:CL:232:GLN:NE2	2.27	0.67
8:Ed:74:PRO:HG3	8:Ed:147:VAL:HG11	1.77	0.67
4:FL:131:LYS:NZ	4:FL:144:CYS:SG	2.67	0.67
1:Hg:807:GLN:O	1:Hg:810:GLN:NE2	2.27	0.67
4:IL:192:PHE:O	4:IL:196:ASN:ND2	2.27	0.67
2:KH:189:TRP:HE3	2:KH:260:GLY:HA2	1.58	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LD:158:TYR:O	8:Ld:137:TYR:OH	2.12	0.67
11:MM:214:ILE:O	11:MM:215:ARG:NH1	2.25	0.67
2:YH:181:PHE:O	2:YH:211:ASN:ND2	2.28	0.67
11:AM:240:GLN:HB3	11:AM:242:LYS:HE3	1.76	0.67
10:LC:239:ILE:HD11	10:MC:131:TYR:HB2	1.75	0.67
8:Dd:148:TYR:HB2	8:Dd:153:VAL:HG12	1.76	0.67
8:HD:77:TYR:O	8:HD:78:ASN:ND2	2.27	0.67
8:ID:86:ASP:OD1	10:DC:87:ARG:NH1	2.27	0.67
8:ID:87:TRP:CD1	8:ID:89:GLY:H	2.13	0.67
9:Kf:246:LEU:HB3	9:Kf:255:LEU:HB3	1.75	0.67
2:WH:108:ASP:OD1	2:WH:108:ASP:N	2.28	0.67
10:AC:107:LEU:HD12	10:AC:108:PRO:HD2	1.77	0.67
2:BH:203:ASN:ND2	2:BH:205:GLN:OE1	2.27	0.67
10:JC:227:VAL:HB	10:JC:250:ILE:HG22	1.77	0.67
5:FN:71:THR:HG22	5:FN:73:HIS:H	1.60	0.67
9:VF:207:ARG:HH22	9:VF:240:GLY:HA3	1.60	0.67
1:FG:951:HIS:H	1:FG:1027:THR:HG22	1.60	0.67
1:GG:931:SER:O	1:GG:1042:THR:OG1	2.13	0.67
3:FK:129:GLU:N	3:FK:129:GLU:OE1	2.28	0.67
8:Hd:148:TYR:HB2	8:Hd:153:VAL:HG12	1.76	0.67
4:KL:115:GLN:HB3	4:KL:126:ILE:HB	1.76	0.67
11:MM:306:GLN:HB3	11:MM:309:LEU:HB2	1.76	0.67
11:DM:273:ALA:HB1	11:DM:277:SER:HB2	1.77	0.67
1:CG:912:MET:HB3	1:CG:944:LEU:HB2	1.76	0.67
1:Lg:791:GLN:N	1:Lg:793:GLU:OE1	2.28	0.67
9:WF:235:GLY:HA2	9:WF:243:MET:HE1	1.77	0.67
9:YF:254:ILE:HB	9:YF:262:ILE:HB	1.77	0.67
11:EM:214:ILE:HB	11:EM:233:VAL:HG12	1.76	0.67
8:Id:76:ALA:HB3	8:Id:79:LEU:HD23	1.76	0.66
3:JK:50:ASP:OD1	3:JK:50:ASP:N	2.27	0.66
5:LN:79:GLN:O	10:GC:84:ASN:ND2	2.28	0.66
4:ML:230:GLU:OE2	4:ML:232:GLN:NE2	2.27	0.66
4:AL:169:THR:HG21	4:AL:178:LYS:HB3	1.76	0.66
11:AM:306:GLN:HB3	11:AM:309:LEU:HB2	1.77	0.66
10:MC:193:ILE:O	10:MC:197:ASN:ND2	2.27	0.66
11:IM:300:ASP:OD2	11:IM:302:ARG:NH2	2.22	0.66
4:JL:219:ILE:HG22	4:JL:222:GLY:H	1.58	0.66
2:AH:107:ILE:HA	2:AH:110:LYS:HE3	1.77	0.66
11:MM:173:LEU:H	11:MM:192:ARG:HH22	1.43	0.66
1:EG:898:LYS:NZ	1:FG:865:THR:O	2.25	0.66
10:FC:216:LEU:HG	10:FC:221:MET:HB2	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AK:114:ILE:HD12	3:AK:182:ILE:HD11	1.78	0.66
3:MK:177:ASN:O	3:MK:179:ARG:NH1	2.28	0.66
4:AL:118:GLU:HG2	4:AL:123:ARG:HG2	1.76	0.66
2:BH:121:PRO:HB2	1:Ag:801:MET:HE1	1.77	0.66
4:BL:221:HIS:O	4:BL:225:GLN:NE2	2.28	0.66
8:HD:29:PRO:HG2	4:HL:225:GLN:HA	1.76	0.66
8:HD:82:ARG:HH21	8:HD:126:GLU:HA	1.61	0.66
1:KG:951:HIS:H	1:KG:1027:THR:HG22	1.59	0.66
8:Dd:76:ALA:HB3	8:Dd:79:LEU:HD23	1.77	0.66
10:BC:262:GLU:OE1	10:BC:262:GLU:N	2.29	0.66
2:KH:190:PRO:HB2	2:KH:231:ARG:HG3	1.78	0.66
3:MK:66:LYS:HB3	3:MK:77:SER:HB3	1.76	0.66
1:OG:871:ALA:HB2	1:OG:889:ILE:HD13	1.77	0.66
11:IM:303:GLU:OE1	11:IM:306:GLN:N	2.29	0.66
1:WG:791:GLN:N	1:WG:793:GLU:OE1	2.28	0.66
10:IC:213:LYS:HE3	8:AD:55:MET:HG3	1.78	0.66
1:JG:898:LYS:HE3	1:KG:864:LYS:HD2	1.76	0.66
5:HN:46:GLY:O	5:HN:61:ASN:ND2	2.29	0.66
1:DG:1006:ILE:O	1:DG:1010:THR:OG1	2.13	0.66
9:VF:219:ARG:NH2	9:VF:231:THR:OG1	2.29	0.66
2:XH:203:ASN:HB3	2:XH:216:GLN:HB3	1.78	0.66
10:AC:216:LEU:HD11	10:AC:221:MET:HE2	1.77	0.66
8:FD:162:TYR:O	10:AC:246:ARG:NH2	2.29	0.66
9:AF:245:LYS:HE3	9:AF:257:SER:HA	1.77	0.66
11:KM:271:SER:OG	11:KM:290:ASP:OD1	2.14	0.66
1:DG:968:PHE:HB3	1:DG:1008:LEU:HD13	1.78	0.66
8:CD:161:ILE:HG12	8:CD:162:TYR:H	1.61	0.66
9:VF:265:SER:HB3	9:VF:268:ASP:HB3	1.76	0.66
1:GG:947:ARG:HE	1:GG:947:ARG:H	1.44	0.66
1:IG:1006:ILE:O	1:IG:1010:THR:OG1	2.14	0.66
1:OG:912:MET:HB3	1:OG:944:LEU:HB2	1.78	0.66
1:OG:931:SER:H	1:OG:1043:GLN:HE22	1.42	0.66
2:HH:184:SER:O	2:HH:255:ARG:NH2	2.28	0.66
2:IH:143:ALA:O	2:JH:131:LYS:NZ	2.29	0.66
11:IM:302:ARG:HH11	11:IM:309:LEU:HD11	1.59	0.66
5:IN:92:TYR:HD1	5:IN:94:GLN:H	1.44	0.66
3:LK:177:ASN:O	3:LK:179:ARG:NH1	2.28	0.66
2:MH:326:ALA:HB3	2:MH:338:GLU:HB3	1.78	0.66
11:BM:293:ALA:O	4:BL:49:ASN:ND2	2.27	0.66
1:IG:1003:ASN:HA	1:IG:1006:ILE:HD12	1.76	0.66
2:EH:238:MET:SD	2:EH:238:MET:N	2.68	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Fd:148:TYR:HB2	8:Fd:153:VAL:HG12	1.77	0.66
9:KF:241:TYR:HB3	9:KF:256:THR:HG21	1.78	0.66
5:LN:48:ILE:HA	5:LN:60:CYS:HA	1.78	0.66
11:AM:246:LEU:O	11:AM:264:SER:OG	2.13	0.66
1:Cg:818:GLN:NE2	2:CH:205:GLN:OE1	2.28	0.66
11:CM:154:LYS:NZ	11:CM:156:GLU:OE2	2.28	0.66
1:IG:951:HIS:H	1:IG:1027:THR:HG22	1.61	0.66
1:NG:1003:ASN:HA	1:NG:1006:ILE:HD12	1.77	0.66
1:PG:912:MET:HB3	1:PG:944:LEU:HB2	1.77	0.66
3:EK:73:ASN:HD21	3:EK:185:ARG:HH21	1.44	0.65
8:Ed:76:ALA:HB3	8:Ed:79:LEU:HD23	1.78	0.65
9:GF:265:SER:HB3	9:GF:268:ASP:HB3	1.77	0.65
11:IM:316:ASN:N	11:IM:316:ASN:OD1	2.28	0.65
1:CG:899:LEU:HD13	1:CG:919:MET:HG2	1.77	0.65
2:KH:190:PRO:HA	2:KH:211:ASN:HB3	1.78	0.65
2:KH:330:SER:OG	2:KH:332:ASP:OD1	2.12	0.65
10:IC:87:ARG:NH1	8:AD:86:ASP:OD1	2.29	0.65
10:KC:51:LYS:HB2	1:MG:938:ASN:HD21	1.60	0.65
1:HG:936:ASP:N	1:HG:941:ARG:O	2.27	0.65
1:NG:969:GLY:HA3	1:NG:1009:ALA:HB2	1.78	0.65
2:EH:249:ASP:N	2:EH:249:ASP:OD1	2.29	0.65
3:EK:129:GLU:OE1	3:EK:129:GLU:N	2.29	0.65
8:Jd:76:ALA:O	8:Jd:80:GLN:NE2	2.26	0.65
9:Jf:245:LYS:NZ	9:Jf:256:THR:O	2.30	0.65
1:Kg:801:MET:HE1	2:LH:115:MET:HE2	1.77	0.65
1:Kg:801:MET:HB3	2:YH:121:PRO:HB2	1.76	0.65
2:VH:170:ARG:NH1	2:VH:249:ASP:OD1	2.29	0.65
11:GM:177:LEU:HD13	11:GM:181:PRO:HG2	1.77	0.65
1:JG:1006:ILE:O	1:JG:1010:THR:OG1	2.13	0.65
9:Gf:245:LYS:NZ	9:Gf:256:THR:O	2.29	0.65
11:HM:201:THR:HG22	11:HM:221:LYS:HD3	1.79	0.65
3:JK:47:GLY:O	3:JK:108:GLN:NE2	2.30	0.65
8:Kd:29:PRO:O	8:Kd:32:ASN:ND2	2.29	0.65
8:Kd:76:ALA:O	8:Kd:80:GLN:NE2	2.27	0.65
11:MM:313:ASP:OD1	11:MM:314:ARG:N	2.29	0.65
11:BM:242:LYS:HA	11:BM:262:GLU:HG2	1.78	0.65
11:FM:249:GLN:OE1	11:FM:267:ASN:ND2	2.29	0.65
11:GM:306:GLN:HB3	11:GM:309:LEU:HB2	1.78	0.65
8:Bd:36:ASP:OD1	8:Bd:36:ASP:N	2.30	0.65
10:FC:249:ARG:NH2	10:FC:250:ILE:O	2.29	0.65
9:EF:219:ARG:HH21	9:EF:231:THR:HG23	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:JM:302:ARG:HH11	11:JM:309:LEU:HD11	1.59	0.65
10:LC:151:TRP:HB3	5:DN:87:TRP:HZ3	1.60	0.65
2:CH:203:ASN:HB3	2:CH:216:GLN:HB3	1.77	0.65
3:EK:146:SER:HB2	8:Ed:29:PRO:HG3	1.79	0.65
3:IK:111:LYS:HD3	3:IK:114:ILE:HD11	1.78	0.65
4:JL:187:GLU:OE1	11:JM:268:HIS:ND1	2.28	0.65
10:CC:93:ILE:HG23	10:CC:94:TYR:HD1	1.61	0.65
11:KM:269:GLN:NE2	11:KM:271:SER:OG	2.29	0.65
1:Lg:811:ASP:O	1:Lg:814:GLN:NE2	2.24	0.65
4:AL:134:MET:HE2	4:AL:141:ASN:HA	1.78	0.65
11:GM:284:LEU:HB3	11:GM:310:LYS:HE3	1.78	0.65
3:BK:129:GLU:OE1	3:BK:129:GLU:N	2.29	0.65
1:CG:869:MET:HG2	1:CG:889:ILE:HD12	1.79	0.65
2:VH:171:LEU:HD11	2:VH:241:LEU:HB2	1.79	0.65
10:EC:97:ASN:OD1	10:EC:97:ASN:N	2.27	0.65
10:KC:102:LEU:HB2	10:KC:106:ILE:HG23	1.78	0.65
1:OG:946:SER:OG	1:OG:1030:GLU:O	2.12	0.65
10:BC:128:ILE:HD11	10:AC:246:ARG:HD3	1.79	0.65
1:Bg:792:GLN:O	1:Bg:795:GLN:NE2	2.30	0.65
11:AM:119:GLU:HG3	11:AM:139:ALA:HB3	1.78	0.65
11:BM:138:LEU:HD11	11:BM:142:GLY:HA3	1.78	0.65
1:JG:972:PHE:HB3	1:JG:1005:VAL:HG22	1.79	0.65
2:FH:324:TRP:HB3	2:FH:339:MET:HE2	1.79	0.65
8:GD:140:GLY:O	8:Gd:60:LYS:NZ	2.29	0.65
2:IH:122:LEU:H	2:IH:122:LEU:HD23	1.62	0.65
2:IH:160:LEU:N	2:IH:257:GLN:OE1	2.29	0.65
4:IL:166:ALA:HA	4:IL:206:GLU:O	1.97	0.65
5:IN:88:HIS:ND1	5:IN:105:ASP:OD2	2.28	0.65
11:EM:210:ASP:OD1	11:EM:210:ASP:N	2.29	0.65
2:BH:341:LYS:HB2	2:BH:361:LEU:HD21	1.77	0.65
3:BK:116:VAL:HB	3:BK:156:THR:HG22	1.79	0.65
4:FL:165:VAL:HG12	4:FL:231:ILE:HG12	1.77	0.65
9:HF:219:ARG:HH22	2:XH:150:LYS:HG3	1.62	0.65
2:HH:275:SER:HA	10:CC:126:ARG:HD3	1.79	0.65
4:HL:166:ALA:HA	4:HL:206:GLU:O	1.97	0.65
9:Hf:233:ARG:NH1	9:Hf:235:GLY:O	2.26	0.65
2:JH:183:ASP:OD1	2:JH:187:ALA:N	2.30	0.65
2:AH:183:ASP:OD1	2:AH:187:ALA:N	2.29	0.65
2:ZH:189:TRP:O	2:ZH:211:ASN:ND2	2.27	0.65
8:Ad:76:ALA:HB3	8:Ad:79:LEU:HB2	1.77	0.65
2:BH:203:ASN:HB3	2:BH:216:GLN:HB3	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GG:969:GLY:HA3	1:GG:1009:ALA:HB2	1.77	0.65
1:IG:871:ALA:HB2	1:IG:889:ILE:HD13	1.77	0.65
1:IG:881:GLU:HG3	1:JG:911:LYS:HE2	1.79	0.65
5:HN:97:SER:O	1:DG:893:LYS:NZ	2.30	0.65
8:Hd:76:ALA:O	8:Hd:80:GLN:NE2	2.30	0.65
1:Kg:807:GLN:O	1:Kg:810:GLN:NE2	2.30	0.65
11:KM:153:GLN:HA	11:KM:173:LEU:HD23	1.79	0.65
1:Lg:792:GLN:O	1:Lg:795:GLN:NE2	2.29	0.65
8:Ld:110:GLY:HA3	8:Ld:158:TYR:HB2	1.79	0.65
1:AG:866:GLY:HA3	1:PG:900:ILE:HD11	1.79	0.64
3:EK:130:ARG:NH1	8:ED:77:TYR:OH	2.29	0.64
9:KF:207:ARG:NH1	9:KF:240:GLY:O	2.30	0.64
1:XG:791:GLN:N	1:XG:793:GLU:OE1	2.30	0.64
1:FG:968:PHE:HB3	1:FG:1008:LEU:HD13	1.79	0.64
2:BH:253:ASP:OD1	2:BH:253:ASP:N	2.30	0.64
4:FL:150:ASN:OD1	4:FL:153:ARG:NH2	2.24	0.64
8:HD:130:GLU:OE2	8:HD:133:ARG:NH1	2.30	0.64
8:Id:73:ILE:HG12	8:Id:75:ASN:H	1.62	0.64
2:VH:251:ARG:NH2	2:CH:160:LEU:O	2.29	0.64
9:CF:213:GLN:O	2:CH:170:ARG:NH2	2.24	0.64
11:FM:119:GLU:HG3	11:FM:139:ALA:HB3	1.77	0.64
11:FM:127:ASN:HB3	11:FM:147:ALA:HB3	1.77	0.64
11:FM:174:GLN:NE2	11:FM:193:GLN:OE1	2.29	0.64
10:LC:108:VAL:HG23	10:LC:207:GLY:HA3	1.78	0.64
10:MC:239:ILE:HG22	10:AC:133:TYR:HB2	1.79	0.64
1:AG:871:ALA:HB2	1:AG:889:ILE:HD13	1.79	0.64
2:EH:319:ILE:HA	2:EH:347:VAL:HG12	1.79	0.64
2:FH:191:ILE:O	2:FH:231:ARG:NH2	2.30	0.64
3:GK:179:ARG:NE	3:GK:181:GLU:OE2	2.28	0.64
4:KL:210:ASP:OD1	4:KL:210:ASP:N	2.29	0.64
7:KX:70:UNK:H2	2:YH:146:GLY:H	1.45	0.64
8:LD:62:ILE:HG22	8:LD:63:THR:HG23	1.79	0.64
3:MK:87:GLN:HB3	3:MK:128:ARG:HH12	1.61	0.64
11:GM:288:ARG:NH2	11:GM:316:ASN:O	2.30	0.64
3:BK:115:THR:OG1	3:BK:183:THR:OG1	2.14	0.64
9:Cf:221:TRP:HE1	9:Cf:229:THR:HB	1.62	0.64
2:EH:190:PRO:HA	2:EH:211:ASN:HB3	1.79	0.64
8:Hd:55:MET:SD	10:CC:213:ARG:NH1	2.70	0.64
2:JH:341:LYS:HB2	2:JH:361:LEU:HD11	1.79	0.64
8:KD:87:TRP:CD1	8:KD:89:GLY:H	2.16	0.64
7:BX:22:UNK:HA	7:BX:77:UNK:HA	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:KC:48:LYS:O	1:MG:938:ASN:ND2	2.31	0.64
10:KC:56:ARG:HH12	10:KC:166:LEU:HD11	1.62	0.64
11:DM:190:ASN:OD1	11:DM:192:ARG:NH2	2.30	0.64
11:DM:201:THR:HG22	11:DM:221:LYS:HB2	1.79	0.64
1:HG:912:MET:HB3	1:HG:944:LEU:HB2	1.78	0.64
8:Dd:82:ARG:NH1	8:Dd:125:ASP:OD1	2.31	0.64
1:AG:911:LYS:HZ1	1:AG:913:VAL:HB	1.63	0.64
3:EK:90:ARG:NH1	3:EK:91:LEU:O	2.31	0.64
9:GF:219:ARG:HH22	2:HH:150:LYS:HG2	1.63	0.64
3:GK:91:LEU:HD21	3:GK:139:VAL:HG11	1.80	0.64
5:IN:85:CYS:N	10:DC:153:ASP:OD2	2.30	0.64
2:AH:143:ALA:O	2:BH:131:LYS:NZ	2.30	0.64
8:KD:158:TYR:O	8:Kd:137:TYR:OH	2.16	0.64
1:Lg:807:GLN:O	1:Lg:810:GLN:NE2	2.31	0.64
11:BM:279:ILE:HB	11:BM:298:VAL:HG22	1.78	0.64
8:Bd:97:ARG:HH21	10:KC:264:ARG:HE	1.43	0.64
1:GG:900:ILE:HD11	1:HG:865:THR:HG22	1.80	0.64
1:JG:919:MET:HG3	1:JG:930:ILE:HG23	1.79	0.64
9:Ef:217:PRO:O	9:Ef:219:ARG:NH2	2.31	0.64
9:Ff:233:ARG:HE	9:Ff:234:GLU:H	1.45	0.64
8:GD:35:ASP:OD2	8:GD:38:THR:N	2.29	0.64
2:HH:297:VAL:HG11	2:HH:302:ALA:HB3	1.79	0.64
8:Ld:60:LYS:NZ	8:Ld:61:VAL:O	2.29	0.64
1:FG:1003:ASN:HA	1:FG:1006:ILE:HD12	1.78	0.64
11:JM:160:ASN:H	11:JM:180:ASP:H	1.45	0.64
1:LG:878:ASN:HD22	1:LG:1030:GLU:HB2	1.62	0.64
2:FH:105:GLU:O	2:FH:109:LYS:NZ	2.27	0.64
6:GU:127:UNK:O	4:HL:232:GLN:NE2	2.31	0.64
1:CG:911:LYS:HB2	1:CG:943:ALA:HA	1.80	0.64
5:IN:46:GLY:O	5:IN:61:ASN:ND2	2.30	0.64
11:LM:275:ASP:HB3	11:LM:294:PHE:HB2	1.78	0.64
11:MM:119:GLU:HG3	11:MM:139:ALA:HB3	1.79	0.64
11:MM:306:GLN:NE2	11:MM:308:ASP:OD1	2.31	0.64
1:FG:899:LEU:HD21	1:FG:916:PHE:HB3	1.79	0.64
3:BK:116:VAL:HG22	3:BK:182:ILE:HG22	1.80	0.64
10:HC:260:GLU:N	10:HC:260:GLU:OE1	2.31	0.64
8:FD:77:TYR:OH	3:FK:130:ARG:NH1	2.30	0.64
2:FH:173:GLN:NE2	2:FH:218:THR:O	2.31	0.64
8:HD:39:ILE:HD13	8:Hd:37:ALA:HB2	1.80	0.64
2:IH:121:PRO:O	1:XG:797:ARG:NH2	2.29	0.64
3:KK:142:GLU:OE2	4:KL:139:ARG:NH1	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:XH:196:LEU:HD21	2:XH:202:PHE:HB2	1.80	0.64
10:DC:145:THR:HG23	10:DC:147:ARG:HE	1.63	0.64
1:OG:900:ILE:HG13	1:OG:918:THR:HB	1.78	0.64
9:CF:208:ILE:HD11	9:CF:224:GLY:HA3	1.80	0.64
2:CH:233:LEU:HD22	2:CH:235:THR:H	1.63	0.64
4:HL:115:GLN:HB3	4:HL:126:ILE:HB	1.80	0.64
2:KH:211:ASN:N	2:KH:211:ASN:OD1	2.30	0.64
11:BM:198:GLY:O	11:BM:219:ALA:HB3	1.98	0.64
3:CK:116:VAL:HG12	3:CK:182:ILE:HG12	1.80	0.64
9:Ff:253:ARG:NH2	11:FM:307:SER:OG	2.31	0.63
11:EM:273:ALA:HB1	11:EM:277:SER:HB2	1.80	0.63
9:BF:230:LEU:HA	2:BH:165:THR:HG21	1.79	0.63
8:DD:87:TRP:HD1	8:DD:89:GLY:H	1.46	0.63
3:DK:129:GLU:OE1	3:DK:129:GLU:N	2.31	0.63
1:NG:1018:GLN:OE1	1:OG:1020:GLN:NE2	2.31	0.63
9:AF:230:LEU:HA	2:AH:165:THR:HG21	1.78	0.63
8:HD:23:MET:N	8:HD:23:MET:SD	2.70	0.63
1:Bg:793:GLU:HB3	1:Bg:796:GLN:HE21	1.63	0.63
11:FM:115:ARG:NH1	11:FM:135:ASP:OD2	2.32	0.63
8:Cd:128:LEU:HD23	8:Cd:128:LEU:H	1.62	0.63
1:PG:931:SER:O	1:PG:1042:THR:OG1	2.16	0.63
1:BG:899:LEU:HD13	1:BG:919:MET:HG2	1.79	0.63
5:IN:71:THR:HG22	5:IN:73:HIS:H	1.63	0.63
2:JH:173:GLN:NE2	2:JH:217:ALA:O	2.31	0.63
3:MK:115:THR:OG1	3:MK:183:THR:OG1	2.16	0.63
11:BM:273:ALA:HB1	11:BM:277:SER:HB2	1.81	0.63
10:LC:125:ARG:HD3	2:DH:275:SER:HA	1.79	0.63
4:CL:165:VAL:HG12	4:CL:231:ILE:HG12	1.80	0.63
2:DH:173:GLN:NE2	2:DH:218:THR:O	2.29	0.63
1:Fg:818:GLN:NE2	2:FH:205:GLN:OE1	2.26	0.63
3:FK:166:THR:HG22	3:FK:168:TYR:H	1.64	0.63
5:GN:88:HIS:ND1	5:GN:105:ASP:OD2	2.30	0.63
11:HM:303:GLU:OE2	11:HM:306:GLN:NE2	2.31	0.63
8:Hd:76:ALA:HB3	8:Hd:79:LEU:HD23	1.80	0.63
9:IF:210:TYR:HA	9:IF:224:GLY:HA2	1.81	0.63
10:CC:146:THR:H	10:CC:149:GLN:HE22	1.45	0.63
10:CC:146:THR:OG1	10:CC:147:TRP:N	2.32	0.63
2:LH:108:ASP:OD1	2:LH:108:ASP:N	2.32	0.63
4:LL:141:ASN:HD21	4:LL:143:ILE:HB	1.62	0.63
2:VH:208:LYS:NZ	1:Dg:822:GLU:O	2.32	0.63
11:GM:138:LEU:HD11	11:GM:142:GLY:HA3	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CN:111:GLU:OE1	5:CN:111:GLU:N	2.30	0.63
1:KG:1003:ASN:HA	1:KG:1006:ILE:HD12	1.80	0.63
2:EH:230:LEU:HB2	2:EH:233:LEU:HB2	1.79	0.63
3:GK:146:SER:HB2	8:Gd:29:PRO:HG3	1.81	0.63
11:IM:157:ALA:O	11:IM:178:LYS:NZ	2.32	0.63
2:AH:230:LEU:HB2	2:AH:233:LEU:HB2	1.80	0.63
2:AH:280:LEU:HD13	2:AH:328:MET:HG3	1.80	0.63
11:KM:163:THR:HB	11:KM:183:VAL:HG12	1.80	0.63
9:Kf:237:LYS:HE2	9:Kf:242:GLY:HA2	1.80	0.63
11:JM:186:SER:HA	11:JM:205:TYR:HB2	1.80	0.63
10:LC:260:GLU:OE1	10:LC:260:GLU:N	2.32	0.63
10:MC:113:ARG:HG2	10:MC:129:ARG:HG2	1.79	0.63
3:CK:117:THR:HA	3:CK:157:GLN:O	1.99	0.63
1:OG:947:ARG:HE	1:OG:947:ARG:H	1.46	0.63
9:If:245:LYS:HE3	9:If:257:SER:HA	1.81	0.63
10:CC:109:VAL:HG13	10:CC:208:GLY:HA3	1.80	0.63
4:LL:165:VAL:HG12	4:LL:231:ILE:HG12	1.81	0.63
11:AM:208:LYS:NZ	9:Af:213:GLN:OE1	2.32	0.63
3:BK:87:GLN:HB3	3:BK:128:ARG:HH12	1.64	0.63
4:CL:161:SER:O	4:CL:202:ARG:NH2	2.31	0.63
8:DD:76:ALA:H	8:DD:79:LEU:HD12	1.64	0.63
4:DL:130:ASP:N	4:DL:130:ASP:OD1	2.31	0.63
4:EL:133:PHE:HA	4:EL:140:LEU:HA	1.79	0.63
11:IM:249:GLN:OE1	11:IM:267:ASN:ND2	2.31	0.63
2:JH:275:SER:HA	10:EC:126:ARG:HD3	1.81	0.63
8:KD:47:SER:OG	10:FC:204:LYS:NZ	2.31	0.63
2:ZH:159:ASN:OD1	2:ZH:257:GLN:NE2	2.31	0.63
11:BM:121:ALA:HA	11:BM:141:GLU:HB3	1.80	0.63
8:BD:87:TRP:CD1	8:BD:89:GLY:H	2.17	0.63
2:BH:318:THR:HB	2:BH:348:SER:HB3	1.80	0.63
2:CH:106:VAL:HA	2:CH:109:LYS:HE2	1.81	0.63
10:AC:111:LEU:HD23	10:AC:213:TYR:HB2	1.81	0.63
1:CG:872:VAL:HA	1:CG:1036:GLY:HA2	1.80	0.63
1:Jg:811:ASP:O	1:Jg:814:GLN:NE2	2.22	0.63
2:KH:108:ASP:N	2:KH:108:ASP:OD1	2.32	0.63
3:AK:130:ARG:NH1	8:AD:77:TYR:OH	2.32	0.63
11:MM:177:LEU:HD13	11:MM:181:PRO:HG2	1.79	0.63
1:EG:875:THR:HA	1:FG:940:ALA:HB1	1.81	0.63
11:AM:138:LEU:HD11	11:AM:142:GLY:HA3	1.81	0.63
11:JM:246:LEU:O	11:JM:264:SER:OG	2.16	0.63
1:GG:1042:THR:OG1	1:GG:1043:GLN:OE1	2.17	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:JC:32:LEU:O	10:JC:36:GLN:NE2	2.32	0.63
10:KC:127:ARG:HD3	2:CH:275:SER:HA	1.79	0.63
10:LC:151:TRP:HB3	5:DN:87:TRP:CZ3	2.33	0.63
2:DH:183:ASP:OD1	2:DH:187:ALA:N	2.30	0.63
2:EH:352:LYS:HG2	3:DK:152:ARG:HD2	1.80	0.63
8:Fd:71:LEU:O	8:Fd:133:ARG:NH1	2.32	0.63
11:HM:177:LEU:HD13	11:HM:181:PRO:HG2	1.80	0.63
1:EG:1006:ILE:O	1:EG:1010:THR:OG1	2.17	0.63
7:VX:70:UNK:H2	2:DH:146:GLY:HA2	1.64	0.63
4:AL:192:PHE:O	4:AL:196:ASN:ND2	2.29	0.63
8:BD:55:MET:HE2	10:JC:211:ILE:HD11	1.81	0.63
10:FC:103:GLU:HG2	10:FC:104:HIS:HD2	1.62	0.63
10:MC:100:LEU:HB2	10:MC:104:ILE:HG23	1.81	0.63
11:CM:302:ARG:HH11	11:CM:309:LEU:HD11	1.64	0.63
3:JK:142:GLU:OE2	4:JL:139:ARG:NH1	2.32	0.62
1:DG:871:ALA:HB2	1:DG:889:ILE:HD13	1.79	0.62
2:XH:280:LEU:HD23	2:XH:328:MET:HE2	1.80	0.62
11:BM:224:LEU:HB2	11:BM:246:LEU:HD22	1.80	0.62
1:JG:969:GLY:HA3	1:JG:1009:ALA:HB2	1.81	0.62
3:FK:92:ASN:O	3:FK:95:SER:OG	2.17	0.62
2:IH:274:PRO:O	10:DC:117:ASN:ND2	2.32	0.62
2:VH:203:ASN:N	2:VH:203:ASN:OD1	2.32	0.62
11:GM:120:GLY:H	11:GM:140:ASN:HB2	1.64	0.62
3:DK:50:ASP:N	3:DK:50:ASP:OD1	2.30	0.62
11:DM:261:ALA:HB1	11:DM:263:ILE:HD11	1.81	0.62
1:PG:969:GLY:HA3	1:PG:1009:ALA:HB2	1.79	0.62
1:BG:912:MET:HB3	1:BG:944:LEU:HB2	1.80	0.62
8:Gd:29:PRO:O	8:Gd:32:ASN:ND2	2.31	0.62
4:HL:191:THR:HG21	11:HM:289:ALA:HB3	1.80	0.62
8:Hd:29:PRO:HB2	8:Hd:32:ASN:HB2	1.80	0.62
2:KH:238:MET:N	2:KH:238:MET:SD	2.72	0.62
4:KL:113:ASP:N	4:KL:113:ASP:OD1	2.32	0.62
8:LD:107:ARG:NH2	8:LD:155:GLU:OE2	2.33	0.62
8:MD:39:ILE:HD12	4:ML:220:ILE:HG13	1.81	0.62
11:AM:117:ARG:HG2	11:AM:137:TYR:HB3	1.81	0.62
3:FK:73:ASN:OD1	3:FK:185:ARG:NH1	2.33	0.62
8:Hd:60:LYS:NZ	8:Hd:61:VAL:O	2.30	0.62
9:JF:219:ARG:HH12	9:JF:233:ARG:HH11	1.45	0.62
1:DG:912:MET:HB3	1:DG:944:LEU:HB2	1.80	0.62
8:LD:105:ARG:HB2	8:LD:153:VAL:HG22	1.80	0.62
8:CD:25:PHE:O	5:BN:62:ASN:ND2	2.28	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AN:77:ASP:OD1	5:AN:79:GLN:NE2	2.29	0.62
10:FC:195:ILE:O	10:FC:199:ASN:ND2	2.29	0.62
3:CK:129:GLU:N	3:CK:129:GLU:OE1	2.32	0.62
1:IG:946:SER:OG	1:IG:1030:GLU:O	2.14	0.62
1:KG:965:LEU:HG	1:KG:1008:LEU:HD23	1.81	0.62
1:BG:1003:ASN:HA	1:BG:1006:ILE:HD12	1.80	0.62
4:GL:216:ASP:OD1	4:GL:217:ASN:N	2.33	0.62
2:HH:322:PRO:HG2	2:HH:339:MET:HE1	1.81	0.62
3:HK:85:ALA:HB3	3:HK:88:SER:HB3	1.82	0.62
4:JL:63:ASP:O	4:JL:88:GLY:N	2.33	0.62
8:CD:27:LYS:NZ	3:BK:71:GLY:O	2.33	0.62
1:EG:1003:ASN:HA	1:EG:1006:ILE:HD12	1.81	0.62
2:XH:126:GLN:HA	2:XH:129:LYS:HE2	1.81	0.62
11:AM:249:GLN:OE1	11:AM:267:ASN:ND2	2.32	0.62
2:BH:235:THR:HG23	2:CH:251:ARG:HH21	1.64	0.62
4:BL:115:GLN:HB3	4:BL:126:ILE:HB	1.81	0.62
10:KC:115:ARG:HG2	10:KC:131:ARG:HG2	1.81	0.62
8:DD:39:ILE:HD12	4:DL:220:ILE:HG13	1.81	0.62
3:DK:142:GLU:OE2	4:DL:139:ARG:NH1	2.32	0.62
1:HG:1003:ASN:HA	1:HG:1006:ILE:HD12	1.82	0.62
1:NG:931:SER:O	1:NG:1042:THR:OG1	2.18	0.62
8:Fd:93:GLU:OE2	10:BC:265:ALA:N	2.32	0.62
4:HL:221:HIS:O	4:HL:225:GLN:NE2	2.33	0.62
1:Bg:807:GLN:HA	1:Bg:810:GLN:HE21	1.62	0.62
9:IF:238:ILE:HD12	9:IF:239:PRO:HD2	1.81	0.62
4:JL:49:ASN:ND2	11:JM:293:ALA:O	2.28	0.62
2:AH:211:ASN:OD1	2:AH:211:ASN:N	2.32	0.62
3:AK:109:PHE:O	3:AK:111:LYS:NZ	2.32	0.62
8:Ad:139:ALA:O	8:Ad:142:LYS:NZ	2.32	0.62
8:Dd:130:GLU:OE1	8:Dd:130:GLU:N	2.23	0.62
1:AG:968:PHE:HB3	1:AG:1008:LEU:HD13	1.82	0.62
9:AF:238:ILE:HB	9:AF:241:TYR:HB2	1.81	0.62
1:DG:969:GLY:HA3	1:DG:1009:ALA:HB2	1.80	0.62
4:ML:134:MET:N	4:ML:134:MET:SD	2.73	0.62
11:FM:131:THR:HG21	11:FM:134:LEU:HD23	1.82	0.62
5:BN:57:ARG:HH22	5:BN:67:THR:HA	1.65	0.62
10:JC:104:HIS:HB2	10:JC:106:ILE:HD11	1.82	0.62
8:DD:88:SER:HA	8:DD:120:SER:HA	1.80	0.62
1:PG:972:PHE:HB3	1:PG:1005:VAL:HG22	1.81	0.62
4:HL:230:GLU:OE2	4:HL:232:GLN:NE2	2.33	0.62
11:HM:275:ASP:HB3	11:HM:294:PHE:HB2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:IL:169:THR:HG21	4:IL:178:LYS:HB3	1.82	0.62
4:KL:166:ALA:HA	4:KL:206:GLU:O	1.98	0.62
9:VF:266:GLN:O	9:CF:233:ARG:NH2	2.33	0.62
9:XF:241:TYR:HB3	9:XF:256:THR:HG21	1.80	0.62
2:XH:183:ASP:HA	2:XH:256:VAL:HG12	1.82	0.62
11:GM:256:HIS:O	11:GM:277:SER:OG	2.17	0.62
1:KG:873:LEU:HB2	1:KG:1037:LEU:HD22	1.81	0.62
1:MG:931:SER:H	1:MG:1043:GLN:HE22	1.48	0.62
4:EL:44:HIS:HB2	4:EL:48:ASN:HA	1.81	0.62
5:FN:63:GLY:HA3	8:GD:27:LYS:HB2	1.82	0.62
1:CG:881:GLU:HG3	1:DG:911:LYS:HE2	1.81	0.62
1:DG:1003:ASN:HA	1:DG:1006:ILE:HD12	1.81	0.62
8:LD:36:ASP:OD2	10:GC:192:ASN:ND2	2.33	0.62
11:EM:311:ASP:OD1	11:EM:312:PHE:N	2.31	0.62
8:BD:140:GLY:O	8:Bd:60:LYS:NZ	2.32	0.62
4:CL:49:ASN:ND2	11:CM:293:ALA:O	2.33	0.62
1:KG:874:ASP:N	1:KG:874:ASP:OD1	2.33	0.62
4:IL:54:ARG:HH21	4:IL:56:ALA:H	1.48	0.62
11:IM:129:LEU:HB3	11:IM:150:ILE:HD11	1.82	0.62
9:KF:263:LYS:NZ	9:KF:264:PHE:O	2.33	0.62
11:AM:306:GLN:NE2	11:AM:308:ASP:OD1	2.32	0.62
10:IC:113:ARG:HG2	10:IC:129:ARG:HG2	1.81	0.62
8:DD:26:LYS:O	4:DL:115:GLN:NE2	2.33	0.62
2:EH:344:VAL:HG11	5:DN:87:TRP:NE1	2.15	0.61
3:IK:90:ARG:NH2	3:IK:92:ASN:OD1	2.33	0.61
10:CC:121:ASP:OD1	10:CC:124:SER:OG	2.16	0.61
8:Ld:132:LEU:HG	8:Ld:145:ILE:HD12	1.82	0.61
11:BM:128:ASN:O	11:BM:130:ARG:NH1	2.33	0.61
5:AN:62:ASN:OD1	5:AN:62:ASN:N	2.29	0.61
1:NG:900:ILE:HG13	1:NG:918:THR:HB	1.82	0.61
1:PG:871:ALA:HB2	1:PG:889:ILE:HD13	1.81	0.61
3:FK:90:ARG:HD3	11:FM:292:MET:HB2	1.82	0.61
9:AF:219:ARG:HH11	9:AF:233:ARG:HB3	1.63	0.61
1:Mg:792:GLN:O	1:Mg:795:GLN:NE2	2.30	0.61
2:MH:176:VAL:HG22	2:MH:216:GLN:HE21	1.64	0.61
3:MK:150:ASP:O	3:MK:152:ARG:NH1	2.32	0.61
4:AL:54:ARG:HH21	4:AL:57:VAL:HG23	1.64	0.61
2:YH:304:ALA:HB1	2:YH:311:MET:HE3	1.82	0.61
1:ZG:818:GLN:NE2	2:ZH:203:ASN:OD1	2.31	0.61
2:ZH:325:LEU:HB2	2:ZH:338:GLU:HG3	1.82	0.61
11:AM:275:ASP:HB3	11:AM:294:PHE:HB2	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:FC:262:GLU:N	10:FC:262:GLU:OE1	2.33	0.61
1:Ig:807:GLN:O	1:Ig:810:GLN:NE2	2.33	0.61
9:LF:223:ILE:HB	9:LF:229:THR:HG22	1.83	0.61
3:AK:129:GLU:N	3:AK:129:GLU:OE1	2.32	0.61
3:AK:179:ARG:NE	3:AK:181:GLU:OE2	2.33	0.61
10:FC:152:LEU:HD21	10:FC:203:ILE:HG21	1.81	0.61
10:FC:169:LYS:N	10:FC:173:GLU:OE2	2.27	0.61
10:KC:107:LEU:HD12	10:KC:108:PRO:HD2	1.82	0.61
4:CL:208:TYR:HB3	4:CL:211:LYS:HD3	1.80	0.61
8:Cd:76:ALA:HB3	8:Cd:79:LEU:HD13	1.82	0.61
8:DD:30:ILE:O	4:DL:131:LYS:NZ	2.31	0.61
2:DH:187:ALA:HB2	2:DH:264:LYS:HB2	1.81	0.61
5:DN:57:ARG:NH1	5:DN:66:SER:O	2.33	0.61
1:JG:871:ALA:HB2	1:JG:889:ILE:HD13	1.83	0.61
8:FD:42:ALA:HB2	8:Fd:41:LEU:HD22	1.82	0.61
9:Ff:218:GLY:H	9:Ff:247:ILE:HD11	1.65	0.61
8:GD:65:PRO:HB3	8:Gd:58:VAL:HG23	1.83	0.61
9:GF:210:TYR:HA	9:GF:224:GLY:HA2	1.81	0.61
3:HK:87:GLN:HB3	3:HK:128:ARG:HH12	1.65	0.61
2:KH:155:SER:OG	2:KH:255:ARG:NH1	2.33	0.61
3:LK:44:ARG:HD2	3:LK:48:ALA:HB3	1.82	0.61
2:XH:173:GLN:NE2	2:XH:218:THR:O	2.33	0.61
1:ZG:794:ILE:HG12	2:BH:107:ILE:HG13	1.81	0.61
10:EC:261:GLU:OE1	10:EC:261:GLU:N	2.33	0.61
4:CL:127:ILE:HB	4:CL:229:ILE:HB	1.81	0.61
2:DH:279:LEU:HD11	2:DH:289:PRO:HB3	1.82	0.61
1:JG:900:ILE:HD11	1:KG:865:THR:HG22	1.80	0.61
8:FD:86:ASP:OD2	3:FK:152:ARG:NH2	2.31	0.61
5:HN:88:HIS:ND1	5:HN:105:ASP:OD2	2.30	0.61
3:IK:87:GLN:NE2	3:IK:173:ASP:OD1	2.34	0.61
11:MM:249:GLN:OE1	11:MM:267:ASN:ND2	2.33	0.61
4:AL:226:ASN:O	4:AL:228:ARG:NH1	2.33	0.61
11:BM:306:GLN:HG3	11:BM:308:ASP:H	1.65	0.61
3:BK:83:LEU:HD12	3:BK:95:SER:HB2	1.82	0.61
10:FC:260:SER:HA	10:FC:263:TRP:CE2	2.34	0.61
10:HC:145:THR:OG1	10:HC:146:TRP:N	2.31	0.61
10:LC:248:ILE:H	10:MC:122:GLN:HB3	1.65	0.61
10:AC:142:ILE:HD11	10:AC:146:PRO:HD3	1.82	0.61
4:EL:124:THR:HA	4:EL:231:ILE:O	2.01	0.61
9:LF:207:ARG:NH1	9:LF:240:GLY:O	2.34	0.61
2:VH:151:PRO:HB2	2:CH:166:PRO:HG3	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:XF:254:ILE:HB	9:XF:262:ILE:HB	1.83	0.61
11:EM:306:GLN:NE2	11:EM:308:ASP:OD1	2.29	0.61
11:FM:273:ALA:HB1	11:FM:277:SER:HB2	1.81	0.61
1:Cg:823:GLY:HA3	2:BH:208:LYS:HD2	1.82	0.61
10:EC:106:LEU:HD12	10:EC:107:PRO:HD2	1.82	0.61
10:IC:148:GLN:OE1	10:IC:148:GLN:N	2.34	0.61
1:Dg:811:ASP:O	1:Dg:814:GLN:NE2	2.32	0.61
5:DN:111:GLU:OE1	5:DN:111:GLU:N	2.32	0.61
1:HG:955:ARG:NH1	1:HG:1023:PHE:O	2.34	0.61
1:IG:969:GLY:HA3	1:IG:1009:ALA:HB2	1.82	0.61
1:JG:951:HIS:H	1:JG:1027:THR:HG22	1.65	0.61
1:OG:1030:GLU:OE2	1:PG:941:ARG:NH2	2.33	0.61
8:FD:62:ILE:HG23	8:FD:63:THR:HG23	1.83	0.61
3:GK:87:GLN:N	3:GK:173:ASP:OD2	2.32	0.61
4:GL:226:ASN:OD1	4:GL:227:ARG:N	2.34	0.61
3:JK:116:VAL:HG22	3:JK:182:ILE:HG22	1.82	0.61
3:AK:76:ILE:HB	3:AK:182:ILE:HG23	1.82	0.61
9:Mf:221:TRP:HE1	9:Mf:229:THR:HB	1.64	0.61
9:WF:238:ILE:HD12	9:WF:239:PRO:HD2	1.83	0.61
11:AM:159:GLY:HA2	11:AM:181:PRO:HG3	1.83	0.61
2:BH:183:ASP:OD1	2:BH:187:ALA:N	2.33	0.61
10:KC:223:SER:OG	10:KC:255:GLU:OE2	2.17	0.61
2:EH:157:PHE:HE1	2:EH:257:GLN:HG2	1.66	0.61
3:EK:92:ASN:O	3:EK:95:SER:OG	2.18	0.61
2:FH:273:PRO:O	10:AC:127:ARG:NH1	2.33	0.61
3:FK:185:ARG:HH22	4:GL:215:SER:HA	1.65	0.61
9:IF:246:LEU:HD13	9:IF:255:LEU:HD12	1.83	0.61
3:IK:53:ILE:HG12	3:IK:108:GLN:HG2	1.82	0.61
4:KL:129:THR:O	4:KL:133:PHE:HB2	2.01	0.61
8:Kd:139:ALA:O	8:Kd:142:LYS:NZ	2.33	0.61
4:LL:192:PHE:O	4:LL:196:ASN:ND2	2.23	0.61
8:Ld:148:TYR:HB2	8:Ld:153:VAL:HG12	1.82	0.61
9:VF:210:TYR:HA	9:VF:224:GLY:HA2	1.82	0.61
10:DC:105:LEU:HD12	10:DC:106:PRO:HD2	1.82	0.61
9:ZF:230:LEU:HA	2:ZH:165:THR:HG21	1.83	0.61
11:JM:163:THR:HB	11:JM:183:VAL:HG12	1.82	0.61
4:BL:125:LEU:HD23	4:BL:233:TRP:HZ3	1.65	0.61
10:HC:248:ILE:HG12	10:IC:122:GLN:HG2	1.83	0.61
10:KC:169:LYS:H	10:KC:173:GLU:HG3	1.65	0.61
1:HG:935:ILE:HG22	1:HG:942:THR:HG22	1.83	0.61
1:IG:869:MET:HG2	1:IG:889:ILE:HD12	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Eg:806:THR:O	1:Eg:810:GLN:NE2	2.34	0.61
10:BC:83:GLN:O	10:BC:87:GLN:NE2	2.34	0.61
1:BG:931:SER:O	1:BG:1042:THR:OG1	2.19	0.61
9:HF:230:LEU:HA	2:HH:165:THR:HG21	1.81	0.61
8:Ld:98:ILE:HD11	8:Ld:128:LEU:HD22	1.82	0.61
2:VH:292:SER:HB2	2:VH:305:TRP:HB3	1.83	0.61
9:CF:245:LYS:NZ	9:CF:256:THR:O	2.27	0.61
2:XH:183:ASP:OD1	2:XH:187:ALA:N	2.30	0.61
11:JM:273:ALA:HB1	11:JM:277:SER:HB2	1.83	0.61
5:AN:49:ASN:HD21	5:AN:61:ASN:HA	1.65	0.61
5:AN:92:TYR:HD1	5:AN:94:GLN:H	1.48	0.61
8:Ad:137:TYR:OH	8:AD:158:TYR:O	2.18	0.61
10:HC:146:TRP:HB2	10:HC:150:LEU:HD23	1.83	0.61
10:LC:147:ARG:HG3	5:DN:87:TRP:CE3	2.36	0.61
5:DN:63:GLY:HA3	8:ED:27:LYS:HB2	1.82	0.61
1:LG:1006:ILE:O	1:LG:1010:THR:OG1	2.19	0.61
4:EL:166:ALA:HA	4:EL:206:GLU:O	1.99	0.61
11:HM:281:TYR:CZ	11:HM:300:ASP:HA	2.36	0.61
8:Ld:136:ASP:HB2	8:Ld:145:ILE:HD11	1.81	0.61
9:YF:210:TYR:HA	9:YF:224:GLY:HA2	1.83	0.61
11:FM:214:ILE:HB	11:FM:233:VAL:HG12	1.82	0.61
10:FC:61:LYS:HD2	10:FC:180:TYR:HE2	1.66	0.61
10:GC:261:GLU:OE1	10:GC:261:GLU:N	2.34	0.61
10:MC:260:GLU:N	10:MC:260:GLU:OE1	2.33	0.61
4:CL:177:HIS:ND1	11:CM:315:TYR:OH	2.29	0.61
1:NG:912:MET:HB3	1:NG:944:LEU:HB2	1.81	0.61
9:FF:245:LYS:NZ	9:FF:256:THR:O	2.33	0.60
8:Fd:82:ARG:NH2	8:Fd:126:GLU:H	1.99	0.60
8:HD:91:ILE:HD11	8:HD:156:LEU:HD11	1.83	0.60
5:KN:89:GLY:HA3	5:KN:104:ASN:HB2	1.83	0.60
11:LM:177:LEU:HD13	11:LM:181:PRO:HG2	1.83	0.60
1:Mg:818:GLN:NE2	2:MH:203:ASN:OD1	2.20	0.60
8:Md:78:ASN:OD1	8:Md:78:ASN:N	2.33	0.60
2:WH:183:ASP:OD1	2:WH:187:ALA:N	2.33	0.60
2:CH:159:ASN:OD1	2:CH:257:GLN:NE2	2.33	0.60
10:AC:115:ARG:HG2	10:AC:131:ARG:HG2	1.83	0.60
5:EN:49:ASN:HB3	5:EN:59:VAL:HG23	1.83	0.60
8:Ed:149:PRO:O	8:Ed:152:GLN:NE2	2.34	0.60
4:FL:230:GLU:OE2	4:FL:232:GLN:NE2	2.27	0.60
4:JL:150:ASN:OD1	4:JL:153:ARG:NH2	2.30	0.60
5:JN:57:ARG:NH1	5:JN:66:SER:O	2.33	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:MD:87:TRP:CD1	8:MD:89:GLY:H	2.19	0.60
11:JM:193:GLN:NE2	11:JM:195:ASP:OD1	2.28	0.60
4:BL:190:MET:HE1	4:BL:203:LEU:HB3	1.83	0.60
2:CH:188:PRO:O	2:CH:262:ASN:ND2	2.34	0.60
8:FD:92:GLU:OE1	8:FD:93:GLU:N	2.34	0.60
3:FK:115:THR:HB	3:FK:183:THR:HG23	1.83	0.60
5:FN:87:TRP:O	5:FN:88:HIS:ND1	2.34	0.60
5:JN:101:VAL:HG12	5:JN:113:SER:HB2	1.82	0.60
4:LL:44:HIS:HB2	4:LL:48:ASN:HA	1.82	0.60
11:LM:249:GLN:OE1	11:LM:267:ASN:ND2	2.34	0.60
10:DC:258:SER:HA	10:DC:261:TRP:CE2	2.36	0.60
1:FG:876:SER:OG	1:FG:1031:VAL:O	2.20	0.60
5:BN:57:ARG:NH1	5:BN:68:CYS:O	2.34	0.60
10:LC:220:VAL:HG12	10:LC:254:LEU:HD23	1.83	0.60
3:CK:92:ASN:O	3:CK:95:SER:OG	2.19	0.60
1:IG:912:MET:HB3	1:IG:944:LEU:HB2	1.82	0.60
1:JG:899:LEU:HD13	1:JG:919:MET:HG2	1.83	0.60
1:MG:1003:ASN:HA	1:MG:1006:ILE:HD12	1.83	0.60
8:HD:29:PRO:HG2	4:HL:225:GLN:HG3	1.82	0.60
3:IK:76:ILE:HD12	3:IK:102:ILE:HD11	1.83	0.60
11:IM:194:LEU:HD11	11:IM:196:MET:HE3	1.82	0.60
1:CG:949:ASN:HA	1:CG:952:TYR:HE2	1.66	0.60
11:MM:257:ASP:OD1	11:MM:257:ASP:N	2.29	0.60
2:XH:320:LEU:HD11	2:XH:348:SER:HB2	1.82	0.60
2:YH:183:ASP:HA	2:YH:256:VAL:HB	1.84	0.60
1:FG:937:PRO:HD3	1:FG:1037:LEU:HA	1.84	0.60
11:EM:177:LEU:HD13	11:EM:181:PRO:HG2	1.84	0.60
10:FC:47:GLN:HA	10:FC:50:GLN:HG2	1.82	0.60
2:CH:155:SER:OG	2:CH:255:ARG:NH1	2.34	0.60
2:EH:266:MET:SD	2:EH:266:MET:N	2.73	0.60
1:BG:968:PHE:HB3	1:BG:1008:LEU:HD13	1.84	0.60
5:JN:47:GLY:O	5:JN:61:ASN:N	2.32	0.60
5:JN:109:SER:OG	5:JN:111:GLU:OE1	2.19	0.60
5:BN:77:ASP:OD1	5:BN:79:GLN:NE2	2.34	0.60
10:FC:90:ASN:OD1	10:FC:90:ASN:N	2.33	0.60
2:DH:189:TRP:HE1	2:DH:232:GLY:H	1.49	0.60
1:HG:876:SER:OG	1:HG:1031:VAL:O	2.20	0.60
8:ED:130:GLU:OE2	8:ED:133:ARG:NH1	2.33	0.60
5:EN:88:HIS:ND1	5:EN:105:ASP:OD2	2.35	0.60
2:FH:359:GLU:OE1	2:FH:359:GLU:N	2.33	0.60
9:Hf:209:ILE:O	9:Hf:225:SER:OG	2.20	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:IM:145:ARG:HH22	11:IM:166:ASN:HB2	1.66	0.60
3:KK:166:THR:HG22	3:KK:168:TYR:H	1.67	0.60
5:AN:86:LEU:HB3	5:AN:87:TRP:HE3	1.66	0.60
10:EC:121:ASP:OD1	10:EC:124:SER:OG	2.20	0.60
10:GC:147:TRP:HB2	10:GC:151:LEU:HD23	1.84	0.60
10:IC:156:LYS:NZ	10:IC:157:PRO:O	2.34	0.60
10:LC:60:GLU:HA	10:LC:63:LEU:HD23	1.81	0.60
1:Dg:818:GLN:NE2	2:DH:205:GLN:OE1	2.34	0.60
4:DL:210:ASP:OD1	4:DL:210:ASP:N	2.31	0.60
10:BC:169:LYS:H	10:BC:173:GLU:HG3	1.65	0.60
2:IH:216:GLN:NE2	2:IH:217:ALA:O	2.27	0.60
2:MH:182:LEU:HB2	2:MH:255:ARG:HD3	1.84	0.60
8:FD:130:GLU:OE2	8:FD:133:ARG:NH1	2.34	0.60
8:HD:86:ASP:OD1	10:CC:88:ARG:NH1	2.34	0.60
11:IM:288:ARG:NH2	11:IM:316:ASN:O	2.35	0.60
4:LL:208:TYR:HB3	4:LL:211:LYS:HD3	1.82	0.60
3:AK:71:GLY:O	8:BD:27:LYS:NZ	2.30	0.60
2:MH:174:GLY:N	2:MH:217:ALA:O	2.35	0.60
11:AM:181:PRO:O	11:AM:201:THR:OG1	2.20	0.60
9:Bf:219:ARG:HA	9:Bf:232:VAL:O	2.02	0.60
1:GG:1003:ASN:HA	1:GG:1006:ILE:HD12	1.83	0.60
2:FH:117:ARG:HH22	1:Eg:797:ARG:HD3	1.67	0.60
2:FH:160:LEU:O	2:WH:251:ARG:NH2	2.35	0.60
4:JL:113:ASP:OD1	4:JL:113:ASP:N	2.33	0.60
4:JL:221:HIS:ND1	4:JL:225:GLN:OE1	2.34	0.60
5:JN:46:GLY:O	5:JN:61:ASN:ND2	2.33	0.60
3:LK:92:ASN:OD1	3:LK:92:ASN:N	2.32	0.60
3:AK:106:LEU:O	3:AK:111:LYS:NZ	2.35	0.60
11:MM:200:GLY:O	11:MM:221:LYS:NZ	2.34	0.60
9:WF:208:ILE:O	9:WF:241:TYR:OH	2.19	0.60
7:BX:15:UNK:O	7:CX:1:UNK:N	2.34	0.60
1:PG:937:PRO:HD3	1:PG:1037:LEU:HA	1.84	0.60
10:AC:116:ASN:HD21	8:ED:114:SER:HA	1.67	0.60
8:FD:93:GLU:N	8:FD:93:GLU:OE1	2.35	0.60
8:Hd:71:LEU:O	8:Hd:133:ARG:NH1	2.34	0.60
8:MD:126:GLU:OE1	8:MD:127:SER:N	2.34	0.60
1:EG:937:PRO:HD3	1:EG:1037:LEU:HA	1.83	0.60
2:ZH:352:LYS:NZ	2:ZH:354:MET:SD	2.75	0.60
11:EM:249:GLN:OE1	11:EM:267:ASN:ND2	2.35	0.60
8:DD:123:THR:OG1	8:DD:124:LYS:N	2.35	0.60
9:EF:222:LEU:HD11	9:EF:232:VAL:HG22	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:Ff:243:MET:O	9:Ff:257:SER:N	2.34	0.59
1:Gg:797:ARG:NH1	1:Gg:800:ASP:OD1	2.34	0.59
1:Gg:807:GLN:O	1:Gg:810:GLN:NE2	2.34	0.59
1:CG:931:SER:O	1:CG:1042:THR:OG1	2.19	0.59
3:JK:130:ARG:NH1	3:JK:162:ASP:OD2	2.35	0.59
8:Md:60:LYS:NZ	8:Md:61:VAL:O	2.34	0.59
4:AL:220:ILE:HG13	8:AD:39:ILE:HD12	1.84	0.59
2:YH:183:ASP:OD1	2:YH:187:ALA:N	2.34	0.59
11:AM:141:GLU:OE2	11:AM:143:THR:OG1	2.20	0.59
11:AM:158:VAL:HA	11:AM:178:LYS:HZ3	1.66	0.59
11:FM:172:ASN:OD1	11:FM:173:LEU:N	2.35	0.59
10:LC:101:GLU:O	8:DD:142:LYS:NZ	2.34	0.59
11:CM:199:LYS:HA	11:CM:219:ALA:HB3	1.83	0.59
1:LG:871:ALA:HB2	1:LG:889:ILE:HD13	1.84	0.59
10:BC:249:ARG:NH2	2:HH:271:GLY:O	2.36	0.59
8:HD:98:ILE:HG21	8:HD:132:LEU:HD11	1.84	0.59
4:HL:54:ARG:HH22	4:HL:56:ALA:HB3	1.66	0.59
4:IL:150:ASN:OD1	4:IL:153:ARG:NH2	2.35	0.59
1:Jg:791:GLN:N	1:Jg:793:GLU:OE1	2.35	0.59
3:JK:129:GLU:OE1	3:JK:129:GLU:N	2.35	0.59
3:AK:85:ALA:HB3	3:AK:88:SER:HB2	1.83	0.59
9:CF:207:ARG:NH1	9:CF:208:ILE:O	2.35	0.59
1:OG:931:SER:O	1:OG:1042:THR:OG1	2.19	0.59
1:OG:951:HIS:H	1:OG:1027:THR:HG22	1.67	0.59
2:EH:115:MET:HG2	1:VG:801:MET:HG3	1.84	0.59
5:FN:62:ASN:OD1	5:FN:62:ASN:N	2.34	0.59
10:BC:98:ASN:ND2	8:GD:118:LEU:O	2.35	0.59
8:BD:29:PRO:HG2	4:BL:225:GLN:HA	1.83	0.59
9:Bf:238:ILE:HG13	9:Bf:241:TYR:HB2	1.85	0.59
10:LC:107:PRO:HD3	10:LC:137:ALA:HB2	1.83	0.59
1:IG:898:LYS:HE2	1:JG:867:ASP:HB3	1.84	0.59
1:KG:972:PHE:O	1:KG:976:ASN:ND2	2.35	0.59
3:EK:116:VAL:HG22	3:EK:182:ILE:HG22	1.84	0.59
10:EC:188:ILE:O	10:EC:192:ASN:ND2	2.35	0.59
1:GG:1024:ASN:OD1	1:GG:1024:ASN:N	2.28	0.59
10:HC:243:ASP:OD2	10:IC:125:ARG:NH2	2.32	0.59
10:JC:260:SER:HA	10:JC:263:TRP:CE2	2.37	0.59
8:DD:86:ASP:OD2	3:DK:152:ARG:NH2	2.35	0.59
4:DL:219:ILE:HG22	4:DL:222:GLY:H	1.66	0.59
1:IG:972:PHE:O	1:IG:976:ASN:ND2	2.35	0.59
1:MG:871:ALA:HB2	1:MG:889:ILE:HD13	1.82	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:EL:173:GLY:O	4:EL:178:LYS:NZ	2.31	0.59
1:CG:898:LYS:NZ	1:DG:865:THR:O	2.34	0.59
5:JN:87:TRP:HD1	2:KH:344:VAL:HG21	1.66	0.59
8:CD:73:ILE:O	8:CD:133:ARG:NH2	2.35	0.59
3:AK:47:GLY:O	3:AK:108:GLN:NE2	2.23	0.59
3:MK:75:LEU:HD12	3:MK:183:THR:HG22	1.85	0.59
10:AC:262:GLU:OE1	10:AC:262:GLU:N	2.35	0.59
11:HM:210:ASP:HA	11:HM:229:ASN:H	1.67	0.59
6:KU:127:UNK:O	4:LL:232:GLN:NE2	2.35	0.59
2:LH:289:PRO:HG2	2:LH:292:SER:HB3	1.84	0.59
8:MD:105:ARG:HB3	8:MD:153:VAL:HG12	1.84	0.59
11:MM:199:LYS:HA	11:MM:219:ALA:HB3	1.84	0.59
2:ZH:207:ASP:OD1	2:ZH:207:ASP:N	2.28	0.59
10:EC:146:THR:HG23	10:EC:148:ARG:HB3	1.83	0.59
8:Ed:66:SER:OG	8:Ed:67:LYS:NZ	2.36	0.59
10:BC:107:LEU:HD12	10:BC:108:PRO:HD2	1.84	0.59
1:Gg:811:ASP:O	1:Gg:814:GLN:NE2	2.20	0.59
5:IN:87:TRP:CD1	10:DC:147:ARG:HD3	2.37	0.59
8:Jd:73:ILE:HG22	8:Jd:75:ASN:H	1.67	0.59
4:KL:208:TYR:HB3	4:KL:211:LYS:HE2	1.85	0.59
2:LH:189:TRP:HE1	2:LH:232:GLY:H	1.50	0.59
11:FM:311:ASP:OD1	11:FM:312:PHE:N	2.31	0.59
10:EC:109:VAL:HG13	10:EC:208:GLY:HA3	1.84	0.59
1:PG:876:SER:OG	1:PG:1031:VAL:O	2.18	0.59
8:ED:23:MET:N	8:ED:23:MET:SD	2.76	0.59
1:AG:899:LEU:HD13	1:AG:919:MET:HG2	1.84	0.59
11:KM:249:GLN:OE1	11:KM:267:ASN:ND2	2.36	0.59
1:DG:931:SER:O	1:DG:1042:THR:OG1	2.19	0.59
8:LD:124:LYS:HZ1	3:LK:145:TRP:CD1	2.20	0.59
2:LH:274:PRO:O	10:GC:118:ASN:ND2	2.36	0.59
2:YH:200:SER:OG	2:YH:219:LYS:NZ	2.36	0.59
1:GG:951:HIS:O	1:GG:955:ARG:NE	2.33	0.59
1:OG:1042:THR:OG1	1:OG:1043:GLN:OE1	2.19	0.59
1:Gg:794:ILE:O	1:Gg:798:THR:N	2.31	0.59
9:HF:245:LYS:HE3	9:HF:257:SER:HA	1.84	0.59
2:JH:225:ASN:HD21	2:KH:176:VAL:HB	1.68	0.59
3:KK:87:GLN:N	3:KK:173:ASP:OD2	2.34	0.59
5:KN:88:HIS:ND1	5:KN:105:ASP:OD2	2.36	0.59
9:Kf:258:SER:OG	9:Kf:260:GLN:NE2	2.36	0.59
8:MD:97:ARG:HH21	3:MK:112:ILE:HG12	1.68	0.59
2:MH:107:ILE:HG23	1:YG:794:ILE:HG23	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:DC:111:GLU:HG3	10:DC:131:TYR:CZ	2.37	0.59
11:AM:214:ILE:HB	11:AM:233:VAL:HG12	1.85	0.59
11:EM:279:ILE:HB	11:EM:298:VAL:HG22	1.85	0.59
8:Bd:130:GLU:OE1	8:Bd:130:GLU:N	2.27	0.59
5:CN:88:HIS:ND1	5:CN:105:ASP:OD2	2.36	0.59
8:DD:87:TRP:CD1	8:DD:89:GLY:H	2.21	0.59
4:DL:124:THR:HG22	4:DL:232:GLN:HG2	1.84	0.59
4:EL:130:ASP:N	4:EL:130:ASP:OD1	2.35	0.59
9:FF:241:TYR:HB3	9:FF:256:THR:HG21	1.84	0.59
2:LH:178:SER:OG	2:YH:238:MET:SD	2.58	0.59
9:MF:213:GLN:O	2:MH:170:ARG:NH1	2.36	0.59
10:JC:107:LEU:HD12	10:JC:108:PRO:HD2	1.85	0.59
10:JC:259:ASN:N	10:JC:259:ASN:OD1	2.30	0.59
10:LC:113:ARG:H	2:DH:328:MET:HE1	1.68	0.59
8:ED:87:TRP:CD1	8:ED:89:GLY:H	2.21	0.59
2:EH:256:VAL:HG12	2:EH:258:GLY:H	1.67	0.58
8:Fd:149:PRO:O	8:Fd:152:GLN:NE2	2.32	0.58
11:HM:199:LYS:HA	11:HM:219:ALA:HB3	1.85	0.58
11:HM:256:HIS:O	11:HM:259:SER:OG	2.20	0.58
8:LD:114:SER:HA	10:HC:114:ASN:HD21	1.67	0.58
11:MM:172:ASN:OD1	11:MM:192:ARG:NH2	2.36	0.58
11:GM:312:PHE:HB2	11:GM:317:LYS:HE2	1.84	0.58
11:JM:276:ALA:H	11:JM:295:ASN:HB2	1.68	0.58
1:Cg:817:THR:OG1	1:Cg:818:GLN:N	2.36	0.58
9:Af:245:LYS:NZ	9:Af:256:THR:O	2.34	0.58
2:BH:167:PRO:HB2	2:BH:239:LEU:HD23	1.85	0.58
8:GD:39:ILE:HD13	8:Gd:37:ALA:HB2	1.85	0.58
9:HF:207:ARG:NH1	9:HF:240:GLY:O	2.33	0.58
1:Bg:802:LEU:HD22	2:VH:115:MET:HG2	1.84	0.58
2:IH:313:VAL:HG22	2:IH:337:TYR:HB2	1.85	0.58
11:IM:205:TYR:OH	9:If:219:ARG:NH2	2.35	0.58
8:JD:140:GLY:O	8:Jd:60:LYS:NZ	2.30	0.58
1:Kg:801:MET:HE3	2:YH:122:LEU:HD21	1.85	0.58
3:LK:115:THR:HB	3:LK:183:THR:HG23	1.83	0.58
4:ML:216:ASP:OD1	4:ML:217:ASN:N	2.36	0.58
11:MM:300:ASP:OD2	11:MM:302:ARG:NE	2.33	0.58
8:Md:119:ILE:HD12	8:Md:135:ILE:HD12	1.84	0.58
8:BD:158:TYR:O	8:Bd:137:TYR:OH	2.19	0.58
10:KC:244:ASP:OD1	10:KC:245:ASP:N	2.35	0.58
11:CM:124:VAL:HB	11:CM:144:THR:HG23	1.84	0.58
1:KG:1006:ILE:O	1:KG:1010:THR:OG1	2.20	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:EH:170:ARG:NH1	9:EF:213:GLN:O	2.34	0.58
3:FK:71:GLY:O	8:GD:27:LYS:NZ	2.36	0.58
2:GH:179:LEU:O	2:GH:212:THR:HA	2.03	0.58
3:HK:75:LEU:HD12	3:HK:183:THR:HG22	1.85	0.58
11:HM:249:GLN:NE2	11:HM:267:ASN:OD1	2.36	0.58
3:IK:49:CYS:O	3:IK:52:THR:OG1	2.17	0.58
2:YH:180:VAL:HG13	2:YH:253:ASP:HA	1.85	0.58
1:FG:955:ARG:NH1	1:FG:1023:PHE:O	2.36	0.58
8:BD:72:THR:HG23	8:BD:73:ILE:HG12	1.85	0.58
2:BH:108:ASP:OD1	2:BH:108:ASP:N	2.35	0.58
1:GG:972:PHE:HB3	1:GG:1005:VAL:HG22	1.84	0.58
1:KG:900:ILE:HG13	1:KG:918:THR:HB	1.85	0.58
3:EK:87:GLN:OE1	3:EK:128:ARG:NH1	2.35	0.58
5:EN:57:ARG:NH1	5:EN:66:SER:O	2.37	0.58
4:FL:116:TYR:OH	4:FL:118:GLU:OE1	2.21	0.58
9:GF:245:LYS:NZ	9:GF:256:THR:O	2.33	0.58
11:HM:242:LYS:HA	11:HM:262:GLU:HB2	1.86	0.58
1:CG:1003:ASN:HA	1:CG:1006:ILE:HD12	1.84	0.58
1:DG:1042:THR:OG1	1:DG:1043:GLN:OE1	2.20	0.58
2:LH:159:ASN:HA	2:LH:257:GLN:HE21	1.67	0.58
4:LL:226:ASN:O	4:LL:228:ARG:NH1	2.35	0.58
2:BH:191:ILE:HG13	2:BH:211:ASN:HA	1.85	0.58
5:BN:47:GLY:O	5:BN:61:ASN:N	2.34	0.58
9:DF:245:LYS:NZ	9:DF:256:THR:O	2.32	0.58
2:FH:256:VAL:HG22	2:FH:258:GLY:H	1.69	0.58
9:XF:233:ARG:HG2	9:XF:236:SER:HB2	1.86	0.58
1:YG:791:GLN:N	1:YG:793:GLU:OE1	2.36	0.58
10:GC:231:LEU:HB2	10:GC:244:ASP:HB3	1.85	0.58
10:LC:145:THR:OG1	10:LC:146:TRP:N	2.35	0.58
10:BC:89:ARG:NH1	10:BC:92:ASP:OD2	2.37	0.58
2:GH:131:LYS:NZ	2:WH:143:ALA:O	2.31	0.58
8:ID:31:ASN:OD1	8:ID:31:ASN:N	2.36	0.58
2:IH:238:MET:HB2	2:JH:250:TYR:CZ	2.38	0.58
11:IM:279:ILE:HB	11:IM:298:VAL:HG22	1.85	0.58
8:LD:82:ARG:HH21	8:LD:126:GLU:HA	1.69	0.58
4:ML:137:SER:HB2	4:ML:139:ARG:HG3	1.84	0.58
1:FG:969:GLY:HA3	1:FG:1009:ALA:HB2	1.84	0.58
8:Cd:73:ILE:HG22	8:Cd:75:ASN:H	1.69	0.58
8:FD:73:ILE:HG13	8:FD:147:VAL:HB	1.84	0.58
1:Ig:811:ASP:O	1:Ig:814:GLN:NE2	2.28	0.58
11:IM:308:ASP:N	11:IM:308:ASP:OD1	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Md:139:ALA:HB1	8:Md:143:ALA:HB3	1.86	0.58
11:AM:313:ASP:HB2	11:AM:316:ASN:HD21	1.67	0.58
11:FM:313:ASP:HB2	11:FM:316:ASN:HD21	1.68	0.58
7:BX:20:UNK:HA	7:BX:79:UNK:HA	1.86	0.58
2:DH:292:SER:HB3	2:DH:307:SER:HB3	1.84	0.58
9:Ff:253:ARG:NH2	11:FM:308:ASP:OD1	2.37	0.58
3:GK:50:ASP:N	3:GK:50:ASP:OD1	2.37	0.58
9:WF:263:LYS:NZ	9:WF:264:PHE:O	2.36	0.58
2:WH:332:ASP:OD1	2:WH:332:ASP:N	2.31	0.58
9:YF:243:MET:O	9:YF:257:SER:N	2.35	0.58
10:DC:244:ARG:HB3	10:EC:127:ILE:HG23	1.86	0.58
4:BL:138:PRO:HB2	4:BL:188:THR:HG21	1.83	0.58
10:IC:225:VAL:HB	10:IC:248:ILE:HG22	1.86	0.58
8:AD:87:TRP:CD1	8:AD:89:GLY:H	2.22	0.58
8:ED:124:LYS:HE3	8:ED:125:ASP:HB2	1.86	0.58
8:FD:158:TYR:O	8:Fd:137:TYR:OH	2.21	0.58
3:HK:44:ARG:HB2	5:HN:67:THR:HG22	1.86	0.58
4:JL:130:ASP:N	4:JL:130:ASP:OD1	2.35	0.58
10:CC:162:ASN:ND2	1:DG:890:VAL:O	2.36	0.58
4:KL:125:LEU:HD23	4:KL:233:TRP:HH2	1.68	0.58
9:LF:208:ILE:HD11	9:LF:224:GLY:HA3	1.84	0.58
3:AK:67:VAL:HG12	3:AK:76:ILE:HG12	1.85	0.58
8:MD:158:TYR:O	8:Md:137:TYR:OH	2.20	0.58
1:Cg:807:GLN:O	1:Cg:810:GLN:NE2	2.37	0.58
5:BN:86:LEU:HB3	5:BN:87:TRP:HE3	1.69	0.58
10:KC:127:ARG:NH1	2:CH:273:PRO:O	2.37	0.58
1:LG:874:ASP:OD1	1:LG:874:ASP:N	2.34	0.58
1:MG:1006:ILE:O	1:MG:1010:THR:OG1	2.22	0.58
1:AG:931:SER:H	1:AG:1043:GLN:HE22	1.52	0.58
10:BC:47:GLN:HA	10:BC:50:GLN:HE21	1.69	0.58
2:IH:238:MET:HB2	2:JH:250:TYR:CE1	2.39	0.58
11:KM:302:ARG:HH11	11:KM:309:LEU:HD11	1.69	0.58
5:KN:110:GLU:OE2	10:FC:191:GLN:NE2	2.37	0.58
3:AK:114:ILE:HD13	3:AK:184:PHE:HB3	1.85	0.58
9:XF:219:ARG:NH1	9:XF:233:ARG:HB3	2.19	0.58
2:YH:357:LYS:NZ	2:YH:358:VAL:O	2.37	0.58
10:FC:107:LEU:HD12	10:FC:108:PRO:HD2	1.86	0.58
10:IC:162:VAL:HB	10:IC:165:LEU:HD21	1.86	0.58
2:DH:184:SER:O	2:DH:255:ARG:NH2	2.37	0.58
11:DM:172:ASN:OD1	11:DM:173:LEU:N	2.36	0.58
10:BC:128:ILE:HG12	10:AC:246:ARG:HB2	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Hg:818:GLN:NE2	2:HH:216:GLN:OE1	2.36	0.57
9:If:244:VAL:HA	9:If:256:THR:HA	1.86	0.57
3:MK:120:SER:N	3:MK:160:GLY:O	2.31	0.57
2:VH:188:PRO:O	2:VH:262:ASN:ND2	2.37	0.57
10:MC:105:LEU:HD12	10:MC:106:PRO:HD2	1.86	0.57
1:MG:965:LEU:HD23	1:MG:1011:VAL:HG23	1.86	0.57
1:OG:969:GLY:HA3	1:OG:1009:ALA:HB2	1.86	0.57
1:Ag:792:GLN:HG2	1:Ag:796:GLN:HE22	1.69	0.57
2:FH:225:ASN:HD21	2:WH:176:VAL:H	1.52	0.57
1:BG:965:LEU:HG	1:BG:1008:LEU:HD23	1.86	0.57
2:IH:203:ASN:N	2:IH:216:GLN:O	2.36	0.57
2:AH:355:GLN:NE2	5:MN:79:GLN:OE1	2.36	0.57
2:LH:110:LYS:O	2:LH:110:LYS:NZ	2.37	0.57
3:AK:91:LEU:HD21	3:AK:139:VAL:HG21	1.85	0.57
4:ML:173:GLY:O	4:ML:178:LYS:NZ	2.37	0.57
1:EG:912:MET:HB3	1:EG:944:LEU:HB2	1.85	0.57
4:EL:210:ASP:N	4:EL:210:ASP:OD1	2.36	0.57
1:Ig:824:THR:H	2:XH:208:LYS:HB3	1.68	0.57
8:KD:77:TYR:OH	3:KK:130:ARG:NH1	2.37	0.57
2:LH:179:LEU:HD13	2:LH:252:VAL:HB	1.85	0.57
5:LN:82:MET:N	5:LN:82:MET:SD	2.77	0.57
8:Ld:33:PRO:HB2	8:Ld:39:ILE:HG22	1.86	0.57
8:Ld:76:ALA:O	8:Ld:80:GLN:NE2	2.29	0.57
9:Lf:238:ILE:HD12	9:Lf:239:PRO:HD2	1.86	0.57
8:Md:110:GLY:HA3	8:Md:158:TYR:HB2	1.84	0.57
2:WH:230:LEU:HB2	2:WH:233:LEU:HB3	1.87	0.57
10:DC:100:LEU:HB2	10:DC:104:ILE:HG23	1.85	0.57
8:BD:162:TYR:OH	10:JC:103:GLU:O	2.21	0.57
8:Bd:52:MET:HE2	10:JC:99:SER:HB2	1.86	0.57
8:Cd:148:TYR:HB2	8:Cd:153:VAL:HG12	1.85	0.57
1:IG:955:ARG:NH1	1:IG:1023:PHE:O	2.36	0.57
9:Df:260:GLN:OE1	9:Df:260:GLN:N	2.33	0.57
1:AG:931:SER:O	1:AG:1042:THR:OG1	2.21	0.57
9:FF:210:TYR:HA	9:FF:224:GLY:HA2	1.86	0.57
8:Fd:33:PRO:HB2	8:Fd:39:ILE:HG22	1.87	0.57
1:BG:869:MET:HB2	1:BG:1041:PHE:HE1	1.69	0.57
8:Gd:49:SER:HA	8:Gd:52:MET:HE2	1.85	0.57
2:IH:170:ARG:HH11	2:IH:247:ALA:HB3	1.69	0.57
11:KM:202:LEU:HB2	11:KM:222:ILE:HG23	1.85	0.57
8:Kd:148:TYR:HB2	8:Kd:153:VAL:HG12	1.84	0.57
2:VH:183:ASP:OD1	2:VH:187:ALA:N	2.36	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:WH:171:LEU:O	2:WH:244:GLY:N	2.37	0.57
11:EM:162:VAL:HG12	11:EM:182:LYS:HB2	1.86	0.57
4:BL:54:ARG:HH21	4:BL:57:VAL:HG13	1.69	0.57
1:GG:946:SER:OG	1:GG:1030:GLU:O	2.17	0.57
10:LC:147:ARG:HG3	5:DN:87:TRP:CD2	2.39	0.57
11:DM:288:ARG:NH2	11:DM:318:GLN:O	2.36	0.57
1:OG:910:ASP:OD1	1:OG:910:ASP:N	2.32	0.57
8:GD:23:MET:SD	8:GD:23:MET:N	2.77	0.57
9:Hf:243:MET:O	9:Hf:257:SER:N	2.38	0.57
8:ID:39:ILE:HD12	4:IL:220:ILE:HG13	1.87	0.57
4:IL:121:ASP:O	4:IL:123:ARG:NH1	2.38	0.57
2:MH:171:LEU:HD21	2:MH:241:LEU:HB3	1.87	0.57
11:EM:288:ARG:NH2	11:EM:316:ASN:O	2.37	0.57
8:Bd:92:GLU:OE2	8:Bd:158:TYR:OH	2.23	0.57
4:CL:173:GLY:O	4:CL:178:LYS:NZ	2.28	0.57
11:CM:116:PHE:HB3	11:CM:136:LEU:HD13	1.86	0.57
11:CM:268:HIS:ND1	11:CM:287:THR:OG1	2.31	0.57
1:IG:890:VAL:HG23	1:IG:891:THR:HG22	1.87	0.57
1:KG:912:MET:HB3	1:KG:944:LEU:HB2	1.86	0.57
2:EH:280:LEU:HD11	2:EH:326:ALA:HB1	1.85	0.57
2:FH:190:PRO:HA	2:FH:211:ASN:HB3	1.86	0.57
8:ID:92:GLU:OE2	8:ID:158:TYR:OH	2.23	0.57
1:CG:1006:ILE:O	1:CG:1010:THR:OG1	2.22	0.57
11:LM:279:ILE:HB	11:LM:298:VAL:HG22	1.87	0.57
1:WG:820:TYR:HD2	2:WH:205:GLN:HB3	1.70	0.57
10:DC:257:ASN:O	10:DC:261:TRP:NE1	2.38	0.57
8:BD:162:TYR:O	10:JC:246:ARG:NH1	2.38	0.57
4:BL:226:ASN:O	4:BL:228:ARG:NH1	2.38	0.57
5:BN:101:VAL:HG22	5:BN:113:SER:HB2	1.87	0.57
8:Bd:148:TYR:HB2	8:Bd:153:VAL:HG12	1.87	0.57
10:GC:106:LEU:HD12	10:GC:107:PRO:HD2	1.87	0.57
2:DH:354:MET:HA	2:DH:354:MET:HE3	1.85	0.57
3:DK:86:ASP:N	3:DK:86:ASP:OD1	2.36	0.57
1:HG:969:GLY:HA3	1:HG:1009:ALA:HB2	1.85	0.57
1:MG:931:SER:O	1:MG:1042:THR:OG1	2.23	0.57
1:MG:1042:THR:OG1	1:MG:1043:GLN:OE1	2.21	0.57
1:OG:968:PHE:HB3	1:OG:1008:LEU:HD13	1.87	0.57
2:EH:330:SER:OG	2:EH:334:THR:OG1	2.18	0.57
9:GF:251:GLN:O	9:GF:263:LYS:NZ	2.38	0.57
9:GF:265:SER:OG	9:GF:267:GLU:OE2	2.22	0.57
4:GL:187:GLU:OE2	11:GM:268:HIS:ND1	2.36	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:ID:41:LEU:HD23	10:DC:198:ILE:HD12	1.85	0.57
2:IH:183:ASP:HA	2:IH:256:VAL:HB	1.86	0.57
8:LD:86:ASP:OD1	10:GC:88:ARG:NH1	2.38	0.57
2:VH:106:VAL:HG23	2:VH:107:ILE:HD12	1.86	0.57
9:BF:219:ARG:HG2	2:CH:148:PRO:HD2	1.85	0.57
10:EC:61:GLU:HA	10:EC:64:LEU:HD23	1.86	0.57
1:GG:1011:VAL:HG12	1:HG:963:SER:HB3	1.85	0.57
10:IC:217:MET:HG2	10:IC:219:MET:HE2	1.86	0.57
1:KG:969:GLY:HA3	1:KG:1009:ALA:HB2	1.87	0.57
2:FH:200:SER:N	1:WG:816:GLU:OE2	2.38	0.57
4:FL:191:THR:HG21	11:FM:289:ALA:HB3	1.86	0.57
1:BG:972:PHE:O	1:BG:976:ASN:ND2	2.38	0.57
4:HL:44:HIS:ND1	4:HL:49:ASN:OD1	2.38	0.57
8:Hd:92:GLU:OE2	8:Hd:158:TYR:OH	2.23	0.57
2:AH:320:LEU:HB2	2:AH:346:LEU:HD23	1.87	0.57
10:CC:91:ASP:HB3	10:CC:147:TRP:HE1	1.69	0.57
11:KM:288:ARG:NH2	11:KM:316:ASN:O	2.38	0.57
8:Ld:97:ARG:HH21	10:HC:262:ARG:HE	1.53	0.57
1:Mg:794:ILE:O	1:Mg:798:THR:N	2.36	0.57
4:ML:127:ILE:HB	4:ML:229:ILE:HB	1.87	0.57
11:MM:186:SER:HA	11:MM:205:TYR:HB2	1.86	0.57
1:XG:818:GLN:NE2	2:XH:203:ASN:OD1	2.38	0.57
11:BM:214:ILE:HB	11:BM:233:VAL:HG12	1.87	0.57
10:GC:201:ARG:O	10:GC:204:GLU:HG3	2.05	0.57
10:HC:244:ARG:HB2	10:IC:126:ILE:HG23	1.87	0.57
10:MC:244:ARG:NH2	8:ED:162:TYR:O	2.37	0.57
2:DH:175:PHE:N	2:DH:216:GLN:HE22	2.02	0.57
8:FD:72:THR:HG23	8:FD:73:ILE:HG22	1.87	0.57
8:FD:147:VAL:HG22	8:FD:154:VAL:HG22	1.86	0.57
10:BC:32:LEU:O	10:BC:36:GLN:NE2	2.38	0.57
4:GL:44:HIS:HB3	4:GL:46:PRO:HD2	1.86	0.57
4:GL:130:ASP:N	4:GL:130:ASP:OD1	2.35	0.57
9:HF:209:ILE:O	9:HF:225:SER:N	2.37	0.57
1:Hg:795:GLN:OE1	1:Hg:795:GLN:N	2.37	0.57
1:Ig:810:GLN:NE2	1:Ig:811:ASP:OD1	2.38	0.57
8:Jd:84:SER:H	10:FC:268:ALA:HB3	1.68	0.57
4:LL:54:ARG:HH21	4:LL:57:VAL:HG13	1.70	0.57
4:ML:115:GLN:HB3	4:ML:126:ILE:HB	1.87	0.57
4:ML:150:ASN:OD1	4:ML:153:ARG:NH2	2.30	0.57
1:VG:797:ARG:HH11	2:DH:121:PRO:HB3	1.70	0.57
10:DC:101:GLU:HG2	10:DC:102:HIS:HD2	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:DC:236:GLY:O	10:EC:255:LEU:N	2.34	0.57
4:BL:118:GLU:HG3	4:BL:123:ARG:HG2	1.85	0.57
5:CN:92:TYR:HD1	5:CN:94:GLN:H	1.53	0.57
1:HG:871:ALA:HB2	1:HG:889:ILE:HD13	1.85	0.57
1:HG:937:PRO:HD3	1:HG:1037:LEU:HA	1.87	0.57
1:AG:1003:ASN:HA	1:AG:1006:ILE:HD12	1.87	0.57
9:AF:266:GLN:OE1	9:ZF:233:ARG:NH2	2.36	0.57
1:BG:969:GLY:HA3	1:BG:1009:ALA:HB2	1.86	0.57
3:HK:90:ARG:NH2	11:HM:293:ALA:O	2.38	0.57
2:AH:115:MET:HB2	1:Mg:798:THR:HG23	1.86	0.57
8:Ld:74:PRO:HG3	8:Ld:147:VAL:HG11	1.86	0.57
11:BM:177:LEU:HD13	11:BM:181:PRO:HG2	1.85	0.57
9:Af:213:GLN:HE21	9:Af:223:ILE:HB	1.70	0.57
4:BL:216:ASP:O	4:BL:226:ASN:ND2	2.35	0.57
10:IC:100:LEU:HB2	10:IC:104:ILE:HG23	1.87	0.57
10:KC:240:GLU:OE2	10:LC:132:LYS:NZ	2.34	0.57
1:Dg:791:GLN:N	1:Dg:793:GLU:OE1	2.38	0.57
1:HG:968:PHE:HB3	1:HG:1008:LEU:HD13	1.87	0.57
1:Ag:810:GLN:NE2	1:Ag:811:ASP:OD1	2.38	0.57
8:Ed:92:GLU:OE1	8:Ed:92:GLU:N	2.30	0.56
10:BC:48:LYS:O	1:BG:938:ASN:ND2	2.38	0.56
8:GD:158:TYR:O	8:Gd:137:TYR:OH	2.19	0.56
2:HH:203:ASN:OD1	2:HH:205:GLN:NE2	2.38	0.56
1:Bg:793:GLU:O	1:Bg:796:GLN:NE2	2.38	0.56
3:JK:119:TYR:HE1	3:JK:159:LEU:HD23	1.68	0.56
2:AH:295:LEU:HD11	2:AH:306:LEU:HB2	1.87	0.56
9:KF:219:ARG:HG2	2:YH:148:PRO:HD2	1.87	0.56
2:KH:183:ASP:OD1	2:KH:185:THR:OG1	2.22	0.56
2:VH:201:SER:HB3	2:VH:219:LYS:HB2	1.87	0.56
2:VH:357:LYS:NZ	2:VH:359:GLU:OE2	2.32	0.56
9:CF:269:SER:OG	9:BF:233:ARG:NH1	2.35	0.56
7:YX:22:UNK:HA	7:YX:77:UNK:HA	1.86	0.56
10:IC:260:GLU:OE1	10:IC:260:GLU:N	2.35	0.56
1:HG:1042:THR:OG1	1:HG:1043:GLN:OE1	2.22	0.56
8:Dd:79:LEU:O	8:Dd:127:SER:OG	2.22	0.56
2:FH:156:GLN:NE2	2:FH:157:PHE:O	2.38	0.56
8:Gd:110:GLY:HA3	8:Gd:158:TYR:HB2	1.86	0.56
4:HL:165:VAL:HG12	4:HL:231:ILE:HG12	1.85	0.56
11:HM:163:THR:HB	11:HM:183:VAL:HG12	1.87	0.56
8:JD:158:TYR:O	8:Jd:137:TYR:OH	2.23	0.56
8:KD:35:ASP:OD2	8:KD:38:THR:N	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:KH:173:GLN:NE2	2:KH:218:THR:O	2.32	0.56
2:LH:339:MET:HE1	2:LH:345:LEU:HD21	1.86	0.56
11:MM:303:GLU:HG3	11:MM:305:GLY:H	1.70	0.56
1:VG:811:ASP:O	1:VG:814:GLN:NE2	2.33	0.56
1:Cg:794:ILE:O	1:Cg:798:THR:N	2.39	0.56
10:KC:149:ARG:HB3	10:KC:149:ARG:HH11	1.69	0.56
11:CM:186:SER:HA	11:CM:205:TYR:HB2	1.88	0.56
5:CN:86:LEU:HB3	5:CN:87:TRP:HE3	1.70	0.56
9:EF:265:SER:HB3	9:EF:268:ASP:HB2	1.87	0.56
9:AF:241:TYR:HB3	9:AF:256:THR:HG21	1.86	0.56
9:HF:219:ARG:NH2	9:HF:231:THR:OG1	2.38	0.56
1:CG:1010:THR:O	1:DG:963:SER:OG	2.16	0.56
8:Id:148:TYR:HB2	8:Id:153:VAL:HG12	1.87	0.56
8:JD:73:ILE:O	8:JD:133:ARG:NH2	2.37	0.56
2:JH:190:PRO:HD2	2:JH:261:PRO:HG2	1.86	0.56
2:AH:160:LEU:HG	2:AH:257:GLN:HG3	1.86	0.56
2:LH:138:GLU:HB3	2:YH:221:TYR:HE2	1.69	0.56
11:LM:174:GLN:NE2	11:LM:193:GLN:O	2.38	0.56
8:MD:114:SER:HA	10:IC:114:ASN:HD21	1.70	0.56
4:ML:116:TYR:OH	4:ML:118:GLU:OE1	2.24	0.56
9:VF:219:ARG:HG2	2:DH:148:PRO:HD2	1.85	0.56
9:ZF:209:ILE:HG12	9:ZF:225:SER:HB3	1.86	0.56
1:FG:931:SER:H	1:FG:1043:GLN:HE22	1.52	0.56
11:BM:284:LEU:HD23	11:BM:310:LYS:HG3	1.88	0.56
11:JM:119:GLU:HG3	11:JM:139:ALA:HB3	1.87	0.56
5:BN:49:ASN:HB3	5:BN:59:VAL:HG23	1.87	0.56
10:EC:214:LYS:NZ	10:EC:218:MET:SD	2.78	0.56
5:CN:86:LEU:HB3	5:CN:87:TRP:CE3	2.40	0.56
2:DH:326:ALA:HB3	2:DH:338:GLU:HB3	1.87	0.56
1:JG:931:SER:O	1:JG:1042:THR:OG1	2.22	0.56
1:PG:900:ILE:HB	1:PG:918:THR:HB	1.86	0.56
8:AD:155:GLU:OE2	8:AD:157:ARG:NH2	2.35	0.56
2:IH:122:LEU:HA	1:XG:801:MET:HE1	1.86	0.56
4:IL:145:TYR:HA	4:IL:148:LEU:HD23	1.88	0.56
4:KL:112:GLN:OE1	4:KL:132:TYR:OH	2.24	0.56
8:LD:125:ASP:OD2	3:LK:138:ARG:NH2	2.36	0.56
3:LK:143:TYR:OH	8:Ld:27:LYS:NZ	2.31	0.56
2:VH:155:SER:OG	2:VH:255:ARG:NH1	2.39	0.56
10:DC:108:VAL:HG21	10:DC:135:LYS:HE2	1.88	0.56
11:EM:191:LEU:HD21	11:EM:194:LEU:HG	1.86	0.56
11:FM:225:ALA:HA	11:FM:246:LEU:HB2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BH:352:LYS:NZ	2:BH:353:VAL:O	2.33	0.56
4:BL:63:ASP:OD1	4:BL:88:GLY:N	2.39	0.56
10:GC:110:LEU:HD23	10:GC:212:TYR:HB2	1.88	0.56
10:HC:247:ARG:HA	10:IC:122:GLN:NE2	2.20	0.56
10:MC:109:LEU:HD23	10:MC:211:TYR:HB2	1.87	0.56
10:MC:168:THR:O	10:MC:172:LYS:HG3	2.05	0.56
4:CL:134:MET:HE2	4:CL:139:ARG:HH12	1.70	0.56
2:DH:278:ASP:OD1	2:DH:278:ASP:N	2.37	0.56
8:Dd:73:ILE:HG22	8:Dd:75:ASN:H	1.70	0.56
3:EK:166:THR:HG22	3:EK:168:TYR:H	1.69	0.56
10:BC:103:GLU:OE2	10:BC:104:HIS:ND1	2.39	0.56
9:GF:207:ARG:HH21	9:GF:208:ILE:HG23	1.70	0.56
2:GH:154:THR:HB	2:GH:156:GLN:HE22	1.71	0.56
5:GN:57:ARG:NH1	5:GN:66:SER:O	2.39	0.56
11:HM:210:ASP:O	11:HM:230:ARG:N	2.30	0.56
9:JF:246:LEU:HD23	9:JF:255:LEU:HD23	1.86	0.56
8:Jd:76:ALA:HB3	8:Jd:79:LEU:HD23	1.87	0.56
6:LU:127:UNK:O	4:ML:232:GLN:NE2	2.36	0.56
8:Ld:76:ALA:HB3	8:Ld:79:LEU:HD23	1.87	0.56
10:DC:149:TYR:HB3	10:DC:201:ILE:HB	1.87	0.56
1:ZG:807:GLN:NE2	1:ZG:810:GLN:OE1	2.39	0.56
11:AM:145:ARG:HH21	11:AM:163:THR:HA	1.70	0.56
11:BM:311:ASP:OD1	11:BM:312:PHE:N	2.34	0.56
10:GC:233:VAL:HA	10:GC:242:ILE:O	2.05	0.56
2:CH:354:MET:HE3	2:CH:355:GLN:H	1.71	0.56
1:OG:937:PRO:HD3	1:OG:1037:LEU:HA	1.86	0.56
10:BC:152:LEU:HD21	10:BC:203:ILE:HG21	1.87	0.56
3:GK:110:ARG:NH1	5:GN:75:VAL:O	2.39	0.56
1:BG:871:ALA:HB2	1:BG:889:ILE:HD13	1.86	0.56
8:ID:132:LEU:HD12	8:ID:145:ILE:HG21	1.88	0.56
1:Ig:798:THR:HA	1:Ig:801:MET:HE2	1.87	0.56
5:KN:101:VAL:HG11	5:KN:112:CYS:HB3	1.88	0.56
11:AM:288:ARG:NH2	11:AM:316:ASN:O	2.38	0.56
9:BF:216:ILE:HD11	9:BF:219:ARG:HB2	1.87	0.56
10:FC:102:LEU:HB2	10:FC:106:ILE:HG13	1.88	0.56
8:DD:82:ARG:NE	8:DD:125:ASP:OD1	2.33	0.56
3:DK:87:GLN:N	3:DK:173:ASP:OD2	2.34	0.56
2:EH:250:TYR:CE2	2:DH:238:MET:HB2	2.40	0.56
1:Gg:824:THR:H	2:WH:208:LYS:HD2	1.71	0.56
1:BG:876:SER:OG	1:BG:1031:VAL:O	2.22	0.56
11:HM:119:GLU:HG3	11:HM:139:ALA:HB3	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:IH:317:LEU:HB3	2:IH:347:VAL:HG11	1.86	0.56
2:JH:324:TRP:HA	2:JH:339:MET:HB3	1.87	0.56
8:KD:32:ASN:N	8:KD:32:ASN:ND2	2.52	0.56
9:KF:235:GLY:HA2	9:KF:243:MET:HE1	1.87	0.56
8:Kd:76:ALA:HB3	8:Kd:79:LEU:HD13	1.88	0.56
1:Lg:824:THR:H	2:YH:208:LYS:HB3	1.71	0.56
3:LK:129:GLU:OE1	3:LK:129:GLU:N	2.38	0.56
5:MN:78:LEU:HD23	5:MN:78:LEU:H	1.71	0.56
2:YH:110:LYS:HA	2:YH:113:LYS:HD3	1.88	0.56
11:BM:172:ASN:OD1	11:BM:173:LEU:N	2.38	0.56
10:HC:187:ILE:O	10:HC:191:ASN:ND2	2.33	0.56
1:LG:951:HIS:O	1:LG:955:ARG:NE	2.37	0.56
1:MG:951:HIS:H	1:MG:1027:THR:HG22	1.70	0.56
1:OG:874:ASP:OD1	1:OG:874:ASP:N	2.37	0.56
1:PG:1003:ASN:HA	1:PG:1006:ILE:HD12	1.88	0.56
10:AC:152:LEU:HD21	10:AC:203:ILE:HG21	1.88	0.56
4:HL:177:HIS:HD1	11:HM:315:TYR:HH	1.53	0.56
8:Id:93:GLU:OE2	10:EC:264:ALA:N	2.32	0.56
3:KK:146:SER:HB2	8:Kd:29:PRO:HG3	1.87	0.56
1:DG:966:GLN:O	1:DG:970:ASN:ND2	2.39	0.56
9:MF:208:ILE:HD11	9:MF:224:GLY:HA3	1.86	0.56
9:XF:266:GLN:O	9:XF:269:SER:OG	2.21	0.56
11:FM:159:GLY:HA2	11:FM:181:PRO:HG3	1.87	0.56
11:JM:235:LEU:HD23	11:JM:255:THR:HG22	1.88	0.56
8:Ad:64:PRO:HG2	8:Ad:67:LYS:HG2	1.88	0.56
10:GC:61:GLU:HA	10:GC:64:LEU:HD12	1.87	0.56
10:LC:117:ASN:OD1	10:LC:118:LEU:N	2.39	0.56
11:CM:117:ARG:HG2	11:CM:137:TYR:HB3	1.88	0.56
8:Cd:82:ARG:HH21	8:Cd:126:GLU:HA	1.71	0.56
3:DK:105:PHE:HD1	3:DK:106:LEU:HD12	1.70	0.56
4:EL:191:THR:HG21	11:EM:289:ALA:HB3	1.88	0.56
3:GK:71:GLY:O	8:HD:27:LYS:NZ	2.38	0.56
9:Gf:243:MET:O	9:Gf:257:SER:N	2.39	0.56
4:HL:127:ILE:HB	4:HL:229:ILE:HB	1.87	0.56
8:JD:86:ASP:OD1	10:EC:88:ARG:NH1	2.39	0.56
9:KF:219:ARG:NH2	9:KF:231:THR:OG1	2.33	0.56
3:KK:54:ILE:HD11	5:KN:44:LYS:HB3	1.88	0.56
4:KL:183:GLN:NE2	4:KL:207:GLY:O	2.34	0.56
2:WH:201:SER:O	2:WH:218:THR:N	2.38	0.56
11:AM:271:SER:OG	11:AM:290:ASP:OD1	2.23	0.56
11:BM:304:TRP:HZ2	3:BK:134:LEU:HD22	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:EM:240:GLN:HB2	11:EM:242:LYS:HE3	1.88	0.56
11:JM:306:GLN:HB3	11:JM:309:LEU:HB2	1.86	0.56
10:IC:224:TYR:H	10:IC:250:ALA:HB3	1.70	0.56
10:JC:151:TYR:HB2	10:JC:152:LEU:HD22	1.88	0.56
10:LC:105:LEU:HD12	10:LC:106:PRO:HD2	1.87	0.56
10:MC:101:GLU:OE1	10:MC:102:HIS:ND1	2.30	0.56
2:CH:184:SER:HB2	2:CH:259:TYR:HE1	1.70	0.56
1:LG:876:SER:OG	1:LG:1031:VAL:O	2.21	0.56
2:GH:148:PRO:HD2	9:WF:219:ARG:HG2	1.87	0.56
2:GH:181:PHE:O	2:GH:211:ASN:ND2	2.31	0.56
2:HH:345:LEU:HB2	2:HH:356:LEU:HB2	1.86	0.56
11:IM:170:SER:OG	11:IM:172:ASN:O	2.23	0.56
11:IM:177:LEU:HD13	11:IM:181:PRO:HG2	1.88	0.56
1:CG:966:GLN:O	1:CG:970:ASN:ND2	2.39	0.56
10:CC:225:TYR:HB2	10:CC:251:ALA:HB3	1.87	0.56
10:CC:261:GLU:OE1	10:CC:261:GLU:N	2.35	0.56
1:Kg:822:GLU:OE1	1:Kg:822:GLU:N	2.39	0.56
4:LL:150:ASN:OD1	4:LL:153:ARG:NH2	2.30	0.56
9:YF:241:TYR:HB3	9:YF:256:THR:HG21	1.87	0.56
1:GG:951:HIS:H	1:GG:1027:THR:HG22	1.70	0.56
1:GG:966:GLN:O	1:GG:970:ASN:ND2	2.39	0.56
10:LC:78:ILE:HD12	10:LC:194:LEU:HD12	1.88	0.56
10:MC:162:VAL:HG12	10:MC:165:LEU:HD11	1.88	0.56
9:FF:213:GLN:O	2:FH:170:ARG:NH2	2.35	0.55
8:GD:54:GLU:HA	8:GD:57:LYS:HD3	1.89	0.55
1:BG:1006:ILE:O	1:BG:1010:THR:OG1	2.22	0.55
2:IH:311:MET:HE3	2:IH:341:LYS:HA	1.86	0.55
2:LH:188:PRO:O	2:LH:262:ASN:ND2	2.39	0.55
11:LM:261:ALA:HB1	11:LM:263:ILE:HD11	1.87	0.55
11:LM:311:ASP:OD1	11:LM:312:PHE:N	2.31	0.55
10:DC:113:ARG:HG2	10:DC:129:ARG:HG2	1.88	0.55
11:FM:158:VAL:HG22	11:FM:178:LYS:HE2	1.87	0.55
11:FM:271:SER:OG	11:FM:290:ASP:OD1	2.24	0.55
10:IC:101:GLU:HG2	10:IC:102:HIS:HD2	1.71	0.55
10:KC:260:SER:HA	10:KC:263:TRP:CE2	2.40	0.55
4:FL:129:THR:HB	4:FL:229:ILE:HD13	1.88	0.55
1:BG:951:HIS:H	1:BG:1027:THR:HG22	1.72	0.55
11:HM:313:ASP:HB2	11:HM:316:ASN:HD21	1.70	0.55
8:JD:92:GLU:OE1	8:JD:93:GLU:N	2.40	0.55
8:JD:155:GLU:OE2	8:JD:157:ARG:NH2	2.38	0.55
11:LM:186:SER:HA	11:LM:205:TYR:HB2	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LM:308:ASP:OD1	11:LM:308:ASP:N	2.39	0.55
9:WF:209:ILE:O	9:WF:225:SER:N	2.38	0.55
10:DC:148:GLN:OE1	10:DC:148:GLN:N	2.29	0.55
11:AM:172:ASN:OD1	11:AM:173:LEU:N	2.39	0.55
11:GM:172:ASN:OD1	11:GM:173:LEU:N	2.39	0.55
10:GC:108:PRO:HD3	10:GC:138:ALA:HB2	1.87	0.55
11:DM:271:SER:OG	11:DM:290:ASP:OD1	2.23	0.55
1:IG:966:GLN:OE1	1:IG:1013:LYS:N	2.40	0.55
1:KG:1011:VAL:HG12	1:LG:963:SER:HB2	1.89	0.55
10:AC:169:LYS:H	10:AC:173:GLU:HG3	1.71	0.55
8:Gd:139:ALA:O	8:Gd:142:LYS:NZ	2.37	0.55
9:HF:233:ARG:NH2	9:XF:269:SER:OG	2.39	0.55
3:IK:120:SER:N	3:IK:160:GLY:O	2.32	0.55
4:IL:124:THR:HA	4:IL:231:ILE:O	2.05	0.55
9:LF:245:LYS:HE3	9:LF:257:SER:HA	1.87	0.55
2:LH:181:PHE:O	2:LH:211:ASN:ND2	2.31	0.55
8:Ad:120:SER:H	8:AD:111:LYS:HZ1	1.53	0.55
2:BH:157:PHE:HA	2:BH:255:ARG:HB2	1.88	0.55
10:HC:109:LEU:HD23	10:HC:211:TYR:HB2	1.88	0.55
10:LC:113:ARG:HH12	10:LC:129:ARG:HH21	1.52	0.55
2:DH:280:LEU:HD21	2:DH:326:ALA:HB1	1.87	0.55
8:AD:72:THR:HG23	8:AD:73:ILE:HG13	1.88	0.55
4:FL:129:THR:O	4:FL:133:PHE:HB2	2.06	0.55
5:FN:47:GLY:O	5:FN:61:ASN:N	2.32	0.55
8:Fd:82:ARG:CZ	8:Fd:83:ALA:H	2.19	0.55
1:BG:1006:ILE:HG12	1:CG:968:PHE:HA	1.87	0.55
1:BG:1011:VAL:HG12	1:CG:963:SER:HB3	1.89	0.55
2:IH:345:LEU:HB2	2:IH:356:LEU:HB2	1.87	0.55
1:CG:948:THR:HG22	1:CG:1029:VAL:HG12	1.88	0.55
1:CG:949:ASN:HA	1:CG:952:TYR:CE2	2.42	0.55
1:Jg:818:GLN:NE2	2:JH:203:ASN:OD1	2.40	0.55
2:JH:200:SER:N	1:Kg:816:GLU:OE2	2.39	0.55
4:JL:170:ASP:OD2	4:JL:227:ARG:NH2	2.28	0.55
9:XF:267:GLU:O	2:XH:150:LYS:NZ	2.37	0.55
1:ZG:807:GLN:O	1:ZG:810:GLN:HG2	2.06	0.55
11:EM:128:ASN:O	11:EM:130:ARG:NH1	2.40	0.55
10:IC:166:PRO:HB2	10:IC:172:LYS:HG3	1.89	0.55
1:KG:917:ASN:HA	1:KG:931:SER:HA	1.87	0.55
1:Fg:798:THR:HG21	2:GH:114:ASP:HB2	1.88	0.55
9:AF:268:ASP:OD2	2:AH:170:ARG:NH1	2.28	0.55
8:HD:109:LEU:HD13	8:HD:155:GLU:HG3	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:HM:279:ILE:HB	11:HM:298:VAL:HG22	1.87	0.55
1:Kg:795:GLN:OE1	1:Kg:795:GLN:N	2.35	0.55
8:LD:42:ALA:HB2	8:Ld:41:LEU:HD22	1.88	0.55
9:LF:230:LEU:HA	2:LH:165:THR:HG21	1.88	0.55
4:LL:124:THR:HA	4:LL:231:ILE:O	2.07	0.55
11:MM:201:THR:HG22	11:MM:221:LYS:HB2	1.89	0.55
1:EG:970:ASN:OD1	1:EG:971:ALA:N	2.39	0.55
11:EM:186:SER:HA	11:EM:205:TYR:HB2	1.87	0.55
5:AN:89:GLY:O	5:AN:104:ASN:ND2	2.40	0.55
8:BD:28:PRO:HG3	4:BL:115:GLN:HB2	1.88	0.55
8:Bd:93:GLU:OE2	10:KC:264:ARG:NH1	2.39	0.55
9:DF:209:ILE:O	9:DF:225:SER:N	2.40	0.55
9:If:261:VAL:O	9:If:263:LYS:NZ	2.40	0.55
8:JD:87:TRP:CD1	8:JD:89:GLY:H	2.25	0.55
3:JK:85:ALA:HB3	3:JK:88:SER:HB2	1.89	0.55
5:JN:46:GLY:HA3	5:JN:61:ASN:HB2	1.88	0.55
2:KH:324:TRP:HA	2:KH:339:MET:HB3	1.88	0.55
4:KL:130:ASP:OD1	4:KL:130:ASP:N	2.38	0.55
3:AK:115:THR:OG1	3:AK:183:THR:OG1	2.25	0.55
1:Mg:797:ARG:NH2	2:ZH:121:PRO:O	2.40	0.55
9:XF:207:ARG:NH1	9:XF:208:ILE:O	2.39	0.55
2:YH:344:VAL:HB	2:YH:355:GLN:HE21	1.72	0.55
1:ZG:811:ASP:O	1:ZG:814:GLN:NE2	2.34	0.55
11:JM:172:ASN:OD1	11:JM:173:LEU:N	2.40	0.55
10:FC:100:LEU:HD12	10:FC:108:PRO:HG3	1.89	0.55
10:IC:140:ILE:HD11	10:IC:143:PRO:HA	1.88	0.55
11:DM:191:LEU:HB3	11:DM:212:LEU:HD11	1.88	0.55
1:IG:900:ILE:HG13	1:IG:918:THR:HB	1.89	0.55
1:Fg:803:THR:O	1:Fg:806:THR:OG1	2.25	0.55
10:BC:227:VAL:HA	10:BC:250:ILE:HA	1.89	0.55
8:HD:87:TRP:CD1	8:HD:89:GLY:H	2.24	0.55
6:JU:127:UNK:O	4:KL:232:GLN:NE2	2.39	0.55
2:KH:196:LEU:HD13	2:KH:226:LEU:HD12	1.89	0.55
2:KH:311:MET:HG3	2:KH:341:LYS:HA	1.89	0.55
3:KK:60:LEU:HG	3:KK:65:ILE:HD11	1.88	0.55
11:LM:168:VAL:H	11:LM:187:GLY:HA3	1.72	0.55
5:MN:87:TRP:CE2	10:HC:147:ARG:HG3	2.41	0.55
9:VF:209:ILE:H	9:VF:225:SER:HB3	1.72	0.55
7:BX:21:UNK:O	7:BX:78:UNK:N	2.39	0.55
10:FC:248:LEU:HB2	10:GC:125:ILE:HG13	1.87	0.55
10:IC:109:LEU:HD23	10:IC:211:TYR:HB2	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:JC:151:TYR:O	10:JC:199:ASN:ND2	2.39	0.55
2:CH:151:PRO:HA	2:CH:248:VAL:HG13	1.89	0.55
1:NG:931:SER:H	1:NG:1043:GLN:NE2	2.05	0.55
1:PG:1006:ILE:O	1:PG:1010:THR:OG1	2.24	0.55
9:FF:219:ARG:HG2	2:WH:148:PRO:HD2	1.89	0.55
5:FN:89:GLY:HA3	5:FN:104:ASN:HB2	1.88	0.55
1:Bg:818:GLN:OE1	2:BH:203:ASN:ND2	2.40	0.55
2:IH:208:LYS:HG3	1:Jg:824:THR:H	1.70	0.55
2:IH:231:ARG:HH22	1:Jg:824:THR:HA	1.72	0.55
4:LL:42:CYS:SG	4:LL:58:LYS:NZ	2.73	0.55
4:ML:129:THR:HG22	4:ML:229:ILE:HG12	1.89	0.55
9:WF:243:MET:O	9:WF:257:SER:N	2.37	0.55
11:BM:145:ARG:HH22	11:BM:162:VAL:HG23	1.71	0.55
11:EM:317:LYS:NZ	8:ED:124:LYS:O	2.36	0.55
8:Ad:134:ASP:OD1	8:Ad:138:GLN:NE2	2.40	0.55
2:BH:166:PRO:HG3	2:CH:151:PRO:HB2	1.88	0.55
11:DM:174:GLN:NE2	11:DM:193:GLN:O	2.39	0.55
8:FD:124:LYS:O	11:FM:317:LYS:NZ	2.40	0.55
8:GD:87:TRP:CD1	8:GD:89:GLY:H	2.25	0.55
5:IN:56:GLY:HA3	5:IN:74:ALA:HB2	1.89	0.55
2:JH:242:ILE:HD12	2:JH:243:PRO:HD2	1.87	0.55
2:AH:229:ARG:HH22	2:BH:210:SER:HB2	1.70	0.55
2:KH:319:ILE:HA	2:KH:347:VAL:HG12	1.89	0.55
11:KM:306:GLN:HB3	11:KM:309:LEU:HB2	1.89	0.55
9:Mf:247:ILE:HA	9:Mf:254:ILE:HG22	1.87	0.55
2:YH:189:TRP:HE1	2:YH:232:GLY:H	1.55	0.55
9:Af:243:MET:HB3	9:Af:257:SER:HB3	1.89	0.55
9:BF:243:MET:O	9:BF:257:SER:N	2.39	0.55
2:DH:190:PRO:HA	2:DH:211:ASN:HB3	1.89	0.55
1:IG:1017:GLN:NE2	1:JG:1020:GLN:OE1	2.39	0.55
1:NG:876:SER:HB3	1:OG:941:ARG:HG2	1.87	0.55
1:NG:968:PHE:HB3	1:NG:1008:LEU:HD13	1.89	0.55
9:Df:218:GLY:H	9:Df:247:ILE:HD11	1.70	0.55
1:AG:1006:ILE:O	1:AG:1010:THR:OG1	2.23	0.55
8:Ed:130:GLU:HG2	8:ED:107:ARG:HH11	1.72	0.55
2:GH:183:ASP:OD1	2:GH:187:ALA:N	2.40	0.55
3:GK:129:GLU:OE1	3:GK:129:GLU:N	2.32	0.55
4:GL:49:ASN:ND2	11:GM:293:ALA:O	2.40	0.55
3:HK:54:ILE:O	3:HK:58:THR:OG1	2.25	0.55
3:JK:103:ALA:O	3:JK:107:LYS:HG2	2.07	0.55
2:KH:145:PRO:HG3	2:YH:128:VAL:HG13	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LH:157:PHE:HA	2:LH:255:ARG:HB3	1.89	0.55
9:MF:221:TRP:CD1	9:MF:231:THR:HB	2.42	0.55
4:ML:108:ASP:OD1	4:ML:112:GLN:NE2	2.38	0.55
9:Mf:253:ARG:N	9:Mf:263:LYS:HZ2	2.05	0.55
11:GM:209:SER:HB3	11:GM:212:LEU:HD21	1.88	0.55
1:Cg:814:GLN:OE1	1:Cg:814:GLN:N	2.39	0.55
11:CM:214:ILE:O	11:CM:215:ARG:NH1	2.37	0.55
8:Cd:76:ALA:O	8:Cd:80:GLN:NE2	2.40	0.55
3:DK:66:LYS:NZ	3:DK:67:VAL:O	2.39	0.55
1:IG:924:ALA:HB3	1:IG:926:LYS:HE3	1.89	0.55
1:LG:862:ILE:HD13	1:LG:1046:THR:HA	1.89	0.55
1:OG:949:ASN:HA	1:OG:952:TYR:CE2	2.42	0.55
2:EH:245:GLN:NE2	9:EF:215:VAL:O	2.38	0.54
2:EH:349:TRP:HB2	2:EH:354:MET:HE2	1.89	0.54
1:BG:965:LEU:O	1:BG:1008:LEU:HB3	2.07	0.54
8:HD:39:ILE:HD12	4:HL:220:ILE:HG13	1.89	0.54
1:Ig:818:GLN:NE2	2:IH:203:ASN:OD1	2.39	0.54
4:IL:165:VAL:HG12	4:IL:231:ILE:HG12	1.89	0.54
8:JD:36:ASP:OD1	10:EC:75:ARG:NH2	2.40	0.54
2:JH:324:TRP:HH2	10:EC:117:LEU:HD23	1.72	0.54
2:AH:230:LEU:HD12	2:AH:233:LEU:HD12	1.90	0.54
1:Kg:794:ILE:HD13	2:LH:107:ILE:HG23	1.89	0.54
11:KM:158:VAL:HG13	11:KM:178:LYS:HE2	1.89	0.54
8:Ld:139:ALA:HB1	8:Ld:143:ALA:HB3	1.87	0.54
4:ML:124:THR:HA	4:ML:231:ILE:O	2.07	0.54
1:EG:972:PHE:O	1:EG:976:ASN:ND2	2.40	0.54
2:XH:325:LEU:HD23	2:XH:339:MET:HA	1.88	0.54
11:FM:190:ASN:O	11:FM:192:ARG:NH2	2.38	0.54
8:Ad:93:GLU:OE2	10:JC:265:ALA:N	2.37	0.54
8:Bd:126:GLU:OE1	8:Bd:131:ILE:HG12	2.08	0.54
10:JC:190:ASP:O	10:JC:194:THR:OG1	2.25	0.54
10:MC:74:ARG:NH2	8:ED:36:ASP:OD1	2.40	0.54
11:DM:210:ASP:N	11:DM:210:ASP:OD1	2.39	0.54
1:PG:899:LEU:HD21	1:PG:916:PHE:HB3	1.89	0.54
10:BC:127:ARG:NH1	2:GH:273:PRO:O	2.38	0.54
9:AF:213:GLN:HA	2:AH:170:ARG:HH21	1.72	0.54
8:GD:29:PRO:HG2	4:GL:225:GLN:HG2	1.88	0.54
1:Ig:798:THR:HG23	2:KH:115:MET:HB2	1.88	0.54
3:IK:107:LYS:NZ	3:IK:148:GLY:O	2.28	0.54
8:Jd:97:ARG:HG3	10:FC:265:ALA:HB3	1.89	0.54
1:Kg:798:THR:HG23	2:LH:115:MET:HB2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DG:876:SER:HB3	1:EG:941:ARG:HG2	1.88	0.54
3:LK:151:SER:O	3:LK:152:ARG:NH1	2.41	0.54
3:MK:65:ILE:HD12	3:MK:78:ILE:HG13	1.89	0.54
11:AM:279:ILE:HB	11:AM:298:VAL:HG22	1.89	0.54
11:BM:131:THR:HG23	11:BM:151:GLY:H	1.71	0.54
8:BD:88:SER:HA	8:BD:120:SER:HA	1.88	0.54
10:HC:107:PRO:HD3	10:HC:137:ALA:HB2	1.88	0.54
8:Cd:79:LEU:O	8:Cd:127:SER:OG	2.25	0.54
8:AD:147:VAL:HG22	8:AD:154:VAL:HG12	1.89	0.54
2:FH:238:MET:N	2:FH:238:MET:SD	2.80	0.54
10:BC:127:ARG:HD3	2:GH:275:SER:HA	1.89	0.54
3:HK:66:LYS:HA	3:HK:66:LYS:HZ2	1.71	0.54
9:JF:243:MET:N	9:JF:257:SER:OG	2.35	0.54
3:JK:92:ASN:O	3:JK:95:SER:OG	2.22	0.54
2:AH:173:GLN:HA	2:AH:217:ALA:HB3	1.89	0.54
2:AH:190:PRO:HA	2:AH:211:ASN:HB3	1.89	0.54
1:DG:1044:ASP:N	1:DG:1044:ASP:OD1	2.38	0.54
11:MM:271:SER:OG	11:MM:290:ASP:OD1	2.25	0.54
1:EG:951:HIS:H	1:EG:1027:THR:HG22	1.72	0.54
5:AN:63:GLY:HA3	8:BD:27:LYS:HB2	1.89	0.54
8:Ad:48:VAL:HG11	10:IC:92:ILE:HD13	1.89	0.54
2:BH:110:LYS:HA	2:BH:113:LYS:HG2	1.88	0.54
4:BL:98:TYR:O	4:BL:101:SER:OG	2.24	0.54
4:BL:133:PHE:HE1	4:BL:138:PRO:HA	1.72	0.54
9:Bf:243:MET:O	9:Bf:257:SER:N	2.40	0.54
10:HC:246:LEU:O	10:IC:122:GLN:NE2	2.28	0.54
5:DN:96:ASN:OD1	5:DN:97:SER:N	2.41	0.54
1:OG:1006:ILE:O	1:OG:1010:THR:OG1	2.25	0.54
8:Dd:149:PRO:O	8:Dd:152:GLN:NE2	2.36	0.54
5:HN:62:ASN:N	5:HN:62:ASN:OD1	2.39	0.54
1:Bg:800:ASP:O	1:Bg:803:THR:OG1	2.23	0.54
2:AH:330:SER:OG	2:AH:332:ASP:OD1	2.19	0.54
8:Kd:74:PRO:HD2	8:Kd:129:ALA:HB1	1.89	0.54
2:MH:183:ASP:OD1	2:MH:187:ALA:N	2.41	0.54
10:FC:115:ARG:HE	10:FC:131:ARG:HH21	1.56	0.54
10:FC:118:LEU:HD12	10:FC:128:ILE:HB	1.88	0.54
10:FC:173:GLU:HA	10:FC:176:ILE:HG12	1.90	0.54
10:HC:105:LEU:HD12	10:HC:106:PRO:HD2	1.89	0.54
5:CN:57:ARG:NH1	5:CN:66:SER:O	2.40	0.54
8:DD:132:LEU:HD12	8:DD:145:ILE:HG21	1.88	0.54
9:DF:233:ARG:NH1	9:EF:269:SER:OG	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Dg:793:GLU:O	1:Dg:796:GLN:NE2	2.41	0.54
9:EF:238:ILE:HD12	9:EF:239:PRO:HD2	1.89	0.54
3:EK:81:SER:OG	3:EK:173:ASP:O	2.25	0.54
3:EK:156:THR:HG23	8:ED:82:ARG:HB2	1.90	0.54
5:GN:94:GLN:HE22	5:GN:96:ASN:HB2	1.72	0.54
5:GN:111:GLU:OE1	5:GN:112:CYS:N	2.41	0.54
8:ID:136:ASP:O	8:Id:60:LYS:NZ	2.36	0.54
11:IM:210:ASP:O	11:IM:230:ARG:N	2.37	0.54
3:JK:162:ASP:N	3:JK:162:ASP:OD1	2.41	0.54
8:KD:72:THR:HG23	8:KD:73:ILE:HG13	1.90	0.54
2:LH:198:ASP:OD1	2:LH:200:SER:OG	2.22	0.54
3:MK:186:ARG:HH21	5:MN:57:ARG:HH12	1.55	0.54
2:WH:283:VAL:HG22	2:WH:289:PRO:HD3	1.89	0.54
11:AM:146:LEU:HB2	11:AM:165:ILE:HG12	1.89	0.54
11:FM:246:LEU:O	11:FM:264:SER:OG	2.21	0.54
11:FM:302:ARG:HH11	11:FM:309:LEU:HD11	1.71	0.54
10:JC:110:VAL:HG13	10:JC:209:GLY:HA3	1.89	0.54
10:KC:259:ASN:OD1	10:KC:259:ASN:N	2.38	0.54
8:FD:23:MET:N	8:FD:23:MET:SD	2.81	0.54
4:HL:121:ASP:O	4:HL:123:ARG:NH1	2.40	0.54
2:IH:324:TRP:HA	2:IH:339:MET:HB3	1.90	0.54
10:CC:245:ARG:HG2	10:CC:247:LEU:HD21	1.88	0.54
1:DG:937:PRO:HD3	1:DG:1037:LEU:HA	1.90	0.54
8:LD:44:ALA:HB1	10:GC:203:LYS:HD2	1.89	0.54
2:LH:296:VAL:HB	2:LH:359:GLU:HB2	1.88	0.54
1:Mg:795:GLN:O	1:Mg:799:SER:N	2.40	0.54
11:MM:150:ILE:HB	11:MM:168:VAL:HG22	1.89	0.54
9:WF:243:MET:HB3	9:WF:257:SER:HB3	1.88	0.54
10:GC:153:MET:N	10:GC:153:MET:SD	2.81	0.54
10:KC:60:LEU:HD11	10:KC:177:TRP:HB2	1.89	0.54
10:KC:195:ILE:O	10:KC:199:ASN:ND2	2.32	0.54
10:LC:129:ARG:NH2	8:Cd:86:ASP:OD1	2.41	0.54
2:CH:230:LEU:HB2	2:CH:233:LEU:HB2	1.89	0.54
11:CM:273:ALA:HB2	11:CM:279:ILE:HD11	1.89	0.54
8:Gd:87:TRP:CD1	8:Gd:94:LEU:HD22	2.43	0.54
8:HD:59:GLU:HA	8:HD:62:ILE:HG12	1.90	0.54
1:CG:931:SER:H	1:CG:1043:GLN:NE2	2.05	0.54
8:Jd:86:ASP:N	8:Jd:86:ASP:OD1	2.41	0.54
11:KM:300:ASP:OD2	11:KM:302:ARG:NE	2.40	0.54
1:DG:931:SER:H	1:DG:1043:GLN:HE22	1.56	0.54
8:LD:28:PRO:HG3	4:LL:115:GLN:HB2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LH:249:ASP:N	2:LH:249:ASP:OD1	2.40	0.54
3:LK:133:THR:HB	3:LK:158:GLY:HA3	1.90	0.54
2:MH:115:MET:HE2	1:YG:801:MET:HE1	1.89	0.54
8:Md:74:PRO:HG3	8:Md:147:VAL:HG11	1.89	0.54
1:FG:972:PHE:O	1:FG:976:ASN:ND2	2.41	0.54
11:AM:144:THR:O	11:AM:145:ARG:NE	2.39	0.54
11:BM:300:ASP:OD2	11:BM:302:ARG:NE	2.41	0.54
11:JM:195:ASP:HB3	11:JM:197:TYR:CE2	2.43	0.54
11:DM:145:ARG:HH22	11:DM:162:VAL:HG23	1.71	0.54
1:HG:931:SER:O	1:HG:1042:THR:OG1	2.25	0.54
1:LG:872:VAL:HA	1:LG:1036:GLY:HA2	1.89	0.54
1:NG:924:ALA:HB3	1:NG:926:LYS:HE3	1.90	0.54
1:NG:951:HIS:H	1:NG:1027:THR:HG22	1.73	0.54
2:FH:297:VAL:HA	2:FH:358:VAL:HG22	1.89	0.54
3:JK:179:ARG:NH2	3:JK:181:GLU:OE2	2.41	0.54
2:AH:179:LEU:HB2	2:AH:213:LEU:HB2	1.90	0.54
2:VH:190:PRO:HA	2:VH:211:ASN:HB3	1.90	0.54
2:XH:309:GLU:O	2:XH:341:LYS:NZ	2.29	0.54
11:FM:240:GLN:HA	11:FM:260:VAL:O	2.08	0.54
11:JM:121:ALA:HA	11:JM:141:GLU:HB3	1.90	0.54
10:MC:235:ASP:OD1	10:MC:238:GLU:N	2.37	0.54
4:DL:118:GLU:OE2	4:DL:123:ARG:NH2	2.40	0.54
11:DM:180:ASP:OD1	11:DM:199:LYS:N	2.36	0.54
1:HG:966:GLN:OE1	1:HG:1013:LYS:N	2.41	0.54
1:PG:910:ASP:OD1	1:PG:910:ASP:N	2.37	0.54
2:FH:229:ARG:NH1	1:WG:820:TYR:OH	2.37	0.54
2:FH:325:LEU:HD11	2:FH:340:GLN:HE22	1.73	0.54
2:GH:140:ALA:HB2	2:HH:124:PRO:HB3	1.90	0.54
4:GL:217:ASN:OD1	4:GL:226:ASN:ND2	2.36	0.54
2:HH:230:LEU:HD12	2:HH:233:LEU:HD12	1.90	0.54
11:HM:197:TYR:HA	11:HM:217:LYS:HB3	1.90	0.54
3:IK:137:SER:HB2	3:IK:156:THR:HG22	1.90	0.54
9:Jf:235:GLY:HA2	9:Jf:243:MET:HE1	1.89	0.54
9:Jf:238:ILE:HG13	9:Jf:241:TYR:HB2	1.90	0.54
8:Ld:123:THR:HG21	8:Ld:126:GLU:HB2	1.89	0.54
2:MH:316:ASN:OD1	2:MH:316:ASN:N	2.41	0.54
4:AL:121:ASP:O	4:AL:123:ARG:NH1	2.41	0.54
10:GC:102:GLU:HG2	10:GC:103:HIS:CD2	2.42	0.54
1:LG:899:LEU:HD21	1:LG:916:PHE:HB3	1.90	0.54
1:PG:899:LEU:HD13	1:PG:919:MET:HG2	1.90	0.54
9:Gf:246:LEU:HD23	9:Gf:255:LEU:HD22	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:IH:148:PRO:HD2	9:XF:219:ARG:HG2	1.90	0.54
8:Id:123:THR:HG21	8:Id:126:GLU:HB2	1.88	0.54
4:JL:116:TYR:OH	4:JL:118:GLU:OE1	2.26	0.54
2:AH:161:SER:O	2:AH:164:SER:OG	2.22	0.54
10:CC:89:ASN:O	10:CC:93:ILE:HG22	2.08	0.54
11:KM:145:ARG:HH22	11:KM:162:VAL:HG23	1.73	0.54
9:Kf:241:TYR:O	9:Kf:258:SER:OG	2.19	0.54
8:CD:55:MET:HE1	8:Cd:55:MET:HG3	1.90	0.54
2:LH:176:VAL:H	2:YH:225:ASN:HD21	1.56	0.54
3:LK:169:THR:HG22	3:LK:177:ASN:HD22	1.73	0.54
11:MM:286:LYS:HA	11:MM:316:ASN:HD21	1.73	0.54
2:ZH:155:SER:OG	2:ZH:255:ARG:NH1	2.41	0.54
11:CM:238:PHE:N	11:CM:258:LYS:O	2.39	0.54
1:JG:1006:ILE:HG12	1:KG:968:PHE:HA	1.89	0.54
10:AC:227:VAL:HB	10:AC:250:ILE:HG22	1.89	0.54
8:Ed:60:LYS:NZ	8:ED:140:GLY:O	2.41	0.53
9:GF:254:ILE:HB	9:GF:262:ILE:HB	1.88	0.53
5:GN:46:GLY:HA3	5:GN:61:ASN:HB2	1.90	0.53
8:Hd:78:ASN:OD1	8:Hd:78:ASN:N	2.41	0.53
4:JL:166:ALA:HB3	4:JL:230:GLU:HG2	1.89	0.53
9:Jf:214:ALA:HB3	11:JM:206:TRP:HZ3	1.74	0.53
8:CD:98:ILE:HD11	8:CD:128:LEU:HD22	1.89	0.53
1:XG:809:VAL:O	1:XG:813:LYS:HG2	2.08	0.53
11:EM:208:LYS:HE2	11:EM:227:ILE:HG12	1.90	0.53
11:EM:238:PHE:N	11:EM:258:LYS:O	2.40	0.53
11:GM:144:THR:O	11:GM:145:ARG:NE	2.41	0.53
11:JM:199:LYS:HA	11:JM:219:ALA:HB3	1.90	0.53
1:Cg:793:GLU:O	1:Cg:796:GLN:NE2	2.41	0.53
11:CM:158:VAL:HA	11:CM:178:LYS:HE2	1.90	0.53
11:DM:228:VAL:HG11	11:DM:231:LEU:HB2	1.90	0.53
1:IG:897:SER:HA	1:IG:922:PRO:HD3	1.90	0.53
2:FH:317:LEU:HB3	2:FH:347:VAL:HG11	1.90	0.53
9:AF:269:SER:OG	9:ZF:233:ARG:NH1	2.41	0.53
2:GH:326:ALA:HB3	2:GH:338:GLU:HB3	1.89	0.53
2:JH:230:LEU:HD12	2:JH:233:LEU:HD12	1.88	0.53
7:JX:27:UNK:O	2:YH:132:GLN:NE2	2.41	0.53
1:Kg:813:LYS:NZ	2:YH:138:GLU:OE2	2.33	0.53
4:LL:129:THR:O	4:LL:133:PHE:HB2	2.08	0.53
3:AK:185:ARG:NH2	4:BL:213:ALA:O	2.42	0.53
2:MH:190:PRO:HB2	2:MH:231:ARG:HE	1.74	0.53
3:MK:117:THR:HA	3:MK:157:GLN:O	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:ML:94:VAL:HA	4:ML:97:ILE:HG12	1.91	0.53
1:YG:797:ARG:O	1:YG:801:MET:HG3	2.07	0.53
11:EM:172:ASN:OD1	11:EM:173:LEU:N	2.41	0.53
9:BF:214:ALA:HB3	9:BF:221:TRP:HB2	1.89	0.53
10:EC:95:ASP:OD2	10:EC:98:SER:OG	2.26	0.53
10:EC:173:LYS:HG2	10:FC:39:ALA:HB1	1.90	0.53
10:HC:258:SER:HA	10:HC:261:TRP:CE2	2.43	0.53
10:MC:104:ILE:HD11	10:MC:137:ALA:HB1	1.90	0.53
10:MC:233:THR:O	10:MC:240:HIS:ND1	2.39	0.53
1:LG:966:GLN:O	1:LG:970:ASN:ND2	2.42	0.53
2:HH:173:GLN:NE2	2:HH:218:THR:O	2.33	0.53
8:Hd:97:ARG:HH21	10:DC:262:ARG:HG3	1.74	0.53
8:JD:73:ILE:HD11	8:JD:133:ARG:HG3	1.90	0.53
2:KH:229:ARG:HH22	2:YH:210:SER:HB2	1.73	0.53
4:KL:130:ASP:OD2	4:KL:227:ARG:NH1	2.32	0.53
11:KM:181:PRO:O	11:KM:201:THR:OG1	2.27	0.53
9:CF:221:TRP:CD2	9:CF:231:THR:HB	2.44	0.53
4:AL:127:ILE:HB	4:AL:229:ILE:HB	1.90	0.53
11:JM:138:LEU:HD11	11:JM:142:GLY:HA3	1.91	0.53
10:EC:103:HIS:CE1	10:EC:226:VAL:HG11	2.43	0.53
10:FC:80:ILE:HD11	10:FC:196:LEU:HD13	1.89	0.53
10:GC:151:LEU:HD21	10:GC:202:ILE:HG21	1.90	0.53
10:GC:218:MET:HG2	10:GC:220:MET:HE2	1.89	0.53
10:HC:200:ARG:O	10:HC:203:GLU:HG3	2.08	0.53
10:IC:108:VAL:HG13	10:IC:207:GLY:HA3	1.88	0.53
10:MC:246:LEU:HB2	10:AC:126:ILE:HG13	1.90	0.53
4:DL:141:ASN:HD21	4:DL:143:ILE:HB	1.74	0.53
4:DL:173:GLY:O	4:DL:178:LYS:NZ	2.38	0.53
1:JG:966:GLN:O	1:JG:970:ASN:ND2	2.42	0.53
10:AC:58:MET:HA	10:AC:61:LYS:HG2	1.90	0.53
1:Ag:794:ILE:O	1:Ag:798:THR:N	2.36	0.53
3:FK:87:GLN:HB3	3:FK:128:ARG:HH12	1.74	0.53
4:FL:216:ASP:OD1	4:FL:217:ASN:N	2.41	0.53
8:Fd:48:VAL:HG11	10:AC:94:ILE:HG13	1.89	0.53
4:GL:129:THR:O	4:GL:133:PHE:HB2	2.08	0.53
2:IH:196:LEU:HD13	2:IH:204:ILE:HD11	1.91	0.53
10:CC:97:ASN:OD1	10:CC:97:ASN:N	2.34	0.53
2:KH:171:LEU:HD11	2:KH:241:LEU:HB2	1.91	0.53
11:KM:257:ASP:OD1	11:KM:257:ASP:N	2.41	0.53
3:AK:52:THR:HG22	3:AK:56:MET:HE3	1.91	0.53
2:MH:172:SER:HB3	2:MH:175:PHE:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:GM:199:LYS:HA	11:GM:219:ALA:HB3	1.90	0.53
11:JM:127:ASN:HB3	11:JM:147:ALA:HB3	1.89	0.53
1:IG:968:PHE:HB3	1:IG:1008:LEU:HD13	1.89	0.53
1:OG:886:LEU:HB3	1:OG:900:ILE:HG22	1.90	0.53
2:EH:208:LYS:HD3	1:Fg:824:THR:H	1.73	0.53
3:EK:162:ASP:N	3:EK:162:ASP:OD1	2.41	0.53
8:Ed:148:TYR:HB2	8:Ed:153:VAL:HG12	1.89	0.53
2:GH:242:ILE:HD12	2:GH:243:PRO:HD2	1.90	0.53
3:GK:93:TRP:CD1	4:GL:46:PRO:HD3	2.43	0.53
8:ID:73:ILE:O	8:ID:133:ARG:NH2	2.40	0.53
1:CG:968:PHE:HB3	1:CG:1008:LEU:HD13	1.90	0.53
6:IU:127:UNK:O	4:JL:232:GLN:NE2	2.41	0.53
8:Id:128:LEU:HD12	8:Id:128:LEU:H	1.74	0.53
10:CC:175:ILE:HA	10:CC:178:ILE:HG12	1.89	0.53
5:MN:47:GLY:O	5:MN:61:ASN:N	2.36	0.53
8:Md:142:LYS:NZ	8:Md:142:LYS:H	2.07	0.53
2:BH:225:ASN:HD21	2:CH:176:VAL:H	1.55	0.53
10:LC:246:LEU:HB2	10:MC:124:ILE:HG13	1.89	0.53
3:CK:86:ASP:OD1	3:CK:86:ASP:N	2.41	0.53
11:CM:116:PHE:HE1	11:CM:118:TYR:HB2	1.72	0.53
11:DM:229:ASN:HA	11:DM:249:GLN:HG2	1.90	0.53
1:JG:966:GLN:OE1	1:JG:1013:LYS:N	2.42	0.53
8:ED:107:ARG:HB3	8:ED:155:GLU:HG2	1.91	0.53
2:EH:146:GLY:H	7:DX:70:UNK:H2	1.56	0.53
2:EH:190:PRO:HB2	2:EH:231:ARG:HH22	1.73	0.53
2:EH:273:PRO:O	10:MC:125:ARG:NH1	2.42	0.53
2:FH:311:MET:HE3	2:FH:341:LYS:HA	1.91	0.53
8:Fd:52:MET:HE2	8:Fd:52:MET:HA	1.90	0.53
5:GN:77:ASP:OD1	5:GN:79:GLN:NE2	2.42	0.53
1:Ig:791:GLN:N	1:Ig:793:GLU:OE2	2.42	0.53
4:JL:124:THR:HA	4:JL:231:ILE:O	2.07	0.53
9:Kf:223:ILE:HG12	9:Kf:229:THR:HG22	1.90	0.53
2:LH:159:ASN:OD1	2:LH:257:GLN:NE2	2.41	0.53
3:LK:92:ASN:O	3:LK:95:SER:OG	2.24	0.53
9:ZF:267:GLU:O	2:ZH:150:LYS:NZ	2.37	0.53
11:JM:271:SER:OG	11:JM:290:ASP:OD1	2.27	0.53
1:Cg:800:ASP:O	1:Cg:803:THR:OG1	2.25	0.53
2:BH:183:ASP:HA	2:BH:256:VAL:HB	1.90	0.53
1:GG:867:ASP:OD1	1:GG:867:ASP:N	2.38	0.53
1:GG:920:SER:HB2	1:HG:865:THR:HB	1.89	0.53
10:LC:238:GLU:HG3	10:MC:132:LYS:HZ1	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:MC:108:VAL:HG13	10:MC:135:LYS:H	1.73	0.53
2:CH:192:ALA:N	2:CH:229:ARG:O	2.41	0.53
8:DD:29:PRO:HG2	4:DL:225:GLN:HA	1.90	0.53
3:DK:168:TYR:CZ	3:DK:170:LEU:HB2	2.43	0.53
1:NG:917:ASN:HA	1:NG:931:SER:HA	1.90	0.53
5:EN:46:GLY:HA3	5:EN:61:ASN:HB2	1.91	0.53
9:Ef:238:ILE:HG13	9:Ef:241:TYR:HB2	1.91	0.53
1:Kg:793:GLU:O	1:Kg:796:GLN:NE2	2.41	0.53
4:ML:216:ASP:OD1	4:ML:218:ALA:N	2.38	0.53
10:DC:89:LEU:HD21	10:DC:146:TRP:CD2	2.44	0.53
11:FM:199:LYS:HA	11:FM:219:ALA:HB3	1.90	0.53
8:Bd:71:LEU:O	8:Bd:133:ARG:NH1	2.39	0.53
10:IC:242:ASP:OD1	10:IC:242:ASP:N	2.42	0.53
1:NG:1006:ILE:HG12	1:OG:968:PHE:HA	1.91	0.53
1:Gg:795:GLN:N	1:Gg:795:GLN:OE1	2.40	0.53
1:BG:1042:THR:OG1	1:BG:1043:GLN:OE1	2.20	0.53
1:Bg:817:THR:OG1	2:BH:203:ASN:OD1	2.24	0.53
3:IK:90:ARG:NH1	3:IK:91:LEU:O	2.42	0.53
2:AH:126:GLN:HA	2:AH:129:LYS:HE2	1.91	0.53
8:KD:149:PRO:O	8:KD:152:GLN:NE2	2.41	0.53
10:CC:61:GLU:HA	10:CC:64:LEU:HD12	1.90	0.53
1:Lg:793:GLU:HB3	1:Lg:796:GLN:HE22	1.74	0.53
2:MH:292:SER:HB2	2:MH:307:SER:HB3	1.90	0.53
3:MK:73:ASN:HD21	3:MK:185:ARG:HH21	1.57	0.53
3:MK:92:ASN:N	3:MK:92:ASN:OD1	2.41	0.53
3:MK:119:TYR:HE1	3:MK:159:LEU:HD23	1.74	0.53
10:DC:101:GLU:HG2	10:DC:102:HIS:CD2	2.44	0.53
11:BM:190:ASN:HD21	11:BM:192:ARG:HH21	1.57	0.53
11:EM:258:LYS:H	11:EM:276:ALA:HB3	1.74	0.53
8:Ad:120:SER:H	8:AD:111:LYS:NZ	2.06	0.53
2:BH:214:MET:SD	2:BH:214:MET:N	2.82	0.53
10:KC:176:ILE:HA	10:KC:179:ILE:HG12	1.89	0.53
3:CK:76:ILE:HD12	3:CK:102:ILE:HD11	1.91	0.53
1:IG:1011:VAL:HG12	1:JG:963:SER:HB2	1.91	0.53
1:JG:949:ASN:HA	1:JG:952:TYR:HE2	1.74	0.53
1:JG:965:LEU:O	1:JG:1008:LEU:HB3	2.09	0.53
1:MG:876:SER:OG	1:MG:1031:VAL:O	2.25	0.53
1:MG:966:GLN:O	1:MG:970:ASN:ND2	2.41	0.53
1:AG:901:GLY:HA3	1:AG:916:PHE:HD1	1.74	0.53
2:EH:288:PRO:HB3	2:EH:305:TRP:CE2	2.44	0.53
8:FD:149:PRO:O	8:FD:152:GLN:NE2	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:FH:181:PHE:O	2:FH:211:ASN:ND2	2.41	0.53
9:Ff:245:LYS:HD3	9:Ff:257:SER:HA	1.91	0.53
5:GN:92:TYR:HD1	5:GN:94:GLN:H	1.56	0.53
1:Hg:794:ILE:HG12	2:IH:107:ILE:HG13	1.89	0.53
1:Ig:804:ALA:O	1:Ig:808:LEU:N	2.41	0.53
8:JD:59:GLU:OE2	8:JD:63:THR:OG1	2.27	0.53
2:JH:238:MET:SD	2:JH:238:MET:N	2.82	0.53
9:Kf:219:ARG:HG2	9:Kf:233:ARG:HD2	1.91	0.53
3:AK:117:THR:HA	3:AK:157:GLN:O	2.08	0.53
1:EG:966:GLN:OE1	1:EG:1013:LYS:N	2.42	0.53
2:XH:108:ASP:N	2:XH:108:ASP:OD1	2.41	0.53
2:XH:160:LEU:H	2:XH:257:GLN:CD	2.15	0.53
11:EM:144:THR:O	11:EM:145:ARG:NE	2.41	0.53
5:BN:49:ASN:HD22	5:BN:50:TYR:HD2	1.56	0.53
1:GG:1006:ILE:O	1:GG:1010:THR:OG1	2.26	0.53
10:IC:174:ILE:HA	10:IC:177:ILE:HG12	1.90	0.53
1:KG:898:LYS:HG3	1:KG:920:SER:HB3	1.90	0.53
1:PG:966:GLN:OE1	1:PG:1013:LYS:N	2.41	0.53
9:EF:219:ARG:HH11	9:EF:233:ARG:HB3	1.74	0.53
8:Ed:128:LEU:H	8:Ed:128:LEU:HD12	1.74	0.53
5:HN:82:MET:N	5:HN:82:MET:SD	2.82	0.53
7:HX:23:UNK:HA	7:HX:33:UNK:HA	1.91	0.53
4:IL:109:LEU:HD12	4:IL:114:ILE:HB	1.90	0.53
4:IL:145:TYR:CG	4:IL:146:PRO:HD3	2.44	0.53
8:KD:32:ASN:N	8:KD:32:ASN:HD22	2.06	0.53
1:Kg:800:ASP:O	1:Kg:803:THR:OG1	2.23	0.53
8:CD:109:LEU:HB3	8:Cd:137:TYR:HD2	1.71	0.53
2:LH:204:ILE:HG12	2:LH:215:ILE:HD12	1.90	0.53
1:VG:814:GLN:NE2	1:VG:814:GLN:O	2.42	0.53
9:WF:254:ILE:HB	9:WF:262:ILE:HB	1.91	0.53
8:Ad:73:ILE:HG12	8:Ad:75:ASN:H	1.74	0.53
2:BH:151:PRO:HA	2:BH:248:VAL:HG13	1.91	0.53
3:BK:96:TYR:CE2	8:Bd:26:LYS:HD3	2.44	0.53
2:CH:230:LEU:HD12	2:CH:233:LEU:HD12	1.91	0.53
1:JG:900:ILE:HD13	1:KG:866:GLY:HA3	1.91	0.53
10:AC:173:GLU:HA	10:AC:176:ILE:HG12	1.91	0.53
1:AG:939:THR:HG22	1:AG:941:ARG:HG3	1.91	0.52
1:AG:970:ASN:OD1	1:AG:971:ALA:N	2.42	0.52
2:FH:234:ASN:OD1	2:WH:211:ASN:ND2	2.31	0.52
9:Ff:251:GLN:NE2	11:FM:306:GLN:OE1	2.42	0.52
1:Gg:800:ASP:OD1	1:Gg:801:MET:N	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BG:966:GLN:OE1	1:BG:1013:LYS:N	2.41	0.52
2:HH:205:GLN:HB2	2:HH:214:MET:HB2	1.90	0.52
8:JD:126:GLU:OE2	11:JM:317:LYS:NZ	2.37	0.52
4:KL:174:SER:HB3	4:KL:177:HIS:HB3	1.91	0.52
2:LH:326:ALA:HB3	2:LH:338:GLU:HB3	1.92	0.52
2:LH:341:LYS:HB2	2:LH:361:LEU:HD21	1.92	0.52
9:Lf:254:ILE:HB	9:Lf:262:ILE:HG23	1.91	0.52
3:MK:50:ASP:OD1	3:MK:50:ASP:N	2.38	0.52
9:YF:263:LYS:HD2	9:YF:264:PHE:H	1.74	0.52
11:BM:271:SER:OG	11:BM:290:ASP:OD1	2.28	0.52
8:BD:23:MET:N	8:BD:23:MET:SD	2.82	0.52
10:IC:80:GLU:HG2	10:IC:81:GLN:N	2.23	0.52
10:LC:148:GLN:OE1	10:LC:148:GLN:N	2.32	0.52
11:CM:191:LEU:HD21	11:CM:194:LEU:HD21	1.91	0.52
1:Dg:817:THR:OG1	1:Dg:818:GLN:N	2.42	0.52
1:MG:972:PHE:O	1:MG:976:ASN:ND2	2.41	0.52
3:EK:71:GLY:O	8:FD:27:LYS:NZ	2.42	0.52
9:AF:207:ARG:NH1	9:AF:240:GLY:O	2.43	0.52
2:GH:161:SER:HB2	2:GH:164:SER:HB3	1.91	0.52
2:GH:277:ASN:HB3	2:GH:280:LEU:HD23	1.91	0.52
2:HH:173:GLN:HA	2:HH:217:ALA:HB3	1.91	0.52
8:ID:105:ARG:HB3	8:ID:153:VAL:HG12	1.91	0.52
4:IL:169:THR:OG1	4:IL:170:ASP:N	2.42	0.52
2:AH:107:ILE:HG23	1:Mg:794:ILE:HD13	1.90	0.52
9:KF:245:LYS:HE3	9:KF:257:SER:HA	1.91	0.52
2:LH:280:LEU:HD13	2:LH:328:MET:HG3	1.90	0.52
9:Mf:218:GLY:H	9:Mf:247:ILE:HD11	1.74	0.52
11:JM:191:LEU:HB3	11:JM:212:LEU:HD11	1.90	0.52
1:PG:968:PHE:CG	1:PG:1008:LEU:HD13	2.44	0.52
1:AG:899:LEU:HD21	1:AG:916:PHE:HB3	1.90	0.52
5:EN:65:TYR:OH	4:FL:221:HIS:HB3	2.10	0.52
5:EN:111:GLU:OE1	5:EN:111:GLU:N	2.34	0.52
8:Ed:29:PRO:O	8:Ed:32:ASN:ND2	2.42	0.52
1:Gg:818:GLN:HB3	2:GH:216:GLN:HG2	1.91	0.52
8:Gd:139:ALA:HB1	8:Gd:143:ALA:HB3	1.91	0.52
9:Gf:246:LEU:HB3	9:Gf:255:LEU:HB2	1.91	0.52
2:HH:206:TRP:NE1	2:HH:210:SER:O	2.42	0.52
11:HM:280:TYR:HE1	11:HM:299:LEU:HD23	1.75	0.52
11:KM:158:VAL:HA	11:KM:178:LYS:HZ3	1.73	0.52
1:DG:899:LEU:HD21	1:DG:916:PHE:HB3	1.89	0.52
5:LN:62:ASN:OD1	5:LN:62:ASN:N	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:Lf:247:ILE:HG22	9:Lf:254:ILE:HD12	1.91	0.52
4:AL:124:THR:HG22	4:AL:232:GLN:HG2	1.91	0.52
4:AL:145:TYR:CD1	4:AL:146:PRO:HD3	2.44	0.52
1:FG:966:GLN:OE1	1:FG:1013:LYS:N	2.42	0.52
2:BH:201:SER:HA	2:BH:219:LYS:HG3	1.92	0.52
8:Bd:76:ALA:O	8:Bd:80:GLN:NE2	2.32	0.52
2:CH:279:LEU:HD11	2:CH:289:PRO:HB3	1.91	0.52
9:DF:207:ARG:NH2	9:DF:208:ILE:O	2.42	0.52
1:MG:968:PHE:HB3	1:MG:1008:LEU:HD13	1.92	0.52
1:NG:1006:ILE:O	1:NG:1010:THR:OG1	2.25	0.52
2:EH:250:TYR:CZ	2:DH:238:MET:HB2	2.44	0.52
2:FH:238:MET:HG2	2:WH:250:TYR:HB3	1.90	0.52
8:Fd:82:ARG:HH12	8:Fd:127:SER:HA	1.74	0.52
1:BG:949:ASN:HA	1:BG:952:TYR:CE2	2.44	0.52
3:IK:111:LYS:NZ	3:IK:150:ASP:O	2.42	0.52
10:CC:106:LEU:HD12	10:CC:107:PRO:HD2	1.91	0.52
2:KH:207:ASP:OD1	2:KH:210:SER:OG	2.27	0.52
11:KM:261:ALA:HB3	11:KM:279:ILE:HG23	1.90	0.52
3:LK:47:GLY:O	3:LK:108:GLN:NE2	2.34	0.52
2:MH:190:PRO:HB2	2:MH:231:ARG:NE	2.24	0.52
2:WH:155:SER:OG	2:WH:255:ARG:NH2	2.42	0.52
2:ZH:170:ARG:HG3	2:ZH:249:ASP:H	1.74	0.52
11:GM:119:GLU:HG3	11:GM:139:ALA:HB3	1.91	0.52
10:FC:57:GLU:OE1	10:FC:58:MET:N	2.42	0.52
10:GC:141:ILE:HD11	10:GC:144:PRO:HA	1.91	0.52
10:HC:101:GLU:HG2	10:HC:102:HIS:CD2	2.44	0.52
10:IC:89:LEU:HD22	10:IC:146:TRP:CG	2.44	0.52
10:IC:101:GLU:O	8:AD:142:LYS:NZ	2.43	0.52
9:DF:243:MET:O	9:DF:257:SER:N	2.34	0.52
11:DM:133:TYR:CE1	11:DM:153:GLN:HG3	2.45	0.52
1:MG:1011:VAL:HG12	1:NG:963:SER:HB2	1.91	0.52
1:NG:951:HIS:O	1:NG:955:ARG:NE	2.36	0.52
8:Ed:138:GLN:HE22	8:ED:111:LYS:HG2	1.75	0.52
2:FH:319:ILE:HA	2:FH:347:VAL:HG22	1.90	0.52
9:AF:219:ARG:HG3	2:BH:148:PRO:HB2	1.92	0.52
8:GD:149:PRO:O	8:GD:152:GLN:NE2	2.42	0.52
8:HD:35:ASP:O	8:HD:39:ILE:HG12	2.10	0.52
5:IN:89:GLY:O	5:IN:104:ASN:ND2	2.42	0.52
8:Id:76:ALA:O	8:Id:80:GLN:NE2	2.29	0.52
3:KK:114:ILE:HG22	3:KK:184:PHE:HB3	1.91	0.52
5:LN:74:ALA:HB3	5:LN:76:MET:HE3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:VG:816:GLU:OE2	2:CH:200:SER:N	2.42	0.52
2:VH:321:SER:OG	2:VH:346:LEU:N	2.37	0.52
10:GC:175:ILE:HA	10:GC:178:ILE:HG12	1.90	0.52
10:LC:146:TRP:HB2	10:LC:150:LEU:HD23	1.91	0.52
10:LC:265:VAL:HA	8:Cd:85:VAL:HG22	1.90	0.52
3:CK:90:ARG:NH1	3:CK:91:LEU:O	2.42	0.52
4:DL:115:GLN:HB2	4:DL:126:ILE:HB	1.91	0.52
1:KG:919:MET:HG3	1:KG:930:ILE:HG23	1.92	0.52
1:MG:939:THR:HG22	1:MG:941:ARG:HG3	1.92	0.52
9:HF:207:ARG:HH21	9:HF:208:ILE:HG23	1.74	0.52
11:HM:300:ASP:OD2	11:HM:302:ARG:NE	2.41	0.52
10:CC:240:ILE:HG12	10:DC:254:LEU:HD13	1.92	0.52
1:Kg:820:TYR:CD2	2:KH:205:GLN:HB3	2.45	0.52
2:MH:189:TRP:CD2	2:MH:230:LEU:HD13	2.44	0.52
8:Md:148:TYR:HB2	8:Md:153:VAL:HG12	1.90	0.52
11:BM:315:TYR:OH	4:BL:177:HIS:ND1	2.40	0.52
11:FM:174:GLN:NE2	11:FM:193:GLN:O	2.38	0.52
11:GM:308:ASP:OD1	11:GM:308:ASP:N	2.42	0.52
7:BX:21:UNK:N	7:BX:78:UNK:O	2.42	0.52
10:GC:168:LYS:O	10:GC:173:LYS:NZ	2.43	0.52
9:DF:215:VAL:HG12	2:DH:245:GLN:HE22	1.75	0.52
2:GH:251:ARG:NH1	2:GH:253:ASP:OD1	2.42	0.52
11:HM:162:VAL:HG12	11:HM:182:LYS:HB2	1.91	0.52
11:HM:271:SER:OG	11:HM:290:ASP:OD1	2.28	0.52
2:AH:282:HIS:HB3	2:AH:287:VAL:HG13	1.90	0.52
1:DG:965:LEU:O	1:DG:1008:LEU:HB3	2.10	0.52
1:EG:1011:VAL:HG12	1:FG:963:SER:HB2	1.91	0.52
1:FG:969:GLY:HA2	1:FG:1005:VAL:HA	1.90	0.52
11:BM:293:ALA:HB1	4:BL:49:ASN:HB3	1.92	0.52
2:BH:229:ARG:HG2	2:BH:236:PRO:HB3	1.90	0.52
4:BL:54:ARG:HB3	4:BL:57:VAL:HG22	1.92	0.52
2:CH:289:PRO:HG2	2:CH:292:SER:HB2	1.91	0.52
4:CL:145:TYR:CD1	4:CL:146:PRO:HD3	2.44	0.52
11:CM:240:GLN:HB3	11:CM:242:LYS:HE3	1.90	0.52
1:KG:884:PRO:HG2	1:LG:1040:LEU:HD11	1.90	0.52
10:AC:202:ARG:O	10:AC:205:GLU:HG3	2.10	0.52
2:FH:230:LEU:HB2	2:FH:233:LEU:HB3	1.92	0.52
1:Gg:793:GLU:HB2	2:XH:107:ILE:HG21	1.91	0.52
8:Gd:28:PRO:HB2	8:Gd:32:ASN:ND2	2.25	0.52
2:LH:302:ALA:O	2:LH:303:ARG:NH1	2.30	0.52
4:LL:169:THR:OG1	4:LL:170:ASP:N	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:MF:246:LEU:HB3	9:MF:255:LEU:HB2	1.91	0.52
9:MF:263:LYS:NZ	9:MF:264:PHE:O	2.43	0.52
2:WH:157:PHE:HD1	2:WH:255:ARG:HB2	1.74	0.52
11:BM:256:HIS:O	11:BM:277:SER:OG	2.28	0.52
11:GM:127:ASN:N	11:GM:127:ASN:OD1	2.42	0.52
11:GM:177:LEU:HD12	11:GM:196:MET:HE1	1.92	0.52
11:GM:216:ALA:HB3	11:GM:235:LEU:HD12	1.92	0.52
2:DH:342:SER:OG	2:DH:344:VAL:O	2.27	0.52
11:DM:129:LEU:HB2	11:DM:150:ILE:HD11	1.91	0.52
1:HG:1019:ALA:O	1:HG:1023:PHE:HB2	2.08	0.52
2:EH:292:SER:HB3	2:EH:307:SER:HB3	1.92	0.52
5:HN:46:GLY:HA3	5:HN:61:ASN:HB2	1.90	0.52
1:Bg:811:ASP:O	1:Bg:814:GLN:NE2	2.39	0.52
9:IF:269:SER:H	2:IH:150:LYS:HZ1	1.58	0.52
8:JD:124:LYS:O	11:JM:317:LYS:NZ	2.43	0.52
8:KD:73:ILE:O	8:KD:133:ARG:NH2	2.37	0.52
2:KH:189:TRP:CE3	2:KH:260:GLY:HA2	2.43	0.52
2:KH:341:LYS:HE3	2:KH:361:LEU:HD11	1.91	0.52
4:KL:169:THR:HG21	4:KL:178:LYS:HB3	1.92	0.52
11:KM:117:ARG:HG2	11:KM:137:TYR:HB3	1.91	0.52
1:DG:1006:ILE:HG12	1:EG:968:PHE:HA	1.91	0.52
9:MF:264:PHE:HB3	9:MF:269:SER:HA	1.92	0.52
1:Mg:817:THR:OG1	1:Mg:818:GLN:N	2.42	0.52
9:Af:221:TRP:HE1	9:Af:229:THR:HG23	1.74	0.52
9:Af:245:LYS:HD3	9:Af:257:SER:HA	1.91	0.52
5:BN:99:GLY:O	5:BN:113:SER:OG	2.23	0.52
8:DD:68:ASP:OD2	8:DD:70:THR:OG1	2.21	0.52
1:IG:966:GLN:O	1:IG:970:ASN:ND2	2.43	0.52
1:JG:924:ALA:HB3	1:JG:926:LYS:HE3	1.92	0.52
1:KG:878:ASN:OD1	1:KG:879:SER:N	2.42	0.52
1:MG:951:HIS:O	1:MG:955:ARG:NE	2.38	0.52
8:Ed:97:ARG:HG3	10:AC:265:ALA:HB3	1.92	0.52
8:FD:119:ILE:HD12	8:FD:138:GLN:HG2	1.91	0.52
9:FF:245:LYS:HD3	9:FF:257:SER:HA	1.91	0.52
8:GD:137:TYR:CZ	8:Gd:57:LYS:HG3	2.45	0.52
8:Hd:128:LEU:H	8:Hd:128:LEU:HD12	1.74	0.52
3:IK:70:VAL:HA	8:JD:27:LYS:HE2	1.92	0.52
11:IM:155:LEU:HB3	11:IM:175:ILE:HD12	1.92	0.52
7:IX:1:UNK:N	7:XX:19:UNK:O	2.42	0.52
4:JL:212:ASN:N	4:JL:212:ASN:OD1	2.43	0.52
9:Jf:222:LEU:HD22	9:Jf:230:LEU:HD12	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LH:313:VAL:HG13	2:LH:337:TYR:HB2	1.92	0.52
4:ML:44:HIS:HB2	4:ML:48:ASN:HA	1.92	0.52
5:MN:102:VAL:HB	5:MN:108:VAL:HG12	1.92	0.52
1:WG:818:GLN:NE2	2:WH:203:ASN:OD1	2.43	0.52
2:BH:302:ALA:C	2:BH:303:ARG:HD2	2.35	0.52
1:GG:886:LEU:HA	1:GG:899:LEU:O	2.09	0.52
9:DF:246:LEU:HB3	9:DF:255:LEU:HD12	1.92	0.52
2:DH:130:LEU:HD23	2:DH:133:ILE:HD11	1.91	0.52
3:DK:53:ILE:HG13	3:DK:108:GLN:HG2	1.91	0.52
4:EL:118:GLU:OE2	4:EL:123:ARG:NE	2.43	0.51
8:FD:136:ASP:O	8:FD:60:LYS:NZ	2.42	0.51
8:FD:160:LYS:NZ	8:FD:161:ILE:O	2.35	0.51
1:Bg:814:GLN:OE1	1:Bg:814:GLN:N	2.40	0.51
5:IN:111:GLU:H	5:IN:111:GLU:CD	2.16	0.51
9:JF:230:LEU:HA	2:JH:165:THR:HG21	1.92	0.51
2:JH:273:PRO:HB3	10:EC:120:ALA:HB2	1.92	0.51
8:CD:73:ILE:HD12	8:CD:147:VAL:HG23	1.91	0.51
8:CD:130:GLU:OE2	8:CD:133:ARG:NH1	2.43	0.51
8:MD:161:ILE:HG13	8:MD:162:TYR:H	1.75	0.51
2:MH:257:GLN:OE1	2:ZH:282:HIS:NE2	2.42	0.51
11:MM:254:LYS:HE2	11:MM:272:LEU:HD23	1.91	0.51
9:VF:258:SER:OG	9:VF:260:GLN:OE1	2.27	0.51
2:WH:311:MET:HE3	2:WH:341:LYS:HB3	1.92	0.51
9:XF:207:ARG:HH21	9:XF:240:GLY:HA3	1.74	0.51
2:ZH:315:THR:HG23	2:ZH:317:LEU:H	1.74	0.51
11:EM:240:GLN:HA	11:EM:260:VAL:O	2.10	0.51
11:FM:228:VAL:HG23	11:FM:246:LEU:HD11	1.91	0.51
11:FM:235:LEU:HD23	11:FM:255:THR:HG22	1.92	0.51
2:BH:152:THR:OG1	2:BH:153:ALA:N	2.43	0.51
10:IC:172:LYS:HG2	10:JC:39:ALA:HB1	1.92	0.51
1:HG:1017:GLN:NE2	1:IG:1020:GLN:OE1	2.43	0.51
1:LG:867:ASP:OD1	1:LG:867:ASP:N	2.32	0.51
8:AD:149:PRO:O	8:AD:152:GLN:NE2	2.43	0.51
3:EK:117:THR:HA	3:EK:157:GLN:O	2.10	0.51
2:HH:157:PHE:HZ	2:HH:257:GLN:HG2	1.76	0.51
4:IL:166:ALA:HB3	4:IL:230:GLU:HG2	1.92	0.51
1:Jg:810:GLN:HA	1:Jg:813:LYS:HB2	1.91	0.51
3:JK:72:GLN:OE1	4:KL:216:ASP:N	2.38	0.51
4:JL:121:ASP:O	4:JL:123:ARG:NH1	2.42	0.51
4:JL:230:GLU:OE2	4:JL:232:GLN:NE2	2.43	0.51
11:MM:118:TYR:CZ	11:MM:124:VAL:HG23	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:VF:243:MET:HB2	9:VF:257:SER:HB3	1.92	0.51
8:Bd:105:ARG:HB3	8:Bd:153:VAL:HG23	1.91	0.51
10:LC:83:ASN:ND2	5:DN:79:GLN:O	2.43	0.51
10:MC:148:GLN:OE1	10:MC:148:GLN:N	2.40	0.51
9:Cf:246:LEU:HB3	9:Cf:255:LEU:HD12	1.93	0.51
3:DK:151:SER:OG	3:DK:152:ARG:N	2.41	0.51
11:DM:119:GLU:HG3	11:DM:139:ALA:HB3	1.91	0.51
1:NG:931:SER:H	1:NG:1043:GLN:HE22	1.56	0.51
5:EN:47:GLY:O	5:EN:61:ASN:N	2.43	0.51
1:Fg:814:GLN:O	1:Fg:814:GLN:NE2	2.43	0.51
5:FN:85:CYS:N	10:AC:155:ASP:OD2	2.39	0.51
8:Fd:109:LEU:HD13	8:Fd:155:GLU:HG3	1.92	0.51
9:Ff:214:ALA:HB3	11:FM:206:TRP:HZ3	1.75	0.51
3:GK:111:LYS:HZ2	3:GK:111:LYS:H	1.58	0.51
2:HH:140:ALA:HB2	2:XH:124:PRO:HB3	1.93	0.51
2:IH:315:THR:OG1	2:IH:316:ASN:N	2.44	0.51
3:KK:53:ILE:HG12	3:KK:108:GLN:HG2	1.92	0.51
4:KL:94:VAL:HA	4:KL:97:ILE:HG12	1.92	0.51
5:KN:47:GLY:O	5:KN:61:ASN:N	2.26	0.51
1:DG:931:SER:H	1:DG:1043:GLN:NE2	2.09	0.51
8:CD:40:LYS:O	8:CD:43:GLU:HG3	2.10	0.51
4:LL:145:TYR:CD1	4:LL:146:PRO:HD3	2.46	0.51
4:ML:191:THR:HG21	11:MM:289:ALA:HB3	1.92	0.51
1:EG:876:SER:OG	1:EG:1031:VAL:O	2.23	0.51
2:VH:145:PRO:HA	7:CX:70:UNK:H2	1.75	0.51
7:YX:21:UNK:O	7:YX:78:UNK:N	2.44	0.51
7:YX:23:UNK:HA	7:YX:33:UNK:HA	1.92	0.51
2:ZH:289:PRO:O	2:ZH:292:SER:OG	2.28	0.51
1:FG:897:SER:HA	1:FG:922:PRO:HD3	1.91	0.51
11:AM:228:VAL:HG12	11:AM:230:ARG:H	1.76	0.51
10:EC:176:TRP:O	10:EC:180:THR:OG1	2.28	0.51
1:GG:1040:LEU:HD23	1:GG:1040:LEU:H	1.75	0.51
3:CK:123:TYR:CD2	3:CK:124:VAL:HG23	2.45	0.51
8:DD:35:ASP:O	8:DD:39:ILE:HG12	2.10	0.51
1:Dg:800:ASP:OD1	1:Dg:800:ASP:N	2.33	0.51
10:AC:166:LEU:HD23	10:AC:166:LEU:H	1.75	0.51
1:Eg:797:ARG:HH21	1:Eg:801:MET:HB3	1.74	0.51
2:FH:151:PRO:HA	2:FH:248:VAL:HG23	1.91	0.51
2:HH:242:ILE:HD12	2:HH:243:PRO:HD2	1.91	0.51
3:HK:108:GLN:OE1	3:HK:108:GLN:N	2.43	0.51
8:Hd:84:SER:OG	8:Hd:123:THR:O	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:IL:217:ASN:HA	4:IL:223:SER:HB2	1.92	0.51
11:IM:228:VAL:HG11	11:IM:231:LEU:HB2	1.93	0.51
1:CG:1006:ILE:HG12	1:DG:968:PHE:HA	1.91	0.51
9:If:254:ILE:HD11	9:If:262:ILE:HB	1.92	0.51
4:JL:145:TYR:CD1	4:JL:146:PRO:HD3	2.46	0.51
4:JL:174:SER:HB3	4:JL:177:HIS:HB3	1.90	0.51
3:KK:92:ASN:O	3:KK:95:SER:OG	2.23	0.51
3:LK:74:TYR:HE1	3:LK:186:ARG:HB2	1.75	0.51
11:AM:202:LEU:O	11:AM:222:ILE:HA	2.11	0.51
11:BM:212:LEU:HD23	11:BM:228:VAL:HG13	1.92	0.51
11:EM:228:VAL:HG11	11:EM:231:LEU:HB2	1.93	0.51
11:JM:123:VAL:HG22	11:JM:143:THR:HB	1.90	0.51
5:AN:111:GLU:H	5:AN:111:GLU:CD	2.19	0.51
10:HC:174:ILE:HA	10:HC:177:ILE:HG12	1.92	0.51
10:LC:149:TYR:HB3	10:LC:201:ILE:HB	1.93	0.51
9:DF:238:ILE:HD12	9:DF:239:PRO:HD2	1.92	0.51
11:DM:256:HIS:O	11:DM:277:SER:OG	2.26	0.51
1:JG:876:SER:HB3	1:KG:941:ARG:HG2	1.91	0.51
9:Df:256:THR:HG1	9:Df:260:GLN:H	1.57	0.51
1:AG:870:PHE:HB3	10:AC:56:ARG:HH22	1.74	0.51
10:BC:31:SER:HB2	10:AC:185:TRP:CZ3	2.46	0.51
3:HK:66:LYS:HB3	3:HK:77:SER:HB3	1.92	0.51
2:JH:230:LEU:HB2	2:JH:233:LEU:HB2	1.93	0.51
10:CC:186:ASN:HA	10:CC:189:ASP:OD2	2.09	0.51
11:KM:273:ALA:HB1	11:KM:277:SER:HB2	1.91	0.51
1:DG:891:THR:OG1	1:DG:892:GLY:N	2.44	0.51
8:CD:109:LEU:HB3	8:Cd:137:TYR:CD2	2.45	0.51
2:LH:184:SER:OG	2:LH:256:VAL:O	2.26	0.51
3:AK:166:THR:HG22	3:AK:168:TYR:H	1.76	0.51
9:MF:219:ARG:NH2	9:MF:231:THR:OG1	2.44	0.51
2:MH:267:PRO:HB2	2:ZH:328:MET:HE3	1.93	0.51
4:AL:210:ASP:OD1	4:AL:210:ASP:N	2.34	0.51
11:GM:125:THR:HG23	11:GM:145:ARG:HB2	1.93	0.51
8:Ad:148:TYR:HB2	8:Ad:153:VAL:HG12	1.92	0.51
3:BK:166:THR:HG22	3:BK:168:TYR:H	1.76	0.51
5:BN:89:GLY:HA3	5:BN:104:ASN:HB2	1.92	0.51
10:FC:237:ASP:OD1	10:FC:240:GLU:N	2.44	0.51
10:GC:79:ILE:HD11	10:GC:195:LEU:HD13	1.92	0.51
10:LC:108:VAL:HG13	10:LC:134:ALA:HB3	1.91	0.51
11:CM:257:ASP:OD1	11:CM:257:ASP:N	2.43	0.51
8:Cd:74:PRO:HG3	8:Cd:147:VAL:HG11	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HG:920:SER:HB2	1:IG:865:THR:HB	1.92	0.51
10:BC:58:MET:O	10:BC:61:LYS:HG2	2.11	0.51
1:CG:966:GLN:OE1	1:CG:1013:LYS:N	2.44	0.51
2:AH:131:LYS:HD3	2:ZH:145:PRO:HD3	1.93	0.51
4:KL:199:ALA:HB3	4:KL:202:ARG:HG3	1.92	0.51
1:DG:878:ASN:OD1	1:DG:879:SER:N	2.44	0.51
2:LH:130:LEU:HA	2:LH:133:ILE:HG22	1.93	0.51
2:MH:132:GLN:O	2:MH:135:GLU:HG2	2.10	0.51
2:ZH:326:ALA:HB3	2:ZH:338:GLU:HB3	1.93	0.51
11:CM:202:LEU:HD21	11:CM:204:LEU:HG	1.93	0.51
9:Df:256:THR:OG1	9:Df:260:GLN:N	2.44	0.51
2:GH:171:LEU:HD11	2:GH:241:LEU:HB3	1.93	0.51
3:GK:56:MET:HE1	3:GK:108:GLN:HG3	1.92	0.51
8:HD:151:SER:O	8:HD:153:VAL:HG13	2.11	0.51
2:HH:207:ASP:N	2:HH:210:SER:OG	2.44	0.51
4:HL:91:VAL:HA	4:HL:94:VAL:HG12	1.92	0.51
4:HL:216:ASP:CG	4:HL:218:ALA:H	2.19	0.51
1:Bg:798:THR:HG22	1:Bg:802:LEU:HD23	1.93	0.51
9:IF:220:ALA:HB3	9:IF:232:VAL:HG23	1.92	0.51
1:CG:898:LYS:HE3	1:DG:866:GLY:O	2.11	0.51
2:JH:311:MET:HG3	2:JH:341:LYS:HA	1.93	0.51
9:Jf:208:ILE:O	9:Jf:241:TYR:OH	2.28	0.51
2:KH:238:MET:HB2	2:YH:250:TYR:CZ	2.45	0.51
1:Lg:810:GLN:NE2	1:Lg:811:ASP:OD1	2.44	0.51
3:AK:92:ASN:O	3:AK:95:SER:OG	2.23	0.51
4:ML:134:MET:HE3	4:ML:139:ARG:HD3	1.92	0.51
1:EG:880:ASP:OD1	1:EG:881:GLU:N	2.42	0.51
9:CF:209:ILE:O	9:CF:225:SER:N	2.43	0.51
9:XF:253:ARG:HG3	9:XF:261:VAL:HG13	1.93	0.51
2:XH:160:LEU:N	2:XH:257:GLN:OE1	2.37	0.51
10:DC:147:ARG:HD2	10:DC:148:GLN:N	2.26	0.51
1:FG:931:SER:O	1:FG:1042:THR:OG1	2.29	0.51
1:FG:1006:ILE:HD13	1:GG:968:PHE:HA	1.93	0.51
11:AM:159:GLY:HA3	11:AM:179:GLY:HA3	1.91	0.51
11:GM:271:SER:OG	11:GM:290:ASP:OD1	2.29	0.51
2:CH:315:THR:OG1	2:CH:316:ASN:N	2.43	0.51
1:OG:965:LEU:O	1:OG:1008:LEU:HB3	2.11	0.51
8:Dd:91:ILE:HG22	8:Dd:119:ILE:HG12	1.92	0.51
2:EH:143:ALA:O	2:FH:131:LYS:NZ	2.44	0.51
3:EK:95:SER:HA	3:EK:98:LEU:HD23	1.92	0.51
10:BC:122:ASP:OD1	10:BC:125:SER:OG	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:GL:134:MET:HE3	4:GL:139:ARG:HH12	1.74	0.51
8:Gd:149:PRO:O	8:Gd:152:GLN:NE2	2.43	0.51
11:HM:303:GLU:HG2	11:HM:305:GLY:H	1.75	0.51
11:IM:127:ASN:HB3	11:IM:147:ALA:HB3	1.92	0.51
8:JD:36:ASP:O	8:JD:40:LYS:HG2	2.11	0.51
8:JD:137:TYR:CZ	8:JD:57:LYS:HD3	2.45	0.51
2:AH:115:MET:HE3	1:Mg:802:LEU:HA	1.93	0.51
2:AH:297:VAL:O	5:MN:72:ARG:NH2	2.44	0.51
8:LD:34:SER:OG	8:Ld:36:ASP:OD1	2.28	0.51
2:MH:285:GLU:HG3	10:HC:203:GLU:HB3	1.92	0.51
2:MH:324:TRP:HA	2:MH:339:MET:HB3	1.91	0.51
9:WF:241:TYR:HB3	9:WF:256:THR:HG21	1.92	0.51
2:XH:343:PRO:HB2	2:XH:357:LYS:HE2	1.92	0.51
11:EM:185:ILE:HB	11:EM:204:LEU:HD22	1.93	0.51
8:Ad:149:PRO:O	8:Ad:152:GLN:NE2	2.42	0.51
10:GC:243:ASP:OD1	10:GC:243:ASP:N	2.42	0.51
1:GG:903:PHE:HB3	1:GG:914:ILE:HD13	1.93	0.51
10:KC:227:VAL:HA	10:KC:250:ILE:HA	1.92	0.51
9:DF:268:ASP:OD1	9:DF:268:ASP:N	2.44	0.51
1:NG:970:ASN:OD1	1:NG:971:ALA:N	2.43	0.51
4:EL:49:ASN:ND2	11:EM:293:ALA:O	2.43	0.51
4:EL:123:ARG:NH1	4:EL:235:THR:OG1	2.42	0.51
1:Fg:795:GLN:OE1	1:Fg:795:GLN:N	2.43	0.51
1:Fg:811:ASP:O	1:Fg:814:GLN:NE2	2.38	0.51
3:GK:53:ILE:HA	3:GK:56:MET:HE2	1.91	0.51
4:HL:49:ASN:O	4:HL:51:GLN:NE2	2.33	0.51
4:HL:99:ARG:HA	4:HL:104:LYS:HG2	1.93	0.51
10:CC:146:THR:H	10:CC:149:GLN:NE2	2.09	0.51
2:KH:204:ILE:HG12	2:KH:215:ILE:HD12	1.92	0.51
11:KM:256:HIS:O	11:KM:277:SER:OG	2.20	0.51
5:KN:92:TYR:HD1	5:KN:94:GLN:H	1.58	0.51
3:AK:152:ARG:HD2	2:BH:352:LYS:HG3	1.92	0.51
1:FG:1042:THR:OG1	1:FG:1043:GLN:OE1	2.24	0.51
9:BF:238:ILE:HD12	9:BF:239:PRO:HD2	1.92	0.51
1:IG:920:SER:HB2	1:JG:865:THR:HB	1.93	0.51
1:LG:967:GLY:HA2	1:LG:970:ASN:HD21	1.76	0.51
1:PG:931:SER:H	1:PG:1043:GLN:NE2	2.07	0.51
8:AD:23:MET:N	8:AD:23:MET:SD	2.84	0.51
9:GF:267:GLU:O	2:GH:150:LYS:NZ	2.36	0.51
3:HK:168:TYR:CZ	3:HK:170:LEU:HB2	2.45	0.51
11:HM:172:ASN:OD1	11:HM:173:LEU:N	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:IH:203:ASN:OD1	2:IH:205:GLN:NE2	2.42	0.51
11:IM:119:GLU:HG3	11:IM:139:ALA:HB3	1.93	0.51
2:AH:316:ASN:N	2:AH:316:ASN:OD1	2.42	0.51
8:KD:92:GLU:N	8:KD:92:GLU:OE1	2.44	0.51
9:Lf:233:ARG:HG3	9:Lf:234:GLU:CD	2.36	0.51
2:YH:190:PRO:HB2	2:YH:231:ARG:HG3	1.93	0.51
11:JM:196:MET:HE3	11:JM:222:ILE:HD11	1.92	0.51
1:Cg:807:GLN:HA	1:Cg:810:GLN:HE21	1.75	0.51
6:AU:127:UNK:O	4:BL:232:GLN:NE2	2.44	0.51
8:Ad:68:ASP:OD1	8:Ad:70:THR:OG1	2.23	0.51
3:BK:60:LEU:HD22	3:BK:65:ILE:HD11	1.93	0.51
4:BL:91:VAL:HA	4:BL:94:VAL:HG22	1.92	0.51
10:KC:155:ASP:N	10:KC:155:ASP:OD1	2.43	0.51
11:CM:306:GLN:OE1	9:Cf:251:GLN:NE2	2.44	0.51
8:Cd:68:ASP:N	8:Cd:68:ASP:OD1	2.44	0.51
1:JG:878:ASN:OD1	1:JG:879:SER:N	2.44	0.51
10:AC:244:ASP:OD1	10:AC:244:ASP:N	2.44	0.51
9:EF:241:TYR:O	9:EF:258:SER:OG	2.29	0.51
9:AF:219:ARG:HH22	2:BH:150:LYS:HG3	1.75	0.50
9:HF:219:ARG:HG2	2:XH:148:PRO:HD2	1.92	0.50
2:HH:171:LEU:O	2:HH:244:GLY:N	2.43	0.50
9:IF:214:ALA:HB3	9:IF:221:TRP:HB2	1.92	0.50
2:IH:295:LEU:HD12	2:IH:304:ALA:HB1	1.93	0.50
1:CG:1042:THR:OG1	1:CG:1043:GLN:OE1	2.22	0.50
9:JF:238:ILE:HD12	9:JF:239:PRO:HD2	1.93	0.50
2:KH:214:MET:N	2:KH:214:MET:SD	2.84	0.50
11:KM:275:ASP:HA	11:KM:295:ASN:H	1.76	0.50
1:Lg:793:GLU:O	1:Lg:796:GLN:NE2	2.45	0.50
11:LM:276:ALA:H	11:LM:295:ASN:HB2	1.76	0.50
2:VH:150:LYS:H	2:VH:247:ALA:HA	1.76	0.50
7:YX:21:UNK:N	7:YX:78:UNK:O	2.44	0.50
11:BM:203:SER:HA	11:BM:223:GLN:O	2.11	0.50
11:GM:129:LEU:HB2	11:GM:150:ILE:HD11	1.93	0.50
5:BN:115:GLN:OE1	10:JC:70:GLN:NE2	2.44	0.50
10:EC:233:VAL:HG12	10:EC:242:ILE:HA	1.92	0.50
2:DH:132:GLN:O	2:DH:135:GLU:HG2	2.11	0.50
1:IG:891:THR:OG1	1:IG:892:GLY:N	2.40	0.50
1:NG:899:LEU:HD21	1:NG:916:PHE:HB3	1.93	0.50
8:Dd:139:ALA:O	8:Dd:142:LYS:NZ	2.40	0.50
9:Ef:243:MET:N	9:Ef:257:SER:OG	2.40	0.50
10:BC:132:THR:OG1	10:AC:241:ILE:O	2.28	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:AF:213:GLN:O	2:AH:245:GLN:NE2	2.44	0.50
2:HH:199:PRO:HD3	1:XG:818:GLN:HA	1.93	0.50
3:HK:120:SER:N	3:HK:160:GLY:O	2.33	0.50
11:IM:284:LEU:HD11	11:IM:302:ARG:HH22	1.76	0.50
4:JL:224:ALA:HA	4:JL:227:ARG:NH1	2.27	0.50
8:Jd:72:THR:OG1	8:Jd:73:ILE:N	2.45	0.50
1:DG:876:SER:N	1:EG:940:ALA:O	2.43	0.50
8:Ld:149:PRO:O	8:Ld:152:GLN:NE2	2.36	0.50
3:MK:45:VAL:HG12	3:MK:48:ALA:HB2	1.93	0.50
4:ML:145:TYR:CG	4:ML:146:PRO:HD3	2.46	0.50
9:VF:238:ILE:HD11	9:VF:256:THR:HG23	1.92	0.50
9:XF:251:GLN:C	2:XH:246:LYS:HZ1	2.20	0.50
4:AL:161:SER:O	4:AL:202:ARG:NH2	2.30	0.50
11:FM:153:GLN:HG2	11:FM:173:LEU:HA	1.93	0.50
9:Bf:208:ILE:HG13	9:Bf:225:SER:HB2	1.93	0.50
10:GC:97:ASN:OD1	10:GC:97:ASN:N	2.42	0.50
10:GC:101:LEU:HB2	10:GC:105:ILE:HG13	1.92	0.50
3:CK:47:GLY:O	3:CK:108:GLN:NE2	2.44	0.50
3:DK:143:TYR:O	3:DK:146:SER:OG	2.24	0.50
1:KG:867:ASP:OD1	1:KG:867:ASP:N	2.44	0.50
1:KG:968:PHE:HB3	1:KG:1008:LEU:HD13	1.92	0.50
2:EH:189:TRP:CD1	2:EH:261:PRO:HD3	2.46	0.50
9:FF:219:ARG:HH21	9:FF:231:THR:HG23	1.76	0.50
2:FH:341:LYS:HE3	2:FH:361:LEU:HD22	1.92	0.50
3:FK:78:ILE:HB	3:FK:180:VAL:HG13	1.92	0.50
8:Fd:36:ASP:O	8:Fd:39:ILE:HG12	2.12	0.50
2:GH:306:LEU:HD11	2:GH:309:GLU:HA	1.93	0.50
2:HH:280:LEU:HB3	2:HH:328:MET:HG3	1.92	0.50
5:IN:47:GLY:O	5:IN:61:ASN:N	2.41	0.50
3:JK:177:ASN:OD1	3:JK:177:ASN:N	2.43	0.50
2:LH:183:ASP:OD1	2:LH:187:ALA:N	2.42	0.50
3:LK:116:VAL:HG12	3:LK:182:ILE:HG23	1.93	0.50
8:MD:130:GLU:OE2	8:MD:133:ARG:NH1	2.44	0.50
11:BM:289:ALA:HB3	4:BL:191:THR:HG21	1.92	0.50
11:GM:246:LEU:O	11:GM:264:SER:OG	2.29	0.50
8:BD:36:ASP:OD1	10:JC:76:ARG:NH2	2.44	0.50
1:GG:900:ILE:HG13	1:GG:918:THR:HB	1.92	0.50
10:KC:249:ARG:NH1	2:DH:270:GLU:OE2	2.42	0.50
10:MC:128:ASP:OD1	10:MC:128:ASP:N	2.44	0.50
4:EL:224:ALA:HA	4:EL:227:ARG:NH1	2.26	0.50
2:FH:253:ASP:HB3	2:FH:255:ARG:HH22	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Fd:79:LEU:HA	8:Fd:128:LEU:HD12	1.92	0.50
10:BC:221:MET:HG2	10:BC:263:TRP:CG	2.47	0.50
8:GD:69:ASN:HD21	8:GD:133:ARG:HB3	1.76	0.50
2:GH:185:THR:HG23	2:GH:259:TYR:HE2	1.77	0.50
11:IM:257:ASP:N	11:IM:257:ASP:OD1	2.45	0.50
1:CG:935:ILE:HG22	1:CG:942:THR:HG22	1.93	0.50
4:JL:91:VAL:HA	4:JL:94:VAL:HG22	1.93	0.50
4:JL:115:GLN:HB3	4:JL:126:ILE:HB	1.93	0.50
2:KH:203:ASN:ND2	2:KH:216:GLN:OE1	2.43	0.50
4:KL:54:ARG:HE	4:KL:57:VAL:HG13	1.76	0.50
2:MH:184:SER:OG	2:MH:257:GLN:O	2.28	0.50
2:XH:151:PRO:HA	2:XH:248:VAL:HG13	1.92	0.50
2:BH:256:VAL:HG12	2:BH:258:GLY:H	1.76	0.50
5:BN:62:ASN:OD1	5:BN:63:GLY:N	2.45	0.50
10:IC:145:THR:OG1	10:IC:146:TRP:N	2.44	0.50
3:DK:66:LYS:HB3	3:DK:77:SER:HB3	1.92	0.50
1:HG:1010:THR:HG21	1:IG:967:GLY:HA3	1.93	0.50
1:OG:882:PRO:HA	1:OG:903:PHE:CE2	2.47	0.50
10:AC:103:GLU:OE1	10:AC:103:GLU:N	2.40	0.50
9:Ef:245:LYS:HG2	9:Ef:255:LEU:HD21	1.94	0.50
2:FH:169:ILE:HG23	2:FH:252:VAL:HG21	1.93	0.50
2:FH:208:LYS:HG3	1:WG:823:GLY:HA2	1.92	0.50
2:FH:278:ASP:OD1	2:FH:278:ASP:N	2.36	0.50
3:FK:72:GLN:NE2	4:GL:225:GLN:OE1	2.45	0.50
8:Fd:92:GLU:OE1	8:Fd:92:GLU:N	2.28	0.50
3:HK:177:ASN:O	3:HK:179:ARG:NH1	2.37	0.50
2:IH:190:PRO:HB2	2:IH:231:ARG:HD3	1.94	0.50
3:IK:100:ASN:OD1	3:IK:143:TYR:OH	2.29	0.50
10:CC:236:ASP:OD1	10:CC:239:GLU:N	2.40	0.50
3:KK:74:TYR:HB2	3:KK:184:PHE:CE1	2.47	0.50
9:Kf:216:ILE:HG13	9:Kf:217:PRO:HD2	1.94	0.50
11:LM:211:THR:HG23	11:LM:230:ARG:HB3	1.93	0.50
8:Ld:142:LYS:NZ	8:Ld:142:LYS:H	2.09	0.50
2:MH:288:PRO:HB3	2:MH:305:TRP:CE2	2.47	0.50
8:Md:123:THR:HG22	8:Md:125:ASP:H	1.76	0.50
9:YF:213:GLN:O	2:YH:170:ARG:NH1	2.44	0.50
4:CL:129:THR:O	4:CL:133:PHE:HB2	2.12	0.50
9:DF:216:ILE:HD11	9:DF:221:TRP:HZ3	1.76	0.50
11:DM:136:LEU:HD13	11:DM:155:LEU:HD13	1.94	0.50
11:DM:275:ASP:HA	11:DM:295:ASN:H	1.76	0.50
1:MG:966:GLN:HG2	1:MG:1012:GLY:HA3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:EH:148:PRO:O	9:DF:219:ARG:NH1	2.44	0.50
8:FD:69:ASN:OD1	8:FD:69:ASN:N	2.44	0.50
4:IL:215:SER:N	4:IL:226:ASN:OD1	2.45	0.50
2:AH:302:ALA:O	2:AH:303:ARG:NH1	2.37	0.50
10:CC:243:ASP:N	10:CC:243:ASP:OD1	2.44	0.50
1:Kg:810:GLN:NE2	1:Kg:811:ASP:OD1	2.45	0.50
2:KH:152:THR:O	2:KH:250:TYR:N	2.37	0.50
11:KM:127:ASN:HB3	11:KM:147:ALA:HB3	1.93	0.50
11:LM:292:MET:HE1	11:LM:298:VAL:HB	1.94	0.50
8:Ld:68:ASP:OD1	8:Ld:68:ASP:N	2.44	0.50
2:XH:349:TRP:O	2:XH:352:LYS:HG2	2.12	0.50
9:YF:216:ILE:HD11	9:YF:219:ARG:HB2	1.93	0.50
9:YF:233:ARG:NE	9:YF:235:GLY:O	2.44	0.50
10:DC:257:ASN:OD1	10:DC:257:ASN:N	2.45	0.50
11:BM:202:LEU:HD21	11:BM:204:LEU:HD23	1.94	0.50
11:GM:214:ILE:HB	11:GM:233:VAL:HG12	1.92	0.50
10:KC:117:THR:HB	10:KC:129:SER:HB3	1.92	0.50
10:KC:155:ASP:HB3	5:CN:84:CYS:HA	1.94	0.50
10:KC:158:LYS:HE2	10:KC:160:GLU:HG3	1.94	0.50
1:MG:931:SER:H	1:MG:1043:GLN:NE2	2.10	0.50
2:EH:130:LEU:HA	2:EH:133:ILE:HG22	1.93	0.50
1:BG:878:ASN:OD1	1:BG:879:SER:N	2.44	0.50
3:HK:66:LYS:HZ2	3:HK:67:VAL:H	1.59	0.50
5:HN:111:GLU:H	5:HN:111:GLU:CD	2.20	0.50
1:Ig:793:GLU:O	1:Ig:796:GLN:NE2	2.44	0.50
5:IN:84:CYS:HA	10:DC:153:ASP:HB3	1.92	0.50
4:JL:145:TYR:CG	4:JL:146:PRO:HD3	2.47	0.50
8:KD:32:ASN:ND2	8:KD:32:ASN:H	2.07	0.50
10:CC:157:LYS:NZ	10:CC:158:PRO:O	2.44	0.50
2:KH:359:GLU:OE1	2:KH:359:GLU:N	2.45	0.50
2:LH:241:LEU:HD23	2:LH:241:LEU:H	1.77	0.50
3:AK:53:ILE:HD13	3:AK:109:PHE:HE1	1.76	0.50
11:MM:131:THR:HG23	11:MM:151:GLY:H	1.77	0.50
11:MM:257:ASP:HA	11:MM:275:ASP:O	2.12	0.50
2:WH:106:VAL:HA	2:WH:109:LYS:HE2	1.93	0.50
2:WH:161:SER:HB2	2:WH:164:SER:HB3	1.93	0.50
10:DC:214:LEU:HG	10:DC:219:MET:HB2	1.93	0.50
1:Cg:792:GLN:NE2	1:Cg:793:GLU:OE2	2.44	0.50
9:Bf:253:ARG:HG2	9:Bf:263:LYS:HE3	1.94	0.50
10:GC:137:GLN:HG2	10:GC:252:LEU:HD13	1.93	0.50
10:KC:80:ILE:HD11	10:KC:196:LEU:HD13	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:LC:258:SER:HA	10:LC:261:TRP:CE2	2.47	0.50
10:MC:145:THR:H	10:MC:148:GLN:NE2	2.09	0.50
3:DK:92:ASN:O	3:DK:95:SER:OG	2.28	0.50
1:HG:878:ASN:HA	1:HG:1030:GLU:HA	1.93	0.50
8:Ed:137:TYR:OH	8:ED:158:TYR:O	2.28	0.50
9:AF:207:ARG:NH2	9:AF:260:GLN:OE1	2.45	0.50
8:GD:35:ASP:O	8:GD:38:THR:OG1	2.29	0.50
1:Gg:798:THR:O	1:Gg:802:LEU:HB2	2.12	0.50
8:CD:70:THR:HA	8:CD:133:ARG:HE	1.76	0.50
1:VG:823:GLY:HA2	2:CH:208:LYS:HE3	1.94	0.50
1:ZG:820:TYR:OH	1:ZG:822:GLU:OE2	2.28	0.50
2:ZH:279:LEU:HD11	2:ZH:289:PRO:HB3	1.93	0.50
11:EM:308:ASP:OD1	11:EM:308:ASP:N	2.43	0.50
9:Af:238:ILE:HD12	9:Af:239:PRO:HD2	1.93	0.50
3:CK:111:LYS:NZ	3:CK:150:ASP:OD1	2.42	0.50
4:DL:169:THR:HG21	4:DL:178:LYS:HB3	1.93	0.50
11:DM:229:ASN:N	11:DM:229:ASN:OD1	2.44	0.50
1:JG:881:GLU:HG3	1:KG:911:LYS:HE2	1.94	0.50
1:NG:910:ASP:OD1	1:NG:910:ASP:N	2.45	0.50
1:PG:952:TYR:CE2	1:PG:1027:THR:HG21	2.47	0.50
8:Ed:78:ASN:OD1	8:Ed:78:ASN:N	2.45	0.50
9:Ef:213:GLN:OE1	11:EM:208:LYS:NZ	2.45	0.50
9:FF:209:ILE:H	9:FF:225:SER:HB3	1.76	0.50
2:HH:298:SER:HB2	2:HH:357:LYS:HB3	1.94	0.50
2:JH:266:MET:SD	2:JH:266:MET:N	2.77	0.50
4:KL:44:HIS:ND1	4:KL:49:ASN:OD1	2.41	0.50
11:LM:172:ASN:OD1	11:LM:173:LEU:N	2.45	0.50
11:LM:257:ASP:N	11:LM:257:ASP:OD1	2.43	0.50
3:MK:47:GLY:O	3:MK:108:GLN:NE2	2.42	0.50
4:ML:145:TYR:CD1	4:ML:146:PRO:HD3	2.46	0.50
5:MN:88:HIS:ND1	5:MN:105:ASP:OD2	2.41	0.50
1:VG:795:GLN:OE1	1:VG:795:GLN:N	2.43	0.50
11:BM:116:PHE:HE1	11:BM:118:TYR:HB2	1.77	0.50
11:EM:257:ASP:HA	11:EM:275:ASP:O	2.11	0.50
4:BL:170:ASP:OD2	4:BL:227:ARG:NH2	2.32	0.50
2:CH:206:TRP:NE1	2:CH:207:ASP:O	2.45	0.50
8:DD:79:LEU:HA	8:DD:128:LEU:HD12	1.94	0.50
2:DH:201:SER:O	2:DH:218:THR:N	2.43	0.50
4:DL:142:GLU:OE1	4:DL:142:GLU:N	2.44	0.50
3:EK:115:THR:HB	3:EK:183:THR:HG23	1.94	0.49
8:Ed:92:GLU:H	8:Ed:92:GLU:CD	2.18	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:FL:145:TYR:CG	4:FL:146:PRO:HD3	2.47	0.49
4:FL:212:ASN:OD1	4:FL:212:ASN:N	2.44	0.49
8:GD:82:ARG:HH21	8:GD:127:SER:HA	1.75	0.49
1:BG:910:ASP:OD1	1:BG:910:ASP:N	2.37	0.49
8:Gd:33:PRO:HB2	8:Gd:39:ILE:HG22	1.94	0.49
8:Gd:80:GLN:C	8:Gd:82:ARG:HH21	2.20	0.49
3:HK:129:GLU:OE1	3:HK:129:GLU:N	2.38	0.49
2:JH:341:LYS:HD3	2:JH:361:LEU:HD21	1.94	0.49
2:MH:200:SER:N	1:ZG:816:GLU:OE2	2.45	0.49
11:GM:268:HIS:HA	11:GM:287:THR:HG23	1.93	0.49
8:BD:77:TYR:OH	3:BK:130:ARG:NH1	2.45	0.49
1:GG:898:LYS:HZ2	1:HG:864:LYS:HE3	1.77	0.49
10:KC:51:LYS:HB2	1:MG:938:ASN:ND2	2.25	0.49
10:KC:241:ILE:HG12	10:LC:254:LEU:HD13	1.93	0.49
1:JG:920:SER:HB2	1:KG:865:THR:HB	1.94	0.49
1:MG:967:GLY:HA2	1:MG:970:ASN:HD21	1.77	0.49
1:NG:949:ASN:HA	1:NG:952:TYR:CE2	2.47	0.49
1:PG:931:SER:H	1:PG:1043:GLN:HE22	1.59	0.49
1:PG:949:ASN:HA	1:PG:952:TYR:HE2	1.77	0.49
1:PG:949:ASN:HA	1:PG:952:TYR:CE2	2.47	0.49
9:Df:220:ALA:HB3	9:Df:232:VAL:HG13	1.94	0.49
2:EH:282:HIS:HB3	2:EH:287:VAL:HG13	1.94	0.49
8:FD:36:ASP:OD1	8:FD:36:ASP:N	2.45	0.49
9:Ff:246:LEU:HB3	9:Ff:255:LEU:HD12	1.95	0.49
4:HL:116:TYR:OH	4:HL:118:GLU:OE1	2.31	0.49
4:KL:145:TYR:CD1	4:KL:146:PRO:HD3	2.47	0.49
11:KM:172:ASN:OD1	11:KM:173:LEU:N	2.46	0.49
2:VH:207:ASP:OD1	2:VH:210:SER:OG	2.22	0.49
1:FG:970:ASN:OD1	1:FG:971:ALA:N	2.45	0.49
11:AM:209:SER:HB3	11:AM:212:LEU:HD21	1.92	0.49
8:Ad:60:LYS:HZ2	8:AD:140:GLY:HA2	1.76	0.49
10:JC:116:ASN:N	10:JC:130:ASP:O	2.39	0.49
10:KC:91:LEU:O	10:KC:94:ILE:HG13	2.12	0.49
10:LC:113:ARG:HH12	10:LC:129:ARG:NH2	2.10	0.49
2:DH:284:LEU:HD21	2:DH:330:SER:HB3	1.94	0.49
1:IG:886:LEU:HB3	1:IG:900:ILE:HG22	1.94	0.49
1:IG:1006:ILE:HG12	1:JG:968:PHE:HA	1.93	0.49
1:OG:1040:LEU:HD23	1:OG:1040:LEU:H	1.77	0.49
2:EH:359:GLU:N	2:EH:359:GLU:OE1	2.46	0.49
9:HF:263:LYS:HG2	9:HF:264:PHE:H	1.77	0.49
4:HL:145:TYR:HA	4:HL:148:LEU:HD13	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:IM:229:ASN:HA	11:IM:249:GLN:HG2	1.94	0.49
8:Jd:148:TYR:HB2	8:Jd:153:VAL:HG12	1.93	0.49
2:KH:341:LYS:HB2	2:KH:361:LEU:HD21	1.94	0.49
4:LL:59:ARG:HH22	4:LL:99:ARG:CZ	2.26	0.49
8:Md:155:GLU:OE2	8:Md:157:ARG:NH2	2.45	0.49
9:Mf:246:LEU:HB3	9:Mf:255:LEU:HD21	1.94	0.49
2:XH:330:SER:OG	2:XH:332:ASP:OD1	2.29	0.49
11:AM:257:ASP:HA	11:AM:275:ASP:O	2.11	0.49
2:BH:130:LEU:HA	2:BH:133:ILE:HG22	1.93	0.49
4:BL:106:ILE:HA	4:BL:109:LEU:HD22	1.94	0.49
4:BL:145:TYR:HA	4:BL:148:LEU:HD13	1.94	0.49
10:EC:89:ASN:O	10:EC:93:ILE:HG22	2.12	0.49
10:FC:151:TYR:CG	10:FC:203:ILE:HD13	2.47	0.49
10:MC:248:ILE:HD11	10:AC:124:GLN:HG2	1.93	0.49
4:DL:109:LEU:HD12	4:DL:114:ILE:HB	1.92	0.49
5:DN:78:LEU:HD23	5:DN:78:LEU:H	1.76	0.49
1:KG:970:ASN:OD1	1:KG:971:ALA:N	2.45	0.49
1:NG:876:SER:N	1:OG:940:ALA:O	2.45	0.49
1:AG:965:LEU:HD23	1:AG:1011:VAL:HG23	1.95	0.49
3:FK:148:GLY:H	8:Fd:30:ILE:HD13	1.78	0.49
10:BC:228:SER:HB3	2:XH:320:LEU:O	2.12	0.49
3:GK:106:LEU:HD21	3:GK:114:ILE:HD13	1.95	0.49
3:GK:166:THR:HG22	3:GK:168:TYR:H	1.76	0.49
2:HH:341:LYS:HB2	2:HH:361:LEU:HD11	1.95	0.49
1:CG:876:SER:OG	1:CG:1031:VAL:O	2.28	0.49
8:Jd:116:PRO:HG2	8:Jd:118:LEU:HD21	1.93	0.49
8:KD:68:ASP:OD1	8:KD:69:ASN:N	2.46	0.49
8:KD:150:ASN:N	8:KD:150:ASN:OD1	2.45	0.49
1:Kg:814:GLN:NE2	1:Kg:814:GLN:O	2.46	0.49
11:KM:313:ASP:O	11:KM:317:LYS:HB2	2.13	0.49
2:VH:347:VAL:HG23	2:VH:354:MET:HE2	1.94	0.49
2:XH:339:MET:SD	2:XH:339:MET:N	2.86	0.49
2:YH:320:LEU:O	10:EC:227:SER:HB2	2.13	0.49
11:AM:144:THR:HB	11:AM:163:THR:HG23	1.94	0.49
11:FM:284:LEU:HD23	11:FM:310:LYS:HG3	1.93	0.49
11:GM:278:ASP:OD1	11:GM:297:SER:OG	2.30	0.49
5:AN:110:GLU:HA	5:AN:113:SER:HB2	1.94	0.49
10:FC:103:GLU:HG2	10:FC:104:HIS:CD2	2.46	0.49
10:IC:78:ILE:HD11	10:IC:194:LEU:HD13	1.94	0.49
10:IC:223:PRO:HD3	10:IC:252:PRO:HG3	1.94	0.49
11:CM:144:THR:O	11:CM:164:GLN:NE2	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:CM:286:LYS:O	11:CM:316:ASN:ND2	2.46	0.49
2:DH:279:LEU:HD21	2:DH:289:PRO:HB3	1.93	0.49
3:DK:117:THR:HA	3:DK:157:GLN:O	2.11	0.49
4:DL:94:VAL:HA	4:DL:97:ILE:HG12	1.94	0.49
11:DM:279:ILE:HB	11:DM:298:VAL:HG22	1.94	0.49
1:KG:1006:ILE:HG12	1:LG:968:PHE:HA	1.93	0.49
1:OG:1003:ASN:HA	1:OG:1006:ILE:HD12	1.92	0.49
1:PG:970:ASN:OD1	1:PG:971:ALA:N	2.44	0.49
1:AG:946:SER:OG	1:AG:1030:GLU:O	2.21	0.49
9:FF:258:SER:OG	9:FF:260:GLN:OE1	2.31	0.49
2:FH:155:SER:OG	2:FH:255:ARG:NH1	2.46	0.49
8:Gd:148:TYR:HB2	8:Gd:153:VAL:HG12	1.94	0.49
11:HM:278:ASP:OD2	11:HM:280:TYR:OH	2.24	0.49
2:IH:285:GLU:OE2	10:DC:202:LYS:NZ	2.45	0.49
8:Jd:128:LEU:H	8:Jd:128:LEU:HD12	1.77	0.49
2:AH:279:LEU:HD12	2:AH:289:PRO:HB3	1.95	0.49
8:KD:36:ASP:OD1	8:KD:36:ASP:N	2.41	0.49
1:Lg:822:GLU:N	1:Lg:822:GLU:OE1	2.45	0.49
1:EG:968:PHE:HB3	1:EG:1008:LEU:HD13	1.94	0.49
1:VG:804:ALA:O	1:VG:807:GLN:HG2	2.11	0.49
9:YF:254:ILE:O	9:YF:261:VAL:HA	2.12	0.49
2:ZH:196:LEU:HD22	2:ZH:204:ILE:HD11	1.93	0.49
1:FG:965:LEU:O	1:FG:1008:LEU:HB3	2.12	0.49
1:FG:1032:TYR:HD1	1:GG:941:ARG:HH22	1.60	0.49
11:BM:228:VAL:HG11	11:BM:231:LEU:HB2	1.94	0.49
10:JC:140:HIS:ND1	10:JC:141:PHE:O	2.43	0.49
1:IG:958:SER:O	1:IG:962:SER:OG	2.31	0.49
1:JG:965:LEU:HD23	1:JG:1011:VAL:HG23	1.94	0.49
1:NG:873:LEU:HD23	1:NG:1037:LEU:HD22	1.95	0.49
9:EF:233:ARG:NE	9:EF:235:GLY:O	2.45	0.49
2:FH:141:LYS:O	2:WH:131:LYS:NZ	2.45	0.49
2:FH:207:ASP:CG	2:FH:210:SER:H	2.20	0.49
3:FK:142:GLU:OE2	4:FL:139:ARG:NH1	2.42	0.49
5:FN:58:LEU:HB2	5:FN:66:SER:HB3	1.94	0.49
10:BC:32:LEU:H	10:AC:185:TRP:HZ3	1.60	0.49
8:HD:28:PRO:HG2	8:HD:29:PRO:HD3	1.93	0.49
8:Id:68:ASP:OD1	8:Id:68:ASP:N	2.44	0.49
2:JH:170:ARG:NE	2:JH:249:ASP:OD1	2.35	0.49
11:KM:256:HIS:O	11:KM:259:SER:OG	2.29	0.49
8:Kd:28:PRO:HB2	8:Kd:32:ASN:ND2	2.27	0.49
8:Kd:128:LEU:H	8:Kd:128:LEU:HD12	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LD:69:ASN:O	8:LD:72:THR:OG1	2.30	0.49
3:LK:86:ASP:OD2	3:LK:87:GLN:NE2	2.44	0.49
9:MF:211:TYR:CG	9:MF:265:SER:HB2	2.48	0.49
4:ML:219:ILE:HG22	4:ML:222:GLY:H	1.78	0.49
11:MM:278:ASP:OD1	11:MM:297:SER:OG	2.31	0.49
1:EG:936:ASP:HB3	1:EG:939:THR:HB	1.95	0.49
2:VH:184:SER:HB2	2:VH:259:TYR:HE1	1.76	0.49
2:XH:308:ASN:OD1	2:XH:308:ASN:N	2.43	0.49
4:AL:59:ARG:HH12	4:AL:99:ARG:HE	1.60	0.49
11:BM:209:SER:HB3	11:BM:212:LEU:HD21	1.93	0.49
8:Bd:128:LEU:H	8:Bd:128:LEU:HD12	1.77	0.49
10:IC:114:ASN:N	10:IC:128:ASP:O	2.42	0.49
10:JC:143:THR:HG21	2:CH:324:TRP:H	1.78	0.49
10:JC:173:GLU:HA	10:JC:176:ILE:HG12	1.94	0.49
10:JC:222:VAL:HG13	10:JC:256:LEU:HD13	1.95	0.49
3:CK:50:ASP:N	3:CK:50:ASP:OD1	2.46	0.49
2:DH:182:LEU:HB2	2:DH:255:ARG:HD2	1.95	0.49
11:DM:210:ASP:O	11:DM:230:ARG:N	2.45	0.49
1:OG:936:ASP:HB3	1:OG:939:THR:HB	1.94	0.49
9:Df:247:ILE:HG22	9:Df:254:ILE:HG23	1.95	0.49
8:AD:35:ASP:O	8:AD:39:ILE:HG12	2.12	0.49
9:EF:235:GLY:HA2	9:EF:243:MET:HE1	1.94	0.49
4:EL:129:THR:O	4:EL:133:PHE:HB2	2.13	0.49
8:FD:81:ALA:O	8:FD:128:LEU:HD23	2.12	0.49
2:GH:284:LEU:HD11	2:GH:330:SER:HB3	1.94	0.49
8:KD:40:LYS:O	8:KD:43:GLU:HG3	2.12	0.49
10:CC:169:THR:HG23	10:CC:172:GLU:H	1.78	0.49
8:CD:69:ASN:OD1	8:CD:69:ASN:N	2.44	0.49
2:LH:148:PRO:HD2	9:YF:219:ARG:HG2	1.95	0.49
2:LH:183:ASP:HA	2:LH:256:VAL:HB	1.94	0.49
2:MH:206:TRP:HB2	2:MH:213:LEU:HD23	1.93	0.49
5:MN:110:GLU:HA	5:MN:113:SER:HB2	1.95	0.49
1:EG:882:PRO:HA	1:EG:903:PHE:CE2	2.48	0.49
9:YF:214:ALA:H	9:YF:221:TRP:HB2	1.78	0.49
4:AL:145:TYR:CG	4:AL:146:PRO:HD3	2.48	0.49
2:YH:161:SER:HB2	2:YH:164:SER:HB3	1.93	0.49
11:AM:225:ALA:HA	11:AM:246:LEU:HB2	1.95	0.49
8:Ad:35:ASP:HB3	8:Ad:38:THR:HG23	1.95	0.49
5:BN:115:GLN:OE1	5:BN:115:GLN:N	2.46	0.49
8:Bd:132:LEU:HD12	8:Bd:145:ILE:HG21	1.94	0.49
2:CH:158:VAL:N	2:CH:255:ARG:O	2.35	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:DL:128:PRO:HG2	4:DL:131:LYS:HB2	1.94	0.49
4:DL:165:VAL:HG12	4:DL:231:ILE:HG12	1.95	0.49
2:EH:109:LYS:O	2:EH:113:LYS:NZ	2.38	0.49
4:FL:118:GLU:HG3	4:FL:123:ARG:HG2	1.94	0.49
5:FN:89:GLY:O	5:FN:104:ASN:ND2	2.46	0.49
10:BC:173:GLU:HA	10:BC:176:ILE:HG12	1.95	0.49
11:HM:300:ASP:OD1	11:HM:302:ARG:N	2.45	0.49
1:Ig:814:GLN:NE2	1:Ig:814:GLN:O	2.43	0.49
3:JK:66:LYS:NZ	3:JK:67:VAL:O	2.46	0.49
11:LM:283:ASN:OD1	11:LM:284:LEU:N	2.45	0.49
8:Ld:70:THR:OG1	8:Ld:133:ARG:NE	2.44	0.49
8:Ld:106:PHE:HD1	8:Ld:154:VAL:HG23	1.77	0.49
2:ZH:157:PHE:HD1	2:ZH:255:ARG:HB2	1.77	0.49
11:JM:300:ASP:CG	11:JM:302:ARG:HB2	2.38	0.49
1:Cg:819:VAL:HG22	2:BH:199:PRO:HG3	1.93	0.49
10:KC:148:TRP:CZ3	10:KC:149:ARG:HG2	2.47	0.49
10:LC:115:THR:HG23	10:LC:127:SER:HB2	1.94	0.49
11:CM:215:ARG:HG3	11:CM:234:GLU:HB3	1.95	0.49
1:JG:936:ASP:HB3	1:JG:939:THR:HB	1.95	0.49
1:KG:944:LEU:HD11	1:KG:1031:VAL:HG12	1.94	0.49
1:LG:972:PHE:O	1:LG:976:ASN:ND2	2.46	0.49
1:MG:921:ILE:HB	1:MG:926:LYS:HD2	1.95	0.49
1:NG:1040:LEU:HD23	1:NG:1040:LEU:H	1.78	0.49
1:OG:897:SER:HA	1:OG:922:PRO:HD3	1.94	0.49
2:EH:191:ILE:HG13	2:EH:211:ASN:HA	1.94	0.49
4:EL:193:LEU:HA	4:EL:196:ASN:HD22	1.77	0.49
8:Ed:29:PRO:HD2	8:Ed:32:ASN:HD21	1.76	0.49
10:BC:221:MET:HG2	10:BC:263:TRP:CD1	2.48	0.49
9:GF:238:ILE:N	9:GF:242:GLY:O	2.45	0.49
3:HK:143:TYR:O	3:HK:146:SER:OG	2.23	0.49
2:IH:214:MET:HE3	2:XH:229:ARG:HD2	1.94	0.49
4:JL:177:HIS:ND1	11:JM:315:TYR:OH	2.37	0.49
2:AH:151:PRO:HG2	9:ZF:231:THR:HG21	1.95	0.49
2:AH:176:VAL:HG22	2:AH:216:GLN:HB3	1.95	0.49
8:KD:91:ILE:O	8:KD:95:THR:HG22	2.13	0.49
4:KL:136:SER:OG	11:KM:314:ARG:NH2	2.28	0.49
11:LM:271:SER:OG	11:LM:290:ASP:OD1	2.31	0.49
11:LM:300:ASP:OD1	11:LM:302:ARG:NE	2.46	0.49
1:EG:973:GLN:HB2	1:EG:1005:VAL:HG11	1.93	0.49
2:VH:189:TRP:HE1	2:VH:231:ARG:HB2	1.76	0.49
1:XG:792:GLN:CD	1:XG:792:GLN:H	2.21	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:YH:330:SER:OG	2:YH:332:ASP:OD1	2.20	0.49
11:GM:262:GLU:HB2	11:GM:282:TYR:HE1	1.78	0.49
11:JM:225:ALA:HA	11:JM:246:LEU:HB2	1.94	0.49
8:Ad:113:PRO:HD3	8:Ad:158:TYR:CE2	2.48	0.49
5:BN:104:ASN:OD1	5:BN:104:ASN:N	2.45	0.49
9:Bf:246:LEU:HG	9:Bf:255:LEU:HB3	1.95	0.49
10:EC:245:ARG:HB3	10:FC:128:ILE:HG23	1.95	0.49
1:GG:931:SER:H	1:GG:1043:GLN:NE2	2.11	0.49
8:DD:77:TYR:HE1	11:DM:304:TRP:HE3	1.58	0.49
11:DM:257:ASP:N	11:DM:257:ASP:OD1	2.46	0.49
2:EH:278:ASP:OD1	2:EH:278:ASP:N	2.44	0.49
3:EK:138:ARG:NH2	8:ED:125:ASP:OD2	2.46	0.49
2:FH:276:ALA:HB2	10:AC:119:ASN:HB2	1.94	0.49
4:FL:49:ASN:O	4:FL:51:GLN:NE2	2.39	0.49
5:FN:86:LEU:HB3	5:FN:87:TRP:CE3	2.48	0.49
9:GF:237:LYS:HD3	9:GF:243:MET:HG3	1.94	0.49
3:GK:109:PHE:HD2	3:GK:184:PHE:HZ	1.60	0.49
11:HM:134:LEU:HD12	11:HM:152:LEU:HB3	1.95	0.49
8:ID:37:ALA:O	8:ID:41:LEU:HG	2.13	0.49
3:IK:70:VAL:HG13	4:JL:214:ILE:HD11	1.95	0.49
2:JH:340:GLN:HE22	2:JH:341:LYS:HG2	1.78	0.49
10:CC:218:MET:HG2	10:CC:220:MET:HE2	1.95	0.49
3:KK:116:VAL:HG12	3:KK:182:ILE:HD12	1.95	0.49
9:Kf:238:ILE:HG13	9:Kf:241:TYR:HB2	1.95	0.49
3:LK:162:ASP:OD1	3:LK:162:ASP:N	2.45	0.49
3:AK:162:ASP:OD1	3:AK:162:ASP:N	2.43	0.49
9:WF:212:ILE:HB	9:WF:264:PHE:HA	1.94	0.49
11:GM:166:ASN:HA	11:GM:186:SER:HB3	1.95	0.49
11:GM:242:LYS:HA	11:GM:262:GLU:HG3	1.93	0.49
10:JC:64:ALA:HB2	10:JC:177:TRP:CD1	2.48	0.49
10:MC:178:TYR:HD1	10:MC:181:ARG:HH11	1.60	0.49
2:CH:341:LYS:HD3	2:CH:361:LEU:HD21	1.94	0.49
11:CM:284:LEU:HD12	11:CM:302:ARG:HH12	1.78	0.49
5:CN:65:TYR:OH	4:DL:221:HIS:HB3	2.13	0.49
2:DH:203:ASN:HB3	2:DH:216:GLN:HB3	1.95	0.49
11:DM:164:GLN:HA	11:DM:184:LEU:HG	1.95	0.49
9:EF:241:TYR:HB3	9:EF:256:THR:HG21	1.95	0.49
8:FD:71:LEU:HD21	8:Fd:64:PRO:HA	1.95	0.48
3:FK:46:ASP:OD1	3:FK:46:ASP:N	2.45	0.48
8:GD:52:MET:O	8:GD:55:MET:HG3	2.13	0.48
1:Hg:796:GLN:O	1:Hg:799:SER:OG	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:HH:191:ILE:O	2:HH:231:ARG:NH2	2.46	0.48
1:Ig:795:GLN:OE1	1:Ig:796:GLN:N	2.46	0.48
1:Ig:805:ALA:HA	1:Ig:808:LEU:HB2	1.95	0.48
2:IH:230:LEU:HB2	2:IH:233:LEU:HB2	1.95	0.48
4:IL:174:SER:HB3	4:IL:177:HIS:HB3	1.94	0.48
1:CG:965:LEU:HD23	1:CG:1011:VAL:HG23	1.94	0.48
9:JF:209:ILE:O	9:JF:225:SER:N	2.46	0.48
2:JH:285:GLU:HG2	10:EC:204:GLU:HB2	1.95	0.48
3:JK:57:MET:HG3	3:JK:67:VAL:HG21	1.95	0.48
2:AH:216:GLN:N	2:AH:216:GLN:HE21	2.11	0.48
2:AH:321:SER:HB3	2:AH:346:LEU:HB3	1.95	0.48
8:Kd:147:VAL:HG13	8:Kd:154:VAL:HG12	1.95	0.48
8:LD:38:THR:HA	8:LD:41:LEU:HD12	1.95	0.48
11:LM:146:LEU:HD23	11:LM:165:ILE:HG12	1.93	0.48
2:ZH:230:LEU:HD12	2:ZH:233:LEU:HD12	1.95	0.48
2:ZH:311:MET:N	2:ZH:339:MET:O	2.44	0.48
11:EM:226:GLY:H	11:EM:246:LEU:HA	1.78	0.48
11:GM:193:GLN:HE21	11:GM:213:THR:HG22	1.76	0.48
11:JM:173:LEU:HD23	11:JM:191:LEU:HG	1.95	0.48
3:BK:168:TYR:CZ	3:BK:170:LEU:HB2	2.48	0.48
1:GG:912:MET:HB3	1:GG:944:LEU:HB2	1.93	0.48
4:DL:124:THR:HA	4:DL:231:ILE:O	2.13	0.48
4:DL:190:MET:HE3	4:DL:203:LEU:HB2	1.95	0.48
1:JG:968:PHE:HB3	1:JG:1008:LEU:HD13	1.94	0.48
1:KG:1014:ALA:HB1	1:LG:959:LEU:HD21	1.95	0.48
1:LG:965:LEU:HD23	1:LG:1011:VAL:HG23	1.94	0.48
1:Ag:814:GLN:NE2	1:Ag:814:GLN:O	2.46	0.48
1:Eg:809:VAL:HA	1:Eg:812:TRP:HD1	1.77	0.48
1:AG:917:ASN:HA	1:AG:931:SER:HA	1.95	0.48
3:HK:65:ILE:HD12	3:HK:78:ILE:HG12	1.95	0.48
8:Id:81:ALA:HB3	8:Id:128:LEU:HD11	1.95	0.48
2:JH:280:LEU:HB3	2:JH:328:MET:HG3	1.95	0.48
4:JL:129:THR:O	4:JL:133:PHE:HB2	2.13	0.48
10:CC:179:TYR:HD1	10:CC:182:ARG:HH11	1.60	0.48
2:LH:106:VAL:HA	2:LH:109:LYS:HE2	1.96	0.48
3:LK:85:ALA:HB3	3:LK:88:SER:HB2	1.95	0.48
4:LL:94:VAL:HA	4:LL:97:ILE:HG12	1.94	0.48
4:ML:57:VAL:HA	4:ML:60:VAL:HG22	1.95	0.48
2:YH:189:TRP:CZ3	2:YH:256:VAL:HG11	2.48	0.48
3:BK:92:ASN:N	3:BK:92:ASN:OD1	2.45	0.48
9:Bf:244:VAL:HA	9:Bf:256:THR:HA	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:HC:67:ALA:HA	10:HC:182:GLY:O	2.13	0.48
10:LC:138:HIS:ND1	10:LC:139:PHE:O	2.45	0.48
10:MC:242:ASP:N	10:MC:242:ASP:OD1	2.43	0.48
3:DK:72:GLN:N	3:DK:72:GLN:OE1	2.46	0.48
4:DL:174:SER:HB3	4:DL:177:HIS:HB3	1.95	0.48
1:NG:891:THR:OG1	1:NG:892:GLY:N	2.44	0.48
1:PG:897:SER:HA	1:PG:922:PRO:HD3	1.95	0.48
10:AC:207:PHE:HA	10:AC:210:MET:HE3	1.95	0.48
2:FH:225:ASN:ND2	2:WH:176:VAL:H	2.12	0.48
4:FL:159:PRO:HG2	4:FL:160:GLN:NE2	2.27	0.48
4:FL:226:ASN:O	4:FL:228:ARG:HD3	2.13	0.48
1:BG:970:ASN:OD1	1:BG:971:ALA:N	2.47	0.48
5:HN:94:GLN:NE2	5:HN:95:LEU:O	2.46	0.48
2:IH:297:VAL:HG11	2:IH:302:ALA:HB3	1.95	0.48
9:If:243:MET:H	9:If:257:SER:HB3	1.79	0.48
4:LL:168:PHE:HB2	4:LL:228:ARG:HG2	1.95	0.48
11:LM:173:LEU:HD22	11:LM:175:ILE:HD11	1.94	0.48
2:YH:157:PHE:HA	2:YH:255:ARG:HB2	1.94	0.48
2:ZH:183:ASP:OD1	2:ZH:187:ALA:N	2.47	0.48
1:FG:1006:ILE:CD1	1:GG:968:PHE:HA	2.43	0.48
11:FM:115:ARG:HG3	11:FM:135:ASP:HB3	1.94	0.48
11:GM:278:ASP:OD2	11:GM:280:TYR:OH	2.24	0.48
11:JM:216:ALA:HB3	11:JM:235:LEU:HD12	1.95	0.48
9:BF:267:GLU:O	2:BH:150:LYS:NZ	2.33	0.48
10:FC:176:ILE:HA	10:FC:179:ILE:HG12	1.95	0.48
1:GG:1014:ALA:HB1	1:HG:959:LEU:HD21	1.94	0.48
10:HC:120:ASP:OD1	10:HC:123:SER:OG	2.23	0.48
10:LC:136:GLN:HG2	10:LC:251:LEU:HD13	1.94	0.48
9:Cf:216:ILE:HG13	9:Cf:217:PRO:HD2	1.95	0.48
2:DH:184:SER:OG	2:DH:256:VAL:O	2.30	0.48
1:LG:900:ILE:HD11	1:MG:866:GLY:HA3	1.95	0.48
1:OG:958:SER:O	1:OG:962:SER:OG	2.31	0.48
1:AG:886:LEU:HA	1:AG:899:LEU:O	2.14	0.48
2:EH:141:LYS:HD3	1:Eg:808:LEU:HD12	1.95	0.48
2:EH:212:THR:HB	2:DH:229:ARG:HH21	1.78	0.48
4:EL:215:SER:HB2	3:DK:72:GLN:HE22	1.79	0.48
5:EN:86:LEU:N	10:MC:153:ASP:OD2	2.34	0.48
10:BC:119:ASN:ND2	2:GH:274:PRO:O	2.45	0.48
11:HM:173:LEU:HD21	11:HM:175:ILE:HD11	1.95	0.48
1:Bg:818:GLN:N	2:BH:216:GLN:OE1	2.45	0.48
2:IH:160:LEU:HG	2:IH:257:GLN:HG3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:IL:124:THR:HG22	4:IL:232:GLN:HG2	1.95	0.48
8:LD:87:TRP:CD1	8:LD:89:GLY:H	2.31	0.48
4:LL:91:VAL:HA	4:LL:94:VAL:HG22	1.94	0.48
9:YF:241:TYR:O	9:YF:258:SER:OG	2.31	0.48
4:AL:216:ASP:CG	4:AL:218:ALA:H	2.22	0.48
2:YH:308:ASN:O	2:YH:309:GLU:HG3	2.13	0.48
11:JM:134:LEU:HD21	11:JM:150:ILE:HG23	1.94	0.48
8:Ad:142:LYS:NZ	8:Ad:142:LYS:H	2.10	0.48
8:BD:35:ASP:O	8:BD:39:ILE:HG12	2.14	0.48
2:BH:238:MET:HE1	2:CH:178:SER:H	1.79	0.48
3:BK:117:THR:HA	3:BK:157:GLN:O	2.14	0.48
5:BN:52:ASP:O	5:BN:56:GLY:N	2.47	0.48
10:JC:44:THR:O	10:JC:48:LYS:HG2	2.14	0.48
3:DK:151:SER:O	3:DK:152:ARG:NH1	2.46	0.48
4:DL:91:VAL:HA	4:DL:94:VAL:HG22	1.95	0.48
5:DN:71:THR:HG22	5:DN:73:HIS:H	1.77	0.48
1:OG:965:LEU:HG	1:OG:1008:LEU:HD23	1.96	0.48
10:AC:58:MET:O	10:AC:62:GLU:HG2	2.13	0.48
1:Eg:806:THR:HA	1:Eg:809:VAL:HG22	1.96	0.48
1:BG:966:GLN:HG2	1:BG:1012:GLY:HA3	1.95	0.48
5:GN:78:LEU:O	5:GN:79:GLN:NE2	2.47	0.48
2:JH:249:ASP:OD1	2:JH:249:ASP:N	2.46	0.48
2:KH:189:TRP:HE1	2:KH:230:LEU:HD22	1.78	0.48
4:KL:216:ASP:N	4:KL:216:ASP:OD1	2.43	0.48
8:LD:73:ILE:O	8:LD:133:ARG:NH2	2.45	0.48
2:VH:194:TYR:CE1	2:VH:204:ILE:HD13	2.49	0.48
9:XF:258:SER:OG	9:XF:260:GLN:OE1	2.26	0.48
11:AM:268:HIS:HA	11:AM:287:THR:HG23	1.95	0.48
11:BM:170:SER:OG	11:BM:172:ASN:O	2.32	0.48
11:GM:117:ARG:HG2	11:GM:137:TYR:HB3	1.96	0.48
2:BH:306:LEU:HD11	2:BH:309:GLU:HA	1.95	0.48
4:BL:102:LYS:HA	4:BL:105:ILE:HD12	1.94	0.48
10:KC:84:LEU:HD21	10:KC:148:TRP:HZ3	1.78	0.48
11:CM:244:LYS:HB2	11:CM:262:GLU:OE2	2.13	0.48
3:DK:132:LEU:HG	3:DK:136:ARG:HD2	1.94	0.48
11:DM:308:ASP:OD1	11:DM:308:ASP:N	2.45	0.48
1:IG:1042:THR:OG1	1:IG:1043:GLN:OE1	2.25	0.48
1:JG:962:SER:HB3	1:JG:1015:TRP:HB3	1.96	0.48
1:OG:897:SER:HB3	1:OG:919:MET:HE1	1.95	0.48
1:Ag:797:ARG:O	1:Ag:801:MET:HG2	2.13	0.48
2:EH:131:LYS:HZ1	2:DH:144:THR:HG22	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Ed:105:ARG:HH22	8:Ed:151:SER:HB2	1.78	0.48
10:BC:155:ASP:OD2	5:GN:85:CYS:N	2.44	0.48
8:GD:28:PRO:HB3	4:GL:128:PRO:HD3	1.96	0.48
8:HD:35:ASP:O	8:HD:38:THR:OG1	2.29	0.48
8:JD:36:ASP:HA	8:JD:39:ILE:HD12	1.95	0.48
11:KM:172:ASN:HA	11:KM:192:ARG:NH2	2.29	0.48
8:LD:35:ASP:O	8:LD:39:ILE:HG12	2.12	0.48
3:LK:52:THR:O	3:LK:56:MET:HG2	2.13	0.48
8:MD:35:ASP:O	8:MD:39:ILE:HG12	2.13	0.48
1:EG:949:ASN:HA	1:EG:952:TYR:CE2	2.48	0.48
9:YF:265:SER:HB3	9:YF:268:ASP:HB3	1.95	0.48
1:GG:1010:THR:O	1:HG:963:SER:OG	2.32	0.48
10:KC:177:TRP:O	10:KC:181:THR:OG1	2.24	0.48
10:LC:166:PRO:O	10:LC:172:LYS:NZ	2.46	0.48
10:MC:258:SER:HA	10:MC:261:TRP:CD1	2.48	0.48
2:CH:278:ASP:N	2:CH:278:ASP:OD1	2.47	0.48
3:DK:83:LEU:HD21	3:DK:98:LEU:HD23	1.95	0.48
1:KG:931:SER:O	1:KG:1042:THR:OG1	2.32	0.48
1:PG:917:ASN:HA	1:PG:931:SER:HA	1.96	0.48
10:AC:140:HIS:ND1	10:AC:141:PHE:O	2.41	0.48
10:AC:170:THR:OG1	10:AC:173:GLU:OE1	2.28	0.48
5:EN:99:GLY:HA3	5:EN:114:LEU:HG	1.95	0.48
3:FK:59:ASP:HA	3:FK:62:LYS:HG2	1.96	0.48
9:AF:263:LYS:HD3	9:AF:264:PHE:N	2.29	0.48
1:Hg:800:ASP:OD1	1:Hg:800:ASP:N	2.45	0.48
1:CG:965:LEU:O	1:CG:1008:LEU:HB3	2.14	0.48
5:IN:101:VAL:N	5:IN:113:SER:OG	2.45	0.48
8:JD:149:PRO:O	8:JD:152:GLN:NE2	2.47	0.48
9:JF:237:LYS:HA	9:JF:243:MET:HA	1.94	0.48
3:JK:97:SER:O	3:JK:100:ASN:ND2	2.44	0.48
8:Jd:68:ASP:N	8:Jd:68:ASP:OD1	2.46	0.48
3:KK:172:GLY:O	3:KK:175:SER:OG	2.31	0.48
11:KM:116:PHE:HE2	11:KM:118:TYR:HB2	1.79	0.48
1:Lg:795:GLN:H	1:Lg:795:GLN:CD	2.22	0.48
2:LH:223:TYR:HB2	2:LH:242:ILE:HG22	1.95	0.48
5:LN:85:CYS:N	10:GC:154:ASP:OD2	2.46	0.48
5:LN:111:GLU:H	5:LN:111:GLU:CD	2.19	0.48
8:MD:149:PRO:O	8:MD:152:GLN:NE2	2.46	0.48
9:CF:263:LYS:HE2	9:CF:264:PHE:HB2	1.95	0.48
2:XH:295:LEU:HD11	2:XH:306:LEU:HB2	1.94	0.48
11:AM:273:ALA:HB1	11:AM:277:SER:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:FM:125:THR:HG23	11:FM:145:ARG:HB2	1.95	0.48
11:FM:171:ARG:HH21	11:FM:192:ARG:HH12	1.61	0.48
11:FM:257:ASP:HA	11:FM:275:ASP:O	2.14	0.48
11:GM:274:THR:HA	11:GM:293:ALA:HB3	1.96	0.48
2:BH:301:ASP:OD1	2:BH:303:ARG:NH1	2.39	0.48
10:GC:249:ILE:H	10:HC:122:GLN:HB3	1.77	0.48
5:DN:46:GLY:HA3	5:DN:61:ASN:HB2	1.95	0.48
1:HG:865:THR:OG1	1:HG:1044:ASP:OD2	2.31	0.48
1:IG:965:LEU:O	1:IG:1008:LEU:HB3	2.14	0.48
1:OG:1011:VAL:HG12	1:PG:963:SER:HB2	1.96	0.48
2:EH:200:SER:OG	1:Fg:816:GLU:OE2	2.31	0.48
4:FL:170:ASP:OD2	4:FL:227:ARG:NH2	2.33	0.48
9:Gf:218:GLY:H	9:Gf:247:ILE:HD11	1.79	0.48
4:HL:129:THR:O	4:HL:133:PHE:CB	2.59	0.48
8:Hd:150:ASN:OD1	8:Hd:150:ASN:N	2.45	0.48
8:ID:158:TYR:O	8:Id:137:TYR:OH	2.28	0.48
2:KH:262:ASN:OD1	2:KH:262:ASN:N	2.47	0.48
11:MM:222:ILE:HB	11:MM:241:PHE:HD1	1.78	0.48
4:AL:200:ALA:HB1	11:AM:230:ARG:HH21	1.78	0.48
2:YH:157:PHE:CZ	2:YH:257:GLN:HG2	2.48	0.48
11:AM:158:VAL:HG13	11:AM:178:LYS:HE2	1.96	0.48
11:FM:303:GLU:HB3	11:FM:306:GLN:HB2	1.96	0.48
11:GM:191:LEU:HD21	11:GM:194:LEU:HG	1.96	0.48
2:BH:171:LEU:O	2:BH:244:GLY:N	2.47	0.48
11:CM:205:TYR:HB3	11:CM:206:TRP:CD1	2.49	0.48
10:AC:116:ASN:OD1	8:ED:114:SER:OG	2.21	0.48
8:ED:58:VAL:HA	8:ED:61:VAL:HG22	1.96	0.48
1:BG:901:GLY:HA3	1:BG:916:PHE:HD1	1.79	0.48
4:GL:133:PHE:HA	4:GL:140:LEU:HA	1.95	0.48
2:HH:270:GLU:OE2	2:XH:327:SER:N	2.47	0.48
2:HH:315:THR:OG1	2:HH:316:ASN:N	2.47	0.48
5:HN:77:ASP:HA	2:IH:354:MET:SD	2.54	0.48
2:IH:320:LEU:N	2:IH:346:LEU:O	2.45	0.48
3:IK:116:VAL:HG22	3:IK:182:ILE:HG23	1.95	0.48
4:IL:127:ILE:HB	4:IL:229:ILE:HB	1.95	0.48
11:IM:225:ALA:HA	11:IM:246:LEU:HB2	1.95	0.48
3:JK:50:ASP:HB2	5:JN:45:MET:HE1	1.96	0.48
8:Jd:98:ILE:HG23	8:Jd:128:LEU:HD23	1.95	0.48
2:AH:315:THR:OG1	2:AH:316:ASN:N	2.46	0.48
10:CC:222:SER:OG	10:CC:254:GLU:HG2	2.14	0.48
1:DG:967:GLY:HA2	1:DG:970:ASN:HD21	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EG:920:SER:HB2	1:FG:865:THR:HB	1.96	0.48
2:YH:325:LEU:HG	2:YH:339:MET:HA	1.96	0.48
2:YH:330:SER:OG	2:YH:334:THR:OG1	2.26	0.48
11:AM:127:ASN:HB3	11:AM:147:ALA:HB3	1.95	0.48
11:EM:119:GLU:HG3	11:EM:139:ALA:HB3	1.96	0.48
11:EM:271:SER:OG	11:EM:290:ASP:OD1	2.31	0.48
8:BD:70:THR:HG23	8:BD:133:ARG:HH21	1.78	0.48
3:BK:133:THR:HB	3:BK:158:GLY:HA3	1.95	0.48
1:GG:968:PHE:CG	1:GG:1008:LEU:HD13	2.48	0.48
10:IC:266:ALA:HB1	8:AD:57:LYS:HE2	1.95	0.48
10:KC:143:THR:HG21	2:DH:324:TRP:H	1.79	0.48
1:IG:899:LEU:HD21	1:IG:916:PHE:HB3	1.96	0.48
1:JG:967:GLY:HA2	1:JG:970:ASN:HD21	1.78	0.48
1:OG:944:LEU:HD11	1:OG:1031:VAL:HA	1.95	0.48
9:Df:230:LEU:HD22	9:Df:232:VAL:HB	1.96	0.48
9:Df:253:ARG:HB2	9:Df:263:LYS:HZ2	1.78	0.48
2:FH:126:GLN:HA	2:FH:129:LYS:HE2	1.95	0.48
2:FH:282:HIS:HA	2:FH:285:GLU:CD	2.39	0.48
8:HD:91:ILE:O	8:HD:95:THR:HG22	2.13	0.48
8:ID:107:ARG:HH11	8:Id:130:GLU:HB3	1.79	0.48
3:IK:129:GLU:N	3:IK:129:GLU:OE1	2.46	0.48
4:IL:130:ASP:OD2	4:IL:227:ARG:NH1	2.41	0.48
9:If:233:ARG:O	9:If:236:SER:OG	2.31	0.48
5:JN:110:GLU:CD	5:JN:110:GLU:H	2.22	0.48
3:KK:49:CYS:O	3:KK:52:THR:OG1	2.24	0.48
8:CD:36:ASP:O	8:CD:40:LYS:HG3	2.14	0.48
2:LH:200:SER:N	1:Mg:816:GLU:OE2	2.47	0.48
11:LM:127:ASN:HB3	11:LM:147:ALA:HB3	1.95	0.48
8:Ld:100:LYS:O	8:Ld:100:LYS:NZ	2.37	0.48
1:Mg:792:GLN:NE2	1:Mg:793:GLU:OE2	2.46	0.48
1:EG:931:SER:O	1:EG:1042:THR:OG1	2.22	0.48
2:VH:324:TRP:HA	2:VH:339:MET:HB3	1.95	0.48
2:YH:225:ASN:N	2:YH:225:ASN:OD1	2.47	0.48
10:DC:167:LYS:N	10:DC:171:GLU:OE1	2.38	0.48
11:BM:257:ASP:HA	11:BM:275:ASP:O	2.14	0.48
11:GM:127:ASN:HB3	11:GM:147:ALA:HB3	1.96	0.48
11:JM:198:GLY:O	11:JM:219:ALA:HB3	2.14	0.48
8:Ad:48:VAL:HG23	8:AD:52:MET:HG2	1.96	0.48
11:DM:152:LEU:H	11:DM:170:SER:HB3	1.78	0.48
1:HG:898:LYS:HD2	1:IG:866:GLY:O	2.13	0.48
1:LG:1006:ILE:HG12	1:MG:968:PHE:HA	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LG:1042:THR:OG1	1:LG:1043:GLN:OE1	2.20	0.48
1:PG:968:PHE:HB3	1:PG:1008:LEU:HD13	1.95	0.48
8:AD:130:GLU:OE2	8:AD:133:ARG:NH1	2.46	0.48
1:AG:876:SER:OG	1:AG:1031:VAL:O	2.20	0.47
2:EH:200:SER:O	2:EH:219:LYS:NZ	2.47	0.47
8:FD:162:TYR:HB3	10:AC:248:LEU:HD21	1.95	0.47
9:AF:208:ILE:HD11	9:AF:224:GLY:HA3	1.95	0.47
8:GD:35:ASP:O	8:GD:39:ILE:HG12	2.14	0.47
8:GD:136:ASP:OD1	8:GD:60:LYS:HE2	2.13	0.47
2:GH:151:PRO:HA	2:GH:248:VAL:HG13	1.96	0.47
8:HD:41:LEU:HD23	10:CC:199:ILE:HD12	1.96	0.47
4:HL:167:GLY:HA2	4:HL:229:ILE:HD13	1.96	0.47
5:HN:110:GLU:OE1	5:HN:110:GLU:N	2.35	0.47
5:IN:58:LEU:HB2	5:IN:66:SER:HB3	1.95	0.47
5:JN:49:ASN:HB3	5:JN:59:VAL:HG23	1.96	0.47
10:CC:111:LEU:HD12	10:CC:133:LYS:HD3	1.95	0.47
1:Kg:818:GLN:N	2:KH:216:GLN:OE1	2.46	0.47
8:Kd:142:LYS:NZ	8:Kd:142:LYS:H	2.12	0.47
2:LH:319:ILE:HD13	2:LH:337:TYR:CE1	2.49	0.47
5:LN:58:LEU:HD12	5:LN:68:CYS:HB2	1.96	0.47
8:Ld:127:SER:HB3	8:Ld:130:GLU:CD	2.39	0.47
2:VH:184:SER:OG	2:VH:256:VAL:O	2.19	0.47
9:CF:250:LEU:HG	9:CF:251:GLN:HG3	1.95	0.47
9:WF:216:ILE:HG12	9:WF:221:TRP:HZ3	1.79	0.47
4:AL:194:TRP:CZ2	11:AM:252:PHE:HB3	2.49	0.47
11:AM:215:ARG:NH1	11:AM:232:ASP:OD2	2.37	0.47
11:FM:202:LEU:HD21	11:FM:204:LEU:HD23	1.96	0.47
8:Bd:110:GLY:HA3	8:Bd:158:TYR:HB2	1.96	0.47
10:MC:90:ASP:HB3	10:MC:146:TRP:HE1	1.79	0.47
3:CK:74:TYR:HB2	3:CK:184:PHE:CE1	2.49	0.47
11:CM:257:ASP:HA	11:CM:275:ASP:O	2.13	0.47
1:Dg:801:MET:HG3	1:Dg:802:LEU:HD22	1.95	0.47
4:DL:150:ASN:OD1	4:DL:153:ARG:NH2	2.29	0.47
1:PG:965:LEU:HD23	1:PG:1011:VAL:HG23	1.96	0.47
4:EL:145:TYR:CG	4:EL:146:PRO:HD3	2.49	0.47
3:FK:117:THR:HA	3:FK:157:GLN:O	2.14	0.47
8:GD:87:TRP:CE3	8:GD:94:LEU:HD13	2.50	0.47
9:LF:219:ARG:NH2	9:LF:231:THR:OG1	2.40	0.47
9:LF:234:GLU:OE1	9:LF:235:GLY:N	2.47	0.47
9:XF:243:MET:O	9:XF:257:SER:N	2.38	0.47
1:YG:818:GLN:NE2	2:YH:216:GLN:OE1	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:DC:178:TYR:HA	10:DC:181:ARG:HD2	1.96	0.47
11:EM:118:TYR:CE1	11:EM:122:GLY:HA3	2.49	0.47
2:BH:277:ASN:OD1	2:BH:278:ASP:N	2.47	0.47
10:LC:198:ILE:HD12	8:DD:41:LEU:HD22	1.95	0.47
11:CM:273:ALA:HB1	11:CM:277:SER:HB2	1.95	0.47
1:IG:1024:ASN:OD1	1:IG:1024:ASN:N	2.46	0.47
1:JG:899:LEU:HD21	1:JG:916:PHE:HB3	1.94	0.47
1:KG:966:GLN:OE1	1:KG:1013:LYS:N	2.47	0.47
1:PG:1042:THR:OG1	1:PG:1043:GLN:OE1	2.17	0.47
1:AG:937:PRO:HB2	10:AC:56:ARG:HD2	1.96	0.47
3:EK:90:ARG:HH22	3:EK:92:ASN:HA	1.79	0.47
10:BC:143:THR:HG21	2:HH:324:TRP:H	1.79	0.47
1:BG:969:GLY:O	1:BG:1005:VAL:HG13	2.15	0.47
9:Gf:215:VAL:HG23	11:GM:245:TYR:HB3	1.97	0.47
8:Hd:149:PRO:O	8:Hd:152:GLN:NE2	2.46	0.47
1:CG:866:GLY:HA2	1:CG:1041:PHE:O	2.14	0.47
1:Jg:793:GLU:OE1	1:Jg:793:GLU:N	2.39	0.47
3:JK:65:ILE:HG23	3:JK:78:ILE:HG13	1.95	0.47
3:KK:126:VAL:HA	3:KK:129:GLU:OE2	2.14	0.47
4:KL:125:LEU:HD23	4:KL:233:TRP:CH2	2.49	0.47
9:LF:208:ILE:HG13	9:LF:225:SER:H	1.78	0.47
2:LH:236:PRO:HD2	2:MH:251:ARG:HH22	1.77	0.47
3:AK:145:TRP:HE3	3:AK:154:ILE:HD12	1.79	0.47
8:Md:128:LEU:H	8:Md:128:LEU:HD12	1.78	0.47
2:XH:134:TYR:O	2:XH:138:GLU:HG2	2.14	0.47
2:XH:184:SER:OG	2:XH:257:GLN:O	2.31	0.47
4:AL:129:THR:O	4:AL:133:PHE:HB2	2.15	0.47
2:YH:123:ASN:N	2:YH:126:GLN:OE1	2.40	0.47
2:ZH:322:PRO:HB2	2:ZH:339:MET:HE2	1.96	0.47
11:AM:275:ASP:HA	11:AM:295:ASN:H	1.79	0.47
8:Ad:87:TRP:CD1	8:Ad:94:LEU:HD22	2.48	0.47
8:BD:38:THR:HA	8:BD:41:LEU:HD12	1.96	0.47
9:Bf:233:ARG:O	9:Bf:236:SER:OG	2.28	0.47
10:EC:102:GLU:OE1	10:EC:103:HIS:ND1	2.45	0.47
10:EC:150:TYR:HB3	10:EC:202:ILE:HB	1.95	0.47
10:LC:174:ILE:HA	10:LC:177:ILE:HG12	1.96	0.47
2:CH:242:ILE:HD12	2:CH:243:PRO:HD2	1.96	0.47
4:CL:118:GLU:HG3	4:CL:123:ARG:HG2	1.96	0.47
9:Cf:246:LEU:HD23	9:Cf:255:LEU:HD12	1.95	0.47
11:DM:279:ILE:O	11:DM:298:VAL:HA	2.14	0.47
1:PG:863:ILE:HB	1:PG:1045:VAL:HG22	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:PG:951:HIS:O	1:PG:955:ARG:NE	2.46	0.47
8:ED:68:ASP:OD1	8:ED:69:ASN:N	2.48	0.47
1:AG:949:ASN:HA	1:AG:952:TYR:CE2	2.49	0.47
3:EK:112:ILE:HD12	8:ED:97:ARG:HH12	1.79	0.47
4:EL:121:ASP:N	4:EL:121:ASP:OD1	2.47	0.47
10:BC:102:LEU:HB2	10:BC:106:ILE:HG23	1.97	0.47
1:BG:898:LYS:HE3	1:CG:866:GLY:HA3	1.95	0.47
2:HH:183:ASP:OD1	2:HH:187:ALA:N	2.47	0.47
11:HM:206:TRP:HZ3	9:Hf:214:ALA:HB3	1.79	0.47
2:AH:188:PRO:HB2	2:AH:211:ASN:HD21	1.80	0.47
2:AH:283:VAL:HG13	2:AH:305:TRP:HZ3	1.80	0.47
10:CC:137:GLN:OE1	10:CC:138:ALA:N	2.46	0.47
2:KH:256:VAL:HG12	2:KH:258:GLY:H	1.79	0.47
8:CD:54:GLU:OE1	10:KC:215:LYS:NZ	2.38	0.47
3:LK:46:ASP:OD1	3:LK:46:ASP:N	2.47	0.47
3:LK:53:ILE:HD13	3:LK:56:MET:HE3	1.96	0.47
8:Ld:87:TRP:CD1	8:Ld:94:LEU:HD22	2.50	0.47
2:MH:158:VAL:HG22	2:MH:254:LEU:HD12	1.96	0.47
11:MM:190:ASN:O	11:MM:192:ARG:NH1	2.47	0.47
11:BM:278:ASP:OD2	11:BM:280:TYR:OH	2.24	0.47
11:GM:275:ASP:HA	11:GM:295:ASN:H	1.78	0.47
11:JM:160:ASN:HA	11:JM:180:ASP:HB2	1.95	0.47
11:JM:288:ARG:HH22	11:JM:318:GLN:H	1.60	0.47
8:BD:61:VAL:HG11	10:JC:267:VAL:O	2.15	0.47
9:BF:211:TYR:CD1	9:BF:265:SER:HB2	2.49	0.47
1:GG:869:MET:HA	1:GG:869:MET:HE3	1.95	0.47
10:HC:108:VAL:HG23	10:HC:134:ALA:HB3	1.96	0.47
10:LC:243:ASP:OD2	10:MC:125:ARG:NH2	2.40	0.47
2:DH:190:PRO:HD2	2:DH:261:PRO:HD2	1.95	0.47
1:KG:968:PHE:CG	1:KG:1008:LEU:HD13	2.49	0.47
2:EH:183:ASP:OD1	2:EH:185:THR:OG1	2.29	0.47
2:EH:207:ASP:OD1	2:EH:210:SER:OG	2.30	0.47
3:EK:99:LEU:O	3:EK:102:ILE:HG22	2.15	0.47
3:EK:186:ARG:HH21	5:EN:65:TYR:HB2	1.77	0.47
8:FD:161:ILE:HG13	8:FD:162:TYR:H	1.80	0.47
8:Fd:92:GLU:H	8:Fd:92:GLU:CD	2.18	0.47
9:Ff:245:LYS:NZ	9:Ff:256:THR:O	2.29	0.47
9:HF:263:LYS:HG2	9:HF:264:PHE:N	2.30	0.47
3:IK:71:GLY:HA3	4:JL:214:ILE:HG12	1.96	0.47
3:JK:74:TYR:HB2	3:JK:184:PHE:CE1	2.50	0.47
8:Jd:84:SER:N	10:FC:268:ALA:HB3	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:KD:81:ALA:O	8:KD:128:LEU:HG	2.15	0.47
2:KH:345:LEU:HB2	2:KH:356:LEU:HB2	1.96	0.47
11:KM:312:PHE:HA	11:KM:316:ASN:HD21	1.80	0.47
2:LH:288:PRO:HB3	2:LH:305:TRP:NE1	2.30	0.47
2:MH:226:LEU:HD23	2:MH:241:LEU:HD11	1.96	0.47
2:MH:230:LEU:HB2	2:MH:233:LEU:HB3	1.97	0.47
3:MK:112:ILE:HD12	3:MK:152:ARG:HG3	1.97	0.47
4:ML:169:THR:OG1	4:ML:170:ASP:N	2.48	0.47
9:VF:246:LEU:HB2	9:VF:255:LEU:HD12	1.96	0.47
2:VH:337:TYR:HB3	2:VH:339:MET:HE1	1.95	0.47
11:FM:185:ILE:HB	11:FM:204:LEU:HD22	1.97	0.47
10:EC:93:ILE:HG23	10:EC:94:TYR:CD1	2.50	0.47
1:GG:911:LYS:HB2	1:GG:943:ALA:HA	1.95	0.47
10:JC:216:LEU:HG	10:JC:221:MET:HB2	1.95	0.47
10:LC:176:CYS:O	10:LC:180:GLU:HG2	2.14	0.47
8:Cd:108:VAL:HG12	8:Cd:156:LEU:HB3	1.96	0.47
1:NG:863:ILE:HB	1:NG:1045:VAL:HG22	1.97	0.47
4:EL:145:TYR:CD1	4:EL:146:PRO:HD3	2.50	0.47
8:Ed:105:ARG:HB2	8:Ed:153:VAL:HG23	1.96	0.47
5:FN:57:ARG:NH1	5:FN:66:SER:O	2.47	0.47
10:BC:143:THR:HG22	10:BC:144:THR:HG23	1.96	0.47
11:HM:257:ASP:HA	11:HM:275:ASP:O	2.14	0.47
9:If:256:THR:OG1	9:If:257:SER:N	2.48	0.47
2:AH:138:GLU:HB3	2:ZH:221:TYR:HE2	1.79	0.47
2:AH:288:PRO:HB3	2:AH:305:TRP:CE2	2.50	0.47
4:KL:159:PRO:HG2	4:KL:160:GLN:NE2	2.29	0.47
1:DG:881:GLU:HG3	1:EG:911:LYS:HE2	1.97	0.47
1:DG:973:GLN:HB2	1:DG:1005:VAL:HG11	1.96	0.47
1:Lg:816:GLU:OE2	2:YH:200:SER:OG	2.30	0.47
4:LL:116:TYR:OH	4:LL:118:GLU:OE1	2.22	0.47
11:LM:275:ASP:HA	11:LM:295:ASN:H	1.80	0.47
9:MF:222:LEU:O	9:MF:229:THR:HA	2.15	0.47
8:Md:82:ARG:HD2	8:Md:127:SER:HB2	1.95	0.47
2:VH:148:PRO:HD2	9:CF:219:ARG:HG2	1.97	0.47
2:YH:311:MET:HB3	2:YH:339:MET:SD	2.54	0.47
10:DC:174:ILE:HA	10:DC:177:ILE:HG12	1.97	0.47
1:FG:965:LEU:HD23	1:FG:1011:VAL:HG23	1.96	0.47
11:BM:154:LYS:HE2	11:BM:174:GLN:HB3	1.96	0.47
11:EM:246:LEU:O	11:EM:264:SER:OG	2.33	0.47
11:GM:210:ASP:N	11:GM:210:ASP:OD1	2.48	0.47
10:LC:149:TYR:CG	10:LC:201:ILE:HD13	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CL:49:ASN:HB3	11:CM:293:ALA:HB1	1.97	0.47
4:CL:131:LYS:NZ	4:CL:144:CYS:SG	2.88	0.47
8:Cd:36:ASP:O	8:Cd:39:ILE:HG12	2.15	0.47
2:EH:308:ASN:O	2:EH:310:LYS:HG3	2.15	0.47
10:BC:249:ARG:HA	10:CC:123:GLN:O	2.15	0.47
1:BG:1044:ASP:OD1	1:BG:1044:ASP:N	2.48	0.47
8:Gd:71:LEU:HB3	8:Gd:133:ARG:HA	1.95	0.47
2:HH:238:MET:HB2	2:XH:250:TYR:HD2	1.80	0.47
2:HH:280:LEU:HD21	2:HH:338:GLU:HB2	1.97	0.47
4:HL:169:THR:HG22	4:HL:209:GLY:HA2	1.96	0.47
11:HM:146:LEU:HD12	11:HM:150:ILE:HD11	1.95	0.47
6:HU:127:UNK:O	4:IL:232:GLN:NE2	2.45	0.47
8:JD:82:ARG:NH2	11:JM:311:ASP:OD1	2.47	0.47
4:JL:175:ARG:HA	4:JL:178:LYS:HZ2	1.79	0.47
4:JL:200:ALA:O	11:JM:230:ARG:NH2	2.48	0.47
2:AH:238:MET:HB2	2:BH:250:TYR:CE2	2.49	0.47
2:AH:285:GLU:HB3	10:IC:203:GLU:HB2	1.96	0.47
10:CC:147:TRP:CZ3	10:CC:148:ARG:HG2	2.49	0.47
4:KL:209:GLY:H	4:KL:211:LYS:NZ	2.13	0.47
1:DG:904:ASN:N	1:DG:904:ASN:OD1	2.45	0.47
1:Lg:792:GLN:NE2	1:Lg:793:GLU:OE2	2.48	0.47
3:LK:50:ASP:N	3:LK:50:ASP:OD1	2.45	0.47
3:LK:123:TYR:CD2	3:LK:124:VAL:HG23	2.50	0.47
4:LL:128:PRO:HG2	4:LL:131:LYS:HB2	1.97	0.47
2:MH:245:GLN:HG2	2:MH:246:LYS:H	1.78	0.47
5:MN:65:TYR:OH	4:AL:221:HIS:HB3	2.15	0.47
8:Md:146:HIS:HB2	8:Md:155:GLU:HG3	1.97	0.47
9:VF:241:TYR:HB3	9:VF:256:THR:HG21	1.96	0.47
2:VH:330:SER:OG	2:VH:334:THR:OG1	2.22	0.47
9:WF:211:TYR:HB3	9:WF:265:SER:HB2	1.97	0.47
2:WH:107:ILE:HG13	1:Eg:794:ILE:HD11	1.97	0.47
10:DC:147:ARG:NH1	10:DC:148:GLN:HB3	2.30	0.47
1:FG:958:SER:O	1:FG:962:SER:OG	2.33	0.47
1:FG:1044:ASP:N	1:FG:1044:ASP:OD1	2.46	0.47
11:AM:201:THR:HG22	11:AM:221:LYS:HB2	1.97	0.47
11:AM:308:ASP:OD2	9:Af:263:LYS:NZ	2.43	0.47
11:EM:205:TYR:HB3	11:EM:206:TRP:CD1	2.49	0.47
5:AN:39:ASP:OD1	5:AN:40:GLY:N	2.48	0.47
2:BH:238:MET:SD	2:CH:178:SER:OG	2.70	0.47
8:Bd:118:LEU:HD22	10:JC:244:ASP:HB2	1.96	0.47
9:Bf:216:ILE:HD12	9:Bf:216:ILE:HA	1.81	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:FC:108:PRO:HG2	10:FC:210:MET:HG2	1.97	0.47
10:FC:155:ASP:N	10:FC:155:ASP:OD1	2.47	0.47
1:GG:876:SER:OG	1:GG:1031:VAL:O	2.20	0.47
10:HC:242:ASP:N	10:HC:242:ASP:OD1	2.46	0.47
10:IC:219:MET:HA	10:IC:255:ASN:HD21	1.78	0.47
10:JC:176:ILE:HA	10:JC:179:ILE:HG12	1.97	0.47
10:KC:117:THR:HG23	2:CH:328:MET:HE1	1.97	0.47
10:KC:183:ARG:HH11	10:KC:183:ARG:HB2	1.78	0.47
10:LC:162:VAL:HB	10:LC:165:LEU:HD21	1.97	0.47
4:CL:91:VAL:HA	4:CL:94:VAL:HG12	1.97	0.47
5:CN:45:MET:SD	5:CN:62:ASN:ND2	2.74	0.47
5:CN:74:ALA:HB3	5:CN:76:MET:HE2	1.95	0.47
8:Cd:35:ASP:O	8:Cd:38:THR:OG1	2.25	0.47
2:DH:289:PRO:HG2	2:DH:292:SER:HB3	1.97	0.47
5:DN:88:HIS:ND1	5:DN:105:ASP:OD2	2.43	0.47
1:JG:935:ILE:HG22	1:JG:942:THR:HG22	1.97	0.47
1:LG:863:ILE:HB	1:LG:1045:VAL:HG22	1.96	0.47
1:NG:882:PRO:HA	1:NG:903:PHE:CE2	2.49	0.47
1:NG:965:LEU:HG	1:NG:1008:LEU:HD23	1.96	0.47
1:NG:966:GLN:HG2	1:NG:1012:GLY:HA3	1.95	0.47
1:PG:965:LEU:O	1:PG:1008:LEU:HB3	2.14	0.47
1:AG:876:SER:N	1:BG:940:ALA:O	2.47	0.47
1:AG:952:TYR:CE2	1:AG:1027:THR:HG21	2.50	0.47
2:EH:106:VAL:HA	2:EH:109:LYS:HE2	1.97	0.47
4:EL:114:ILE:HD12	4:EL:127:ILE:HG13	1.95	0.47
5:HN:52:ASP:OD1	5:HN:55:ALA:N	2.43	0.47
9:IF:246:LEU:HB3	9:IF:255:LEU:HB2	1.96	0.47
2:JH:349:TRP:CG	2:JH:350:HIS:HD1	2.32	0.47
3:KK:177:ASN:OD1	3:KK:178:ALA:N	2.46	0.47
8:Kd:130:GLU:HA	8:Kd:133:ARG:HB2	1.96	0.47
1:Mg:795:GLN:CD	1:Mg:795:GLN:H	2.23	0.47
2:MH:275:SER:O	10:HC:117:ASN:HB3	2.15	0.47
2:VH:229:ARG:HH22	2:DH:210:SER:HB2	1.80	0.47
2:YH:127:VAL:O	2:YH:130:LEU:HG	2.15	0.47
11:JM:275:ASP:OD1	11:JM:275:ASP:N	2.46	0.47
2:BH:111:ALA:O	2:BH:115:MET:HE2	2.15	0.47
3:BK:45:VAL:HG12	3:BK:48:ALA:HB2	1.95	0.47
10:GC:71:GLY:HA2	10:GC:184:TRP:HD1	1.79	0.47
10:MC:258:SER:HA	10:MC:261:TRP:CE2	2.50	0.47
1:HG:970:ASN:OD1	1:HG:971:ALA:N	2.47	0.47
1:OG:898:LYS:HE3	1:PG:866:GLY:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:OG:966:GLN:OE1	1:OG:1013:LYS:N	2.48	0.47
1:AG:911:LYS:HE2	1:PG:881:GLU:HG3	1.96	0.47
2:EH:322:PRO:HB2	2:EH:339:MET:HE1	1.97	0.47
4:EL:91:VAL:HA	4:EL:94:VAL:HG12	1.97	0.47
9:Ef:218:GLY:H	9:Ef:247:ILE:HD11	1.79	0.47
9:Ef:237:LYS:HZ3	9:Ef:243:MET:N	2.12	0.47
9:FF:266:GLN:OE1	9:EF:233:ARG:NH2	2.47	0.47
2:FH:282:HIS:O	2:FH:285:GLU:HG2	2.15	0.47
3:FK:134:LEU:HD13	11:FM:304:TRP:HZ2	1.80	0.47
4:FL:124:THR:HA	4:FL:231:ILE:O	2.15	0.47
4:FL:148:LEU:H	4:FL:148:LEU:HD12	1.79	0.47
3:GK:117:THR:HA	3:GK:157:GLN:O	2.15	0.47
11:HM:186:SER:HA	11:HM:205:TYR:HB2	1.97	0.47
8:ID:95:THR:HA	8:ID:98:ILE:HG22	1.97	0.47
8:Id:33:PRO:HB2	8:Id:39:ILE:HG22	1.95	0.47
2:JH:207:ASP:N	2:JH:207:ASP:OD1	2.48	0.47
10:CC:258:ASN:HB2	10:CC:261:GLU:OE1	2.15	0.47
1:Kg:800:ASP:OD1	1:Kg:801:MET:N	2.47	0.47
2:KH:203:ASN:OD1	2:KH:218:THR:OG1	2.21	0.47
8:Kd:150:ASN:OD1	8:Kd:150:ASN:N	2.48	0.47
1:Lg:793:GLU:HB2	2:ZH:107:ILE:HG21	1.97	0.47
1:EG:1002:GLU:HB2	1:FG:972:PHE:HE1	1.80	0.47
2:VH:132:GLN:O	2:VH:135:GLU:HG2	2.15	0.47
2:VH:190:PRO:HB2	2:VH:231:ARG:HE	1.80	0.47
2:VH:219:LYS:HG3	2:VH:222:ASN:HD22	1.80	0.47
2:XH:284:LEU:O	2:XH:314:ARG:NH1	2.46	0.47
11:BM:229:ASN:N	11:BM:229:ASN:OD1	2.48	0.47
11:EM:144:THR:HB	11:EM:163:THR:HG23	1.96	0.47
11:EM:278:ASP:OD1	11:EM:297:SER:OG	2.33	0.47
5:BN:45:MET:HE1	5:BN:64:PHE:HB2	1.97	0.47
10:IC:132:LYS:NZ	10:IC:133:VAL:O	2.48	0.47
10:IC:258:SER:HA	10:IC:261:TRP:CD2	2.50	0.47
11:CM:206:TRP:HZ3	9:Cf:214:ALA:HB3	1.80	0.47
2:DH:125:GLU:H	2:DH:125:GLU:CD	2.20	0.47
2:DH:289:PRO:O	2:DH:292:SER:OG	2.24	0.47
1:HG:1014:ALA:HB1	1:IG:959:LEU:HD21	1.97	0.47
1:OG:891:THR:OG1	1:OG:892:GLY:N	2.47	0.47
10:AC:58:MET:SD	10:AC:58:MET:N	2.88	0.47
3:FK:185:ARG:HH12	4:GL:215:SER:HA	1.79	0.47
4:FL:224:ALA:HA	4:FL:227:ARG:NH1	2.29	0.47
9:Ff:212:ILE:HG12	9:Ff:264:PHE:HA	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:GD:124:LYS:HE3	3:GK:145:TRP:CD1	2.50	0.47
1:Gg:797:ARG:HG3	2:XH:107:ILE:HG22	1.96	0.47
4:GL:63:ASP:O	4:GL:88:GLY:N	2.48	0.47
4:HL:225:GLN:HE21	4:HL:225:GLN:HB2	1.60	0.47
11:HM:303:GLU:OE1	11:HM:303:GLU:N	2.31	0.47
8:ID:70:THR:HG23	8:ID:133:ARG:NH2	2.29	0.47
4:IL:142:GLU:CD	4:IL:142:GLU:H	2.21	0.47
1:CG:951:HIS:H	1:CG:1027:THR:HG22	1.80	0.47
11:KM:144:THR:O	11:KM:145:ARG:NE	2.47	0.47
9:VF:246:LEU:HD13	9:VF:255:LEU:HD12	1.97	0.47
9:CF:267:GLU:O	2:CH:150:LYS:NZ	2.33	0.47
9:WF:245:LYS:HE3	9:WF:257:SER:HA	1.98	0.47
1:YG:793:GLU:CD	1:YG:793:GLU:H	2.23	0.47
2:ZH:125:GLU:H	2:ZH:125:GLU:CD	2.23	0.47
2:ZH:282:HIS:HB3	2:ZH:287:VAL:HG13	1.97	0.47
11:EM:257:ASP:OD1	11:EM:257:ASP:N	2.44	0.47
11:FM:308:ASP:OD1	11:FM:308:ASP:N	2.47	0.47
10:EC:63:ALA:HB2	10:EC:176:TRP:CD1	2.50	0.47
1:GG:949:ASN:HA	1:GG:952:TYR:CE2	2.50	0.47
1:GG:1044:ASP:N	1:GG:1044:ASP:OD1	2.48	0.47
10:JC:32:LEU:H	10:JC:32:LEU:HD12	1.80	0.47
10:MC:120:ASP:N	10:MC:123:SER:OG	2.46	0.47
2:CH:183:ASP:HB3	2:CH:260:GLY:H	1.79	0.47
4:CL:174:SER:O	4:CL:178:LYS:HG3	2.15	0.47
1:JG:949:ASN:HA	1:JG:952:TYR:CE2	2.50	0.47
1:NG:878:ASN:ND2	1:NG:1030:GLU:OE1	2.48	0.47
1:AG:931:SER:H	1:AG:1043:GLN:NE2	2.13	0.46
2:EH:151:PRO:HG3	9:DF:221:TRP:HZ2	1.80	0.46
2:FH:225:ASN:N	2:FH:225:ASN:OD1	2.48	0.46
2:GH:183:ASP:HB2	2:GH:259:TYR:HA	1.97	0.46
2:GH:189:TRP:CE2	2:GH:260:GLY:HA2	2.50	0.46
3:GK:177:ASN:O	3:GK:179:ARG:NH1	2.39	0.46
9:If:238:ILE:HD12	9:If:239:PRO:HD2	1.96	0.46
8:JD:38:THR:HA	8:JD:41:LEU:HD12	1.97	0.46
1:Kg:801:MET:HE2	1:Kg:801:MET:HB2	1.83	0.46
8:CD:137:TYR:CZ	8:Cd:57:LYS:HG3	2.51	0.46
3:LK:117:THR:HA	3:LK:157:GLN:O	2.15	0.46
4:LL:174:SER:O	4:LL:178:LYS:HG3	2.15	0.46
11:MM:244:LYS:HE2	11:MM:244:LYS:HB2	1.73	0.46
11:MM:275:ASP:HA	11:MM:295:ASN:H	1.78	0.46
2:VH:311:MET:HB2	2:VH:341:LYS:HA	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:WG:797:ARG:HA	1:WG:800:ASP:OD2	2.15	0.46
2:WH:284:LEU:HD11	2:WH:330:SER:HB3	1.98	0.46
2:ZH:325:LEU:HG	2:ZH:339:MET:HA	1.97	0.46
11:BM:181:PRO:O	11:BM:201:THR:OG1	2.32	0.46
11:JM:133:TYR:HE1	11:JM:153:GLN:H	1.62	0.46
11:JM:288:ARG:NH2	11:JM:316:ASN:O	2.47	0.46
1:GG:969:GLY:O	1:GG:1005:VAL:HG13	2.15	0.46
10:IC:213:LYS:HA	10:IC:213:LYS:HE2	1.96	0.46
10:JC:109:PRO:HD3	10:JC:139:ALA:HB2	1.97	0.46
2:CH:198:ASP:OD2	2:CH:200:SER:OG	2.29	0.46
5:CN:63:GLY:HA3	8:DD:27:LYS:HB2	1.97	0.46
1:HG:1006:ILE:HD13	1:IG:968:PHE:HA	1.96	0.46
1:JG:958:SER:O	1:JG:962:SER:OG	2.33	0.46
1:NG:1014:ALA:HB1	1:OG:959:LEU:HD21	1.97	0.46
8:AD:35:ASP:OD2	8:AD:38:THR:N	2.38	0.46
8:GD:87:TRP:CG	8:GD:94:LEU:HD22	2.51	0.46
3:HK:104:ALA:HA	3:HK:107:LYS:HZ3	1.81	0.46
2:IH:112:PHE:CZ	2:XH:129:LYS:HE3	2.50	0.46
1:CG:899:LEU:HD21	1:CG:916:PHE:HB3	1.97	0.46
9:JF:216:ILE:HG13	9:JF:219:ARG:O	2.16	0.46
4:JL:171:ASN:OD1	4:JL:217:ASN:ND2	2.49	0.46
2:AH:125:GLU:H	2:AH:125:GLU:CD	2.22	0.46
2:AH:134:TYR:HA	2:BH:120:TYR:HE2	1.80	0.46
2:AH:251:ARG:CZ	2:ZH:235:THR:HG23	2.46	0.46
2:LH:225:ASN:HD21	2:MH:176:VAL:N	2.13	0.46
4:LL:59:ARG:HH12	4:LL:99:ARG:HD2	1.81	0.46
2:MH:190:PRO:HA	2:MH:211:ASN:HB3	1.97	0.46
4:ML:210:ASP:OD1	4:ML:210:ASP:N	2.46	0.46
9:Mf:263:LYS:HG3	9:Mf:264:PHE:H	1.81	0.46
11:AM:131:THR:HG21	11:AM:134:LEU:HD23	1.98	0.46
11:AM:276:ALA:H	11:AM:295:ASN:HB2	1.79	0.46
1:Cg:822:GLU:OE2	1:Cg:824:THR:OG1	2.30	0.46
8:Ad:110:GLY:HA3	8:Ad:158:TYR:HB2	1.96	0.46
10:HC:239:ILE:HG13	10:IC:131:TYR:HB2	1.98	0.46
2:CH:313:VAL:HG13	2:CH:337:TYR:HB2	1.96	0.46
1:HG:915:THR:HG23	1:HG:933:TYR:HE1	1.80	0.46
1:HG:965:LEU:O	1:HG:1008:LEU:HB3	2.15	0.46
1:LG:1014:ALA:HB1	1:MG:959:LEU:HD21	1.97	0.46
8:ED:35:ASP:O	8:ED:39:ILE:HG12	2.14	0.46
8:Ed:33:PRO:HB2	8:Ed:39:ILE:HG22	1.97	0.46
8:Fd:82:ARG:NH2	8:Fd:83:ALA:H	2.13	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BG:877:VAL:H	1:BG:1031:VAL:HG22	1.80	0.46
9:HF:209:ILE:HB	9:HF:225:SER:HB3	1.96	0.46
2:HH:107:ILE:HG23	1:WG:794:ILE:HG12	1.97	0.46
8:ID:119:ILE:HD13	8:ID:119:ILE:HA	1.85	0.46
1:Ig:794:ILE:HD13	2:KH:107:ILE:HG23	1.97	0.46
10:CC:242:ILE:HG13	10:DC:129:ARG:HB2	1.96	0.46
3:KK:85:ALA:HB3	3:KK:88:SER:HB2	1.97	0.46
8:CD:82:ARG:HB3	3:CK:156:THR:HG23	1.96	0.46
3:AK:120:SER:N	3:AK:160:GLY:O	2.36	0.46
11:MM:172:ASN:OD1	11:MM:173:LEU:N	2.48	0.46
2:VH:169:ILE:HD12	2:VH:252:VAL:HG21	1.96	0.46
10:DC:149:TYR:CD2	10:DC:201:ILE:HD13	2.50	0.46
11:BM:206:TRP:CZ3	9:Bf:221:TRP:HB2	2.50	0.46
8:Bd:87:TRP:CD1	8:Bd:94:LEU:HD22	2.50	0.46
8:Bd:106:PHE:HD1	8:Bd:154:VAL:HG23	1.80	0.46
10:LC:109:LEU:HD23	10:LC:214:LEU:HD22	1.97	0.46
3:CK:67:VAL:HG22	3:CK:76:ILE:HG22	1.97	0.46
11:CM:313:ASP:O	11:CM:317:LYS:N	2.48	0.46
5:CN:82:MET:HG3	5:CN:83:GLY:H	1.80	0.46
8:DD:127:SER:OG	8:DD:130:GLU:OE1	2.29	0.46
1:HG:876:SER:N	1:IG:940:ALA:O	2.43	0.46
1:HG:1006:ILE:CD1	1:IG:968:PHE:HA	2.45	0.46
1:JG:968:PHE:CG	1:JG:1008:LEU:HD13	2.49	0.46
2:FH:150:LYS:H	2:FH:247:ALA:HA	1.81	0.46
3:FK:73:ASN:CG	3:FK:185:ARG:HD3	2.40	0.46
9:HF:212:ILE:H	9:HF:264:PHE:HA	1.80	0.46
8:ID:123:THR:OG1	8:ID:124:LYS:N	2.49	0.46
8:Id:151:SER:O	8:Id:153:VAL:N	2.49	0.46
1:Kg:812:TRP:HE1	2:KH:141:LYS:HD3	1.80	0.46
1:DG:939:THR:HG22	1:DG:941:ARG:HG3	1.97	0.46
8:CD:85:VAL:HG23	3:CK:153:ILE:HG12	1.98	0.46
8:CD:136:ASP:C	8:Cd:60:LYS:HZ1	2.23	0.46
2:MH:302:ALA:O	2:MH:303:ARG:NH1	2.35	0.46
3:MK:72:GLN:OE1	3:MK:72:GLN:N	2.49	0.46
1:EG:878:ASN:HD22	1:EG:1030:GLU:HB2	1.81	0.46
1:ZG:814:GLN:NE2	1:ZG:814:GLN:O	2.48	0.46
1:FG:1024:ASN:OD1	1:FG:1024:ASN:N	2.34	0.46
11:EM:284:LEU:O	11:EM:310:LYS:NZ	2.32	0.46
11:JM:220:ALA:HB1	11:JM:222:ILE:HD13	1.98	0.46
10:IC:166:PRO:HA	10:IC:171:GLU:CD	2.40	0.46
10:KC:98:ASN:OD1	10:KC:98:ASN:N	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:KC:214:ARG:NH1	8:Cd:55:MET:SD	2.89	0.46
8:DD:35:ASP:O	8:DD:38:THR:OG1	2.26	0.46
9:DF:230:LEU:HD13	9:DF:231:THR:H	1.79	0.46
2:DH:105:GLU:CD	2:DH:105:GLU:H	2.23	0.46
1:HG:880:ASP:OD1	1:HG:881:GLU:N	2.49	0.46
1:JG:898:LYS:HB2	1:JG:898:LYS:HZ2	1.80	0.46
1:KG:948:THR:HG22	1:KG:1029:VAL:HG12	1.98	0.46
1:LG:1030:GLU:OE2	1:MG:941:ARG:NH2	2.48	0.46
10:AC:60:LEU:H	10:AC:60:LEU:HD12	1.80	0.46
2:EH:132:GLN:NE2	2:EH:132:GLN:O	2.49	0.46
2:EH:288:PRO:HB3	2:EH:305:TRP:NE1	2.31	0.46
2:EH:311:MET:HE3	2:EH:341:LYS:HA	1.97	0.46
3:EK:183:THR:HG21	6:EU:123:UNK:HA	1.98	0.46
4:EL:141:ASN:OD1	4:EL:142:GLU:N	2.48	0.46
4:EL:190:MET:HG2	4:EL:203:LEU:HD23	1.97	0.46
8:Ed:41:LEU:HD22	8:ED:42:ALA:HB2	1.98	0.46
8:Fd:105:ARG:HB2	8:Fd:153:VAL:HG23	1.97	0.46
10:BC:257:ASN:CG	10:BC:263:TRP:HE1	2.23	0.46
2:GH:232:GLY:HA3	2:GH:261:PRO:HD3	1.98	0.46
8:Gd:144:SER:HB2	8:Gd:157:ARG:HB3	1.98	0.46
2:HH:106:VAL:HA	2:HH:109:LYS:HE2	1.98	0.46
8:Hd:31:ASN:OD1	8:Hd:31:ASN:N	2.41	0.46
9:Hf:216:ILE:HD12	9:Hf:216:ILE:HA	1.80	0.46
11:IM:254:LYS:HE3	11:IM:254:LYS:HB2	1.82	0.46
9:JF:236:SER:O	9:JF:244:VAL:N	2.45	0.46
2:JH:166:PRO:HG3	2:KH:151:PRO:HB2	1.97	0.46
3:JK:45:VAL:HG23	3:JK:48:ALA:HB2	1.98	0.46
5:JN:62:ASN:OD1	5:JN:63:GLY:N	2.49	0.46
4:KL:145:TYR:CG	4:KL:146:PRO:HD3	2.50	0.46
5:LN:69:TYR:CD1	5:LN:76:MET:HE1	2.51	0.46
8:Ld:71:LEU:HD21	8:Ld:147:VAL:HG12	1.97	0.46
1:EG:876:SER:HB2	1:EG:1033:SER:N	2.30	0.46
2:WH:168:VAL:HG13	2:WH:240:THR:HG23	1.98	0.46
10:DC:193:ILE:O	10:DC:196:GLU:HG2	2.16	0.46
10:FC:249:ARG:NH2	10:GC:123:GLN:HB3	2.31	0.46
4:CL:176:SER:O	4:CL:179:ARG:HG2	2.14	0.46
8:DD:69:ASN:O	8:DD:73:ILE:HG22	2.16	0.46
11:DM:311:ASP:OD1	11:DM:312:PHE:N	2.37	0.46
1:OG:1006:ILE:HG12	1:PG:968:PHE:HA	1.95	0.46
10:AC:267:VAL:HG22	10:AC:268:ALA:H	1.80	0.46
9:Df:243:MET:H	9:Df:257:SER:HG	1.57	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AD:69:ASN:HD21	8:AD:133:ARG:HB3	1.80	0.46
2:EH:275:SER:HA	10:MC:125:ARG:HD3	1.98	0.46
9:FF:254:ILE:HB	9:FF:262:ILE:HB	1.98	0.46
10:BC:122:ASP:N	10:BC:125:SER:OG	2.48	0.46
8:GD:47:SER:HA	8:GD:50:ASP:OD2	2.15	0.46
1:BG:972:PHE:HB3	1:BG:1005:VAL:HG22	1.97	0.46
4:HL:54:ARG:NH1	4:HL:54:ARG:HA	2.30	0.46
2:IH:151:PRO:HA	2:IH:248:VAL:HG13	1.98	0.46
2:IH:341:LYS:HB2	2:IH:361:LEU:HD11	1.96	0.46
5:JN:85:CYS:N	10:EC:154:ASP:OD2	2.45	0.46
4:KL:57:VAL:HA	4:KL:60:VAL:HG22	1.97	0.46
11:KM:254:LYS:HE2	11:KM:272:LEU:HD23	1.98	0.46
9:CF:212:ILE:HA	9:CF:222:LEU:HD13	1.97	0.46
2:XH:231:ARG:NH1	2:XH:231:ARG:HB2	2.31	0.46
2:ZH:319:ILE:HG22	2:ZH:347:VAL:HG22	1.98	0.46
11:JM:149:ASN:N	11:JM:149:ASN:OD1	2.49	0.46
9:BF:254:ILE:HB	9:BF:262:ILE:HB	1.98	0.46
11:DM:116:PHE:HE1	11:DM:118:TYR:HB2	1.79	0.46
11:DM:145:ARG:HE	11:DM:164:GLN:HB3	1.80	0.46
1:LG:944:LEU:HD13	1:LG:945:ALA:N	2.31	0.46
10:AC:90:ASN:N	10:AC:90:ASN:OD1	2.47	0.46
10:AC:176:ILE:HA	10:AC:179:ILE:HG12	1.98	0.46
2:EH:233:LEU:HD23	2:EH:233:LEU:HA	1.82	0.46
2:GH:125:GLU:H	2:GH:125:GLU:CD	2.24	0.46
4:HL:113:ASP:N	4:HL:113:ASP:OD1	2.39	0.46
11:HM:162:VAL:HA	11:HM:182:LYS:O	2.15	0.46
4:IL:127:ILE:HD13	4:IL:189:MET:HE2	1.98	0.46
4:IL:129:THR:HG22	4:IL:229:ILE:HG12	1.97	0.46
8:Kd:142:LYS:HE2	8:Kd:142:LYS:HB2	1.83	0.46
11:LM:158:VAL:HA	11:LM:178:LYS:HE2	1.98	0.46
5:LN:87:TRP:CE2	10:GC:148:ARG:HB3	2.50	0.46
9:MF:214:ALA:HB3	9:MF:221:TRP:HB2	1.97	0.46
1:EG:969:GLY:CA	1:EG:1009:ALA:HB2	2.41	0.46
2:XH:157:PHE:CZ	2:XH:257:GLN:HG2	2.50	0.46
2:YH:253:ASP:N	2:YH:253:ASP:OD1	2.47	0.46
8:Ad:28:PRO:HB2	8:Ad:32:ASN:ND2	2.31	0.46
5:BN:111:GLU:CD	5:BN:111:GLU:H	2.22	0.46
10:GC:186:ASN:HA	10:GC:189:ASP:OD2	2.16	0.46
10:MC:102:HIS:CD2	10:MC:225:VAL:HG11	2.51	0.46
3:CK:87:GLN:N	3:CK:173:ASP:OD2	2.47	0.46
5:CN:89:GLY:HA3	5:CN:104:ASN:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HG:931:SER:H	1:HG:1043:GLN:NE2	2.13	0.46
1:JG:898:LYS:NZ	1:KG:865:THR:O	2.41	0.46
1:KG:969:GLY:HA3	1:KG:1009:ALA:N	2.31	0.46
1:LG:969:GLY:O	1:LG:1005:VAL:HG13	2.15	0.46
1:NG:904:ASN:OD1	1:NG:904:ASN:N	2.49	0.46
10:AC:110:VAL:HG13	10:AC:209:GLY:HA3	1.98	0.46
2:EH:168:VAL:HG21	9:EF:221:TRP:CD1	2.51	0.46
2:EH:297:VAL:HG22	2:EH:358:VAL:HA	1.98	0.46
8:Ed:151:SER:O	8:Ed:153:VAL:N	2.49	0.46
3:FK:56:MET:HG3	3:FK:105:PHE:HD1	1.81	0.46
8:Fd:64:PRO:HG2	8:Fd:67:LYS:HG2	1.98	0.46
9:AF:233:ARG:NH1	9:BF:269:SER:OG	2.49	0.46
9:GF:223:ILE:HA	9:GF:229:THR:HA	1.96	0.46
1:Gg:804:ALA:O	1:Gg:808:LEU:N	2.45	0.46
8:Hd:81:ALA:HB3	8:Hd:128:LEU:HD11	1.98	0.46
2:IH:152:THR:O	2:IH:250:TYR:N	2.30	0.46
2:IH:194:TYR:CE2	2:IH:204:ILE:HG21	2.51	0.46
3:IK:143:TYR:O	3:IK:146:SER:OG	2.26	0.46
9:If:241:TYR:HB3	9:If:256:THR:HG21	1.98	0.46
9:KF:233:ARG:NH1	9:YF:269:SER:OG	2.49	0.46
2:KH:150:LYS:H	2:KH:247:ALA:HA	1.80	0.46
4:KL:133:PHE:HE2	4:KL:138:PRO:HA	1.81	0.46
1:Lg:814:GLN:NE2	1:Lg:814:GLN:O	2.43	0.46
11:MM:205:TYR:HD1	11:MM:205:TYR:HA	1.65	0.46
9:VF:256:THR:HB	9:VF:260:GLN:H	1.79	0.46
9:WF:212:ILE:HG12	9:WF:222:LEU:HD22	1.98	0.46
9:YF:219:ARG:HD2	9:YF:233:ARG:HA	1.98	0.46
2:YH:115:MET:HE3	2:YH:115:MET:HB2	1.77	0.46
11:AM:199:LYS:HA	11:AM:219:ALA:HB3	1.98	0.46
11:GM:235:LEU:HD23	11:GM:255:THR:HG22	1.98	0.46
10:FC:237:ASP:CG	10:FC:239:SER:H	2.24	0.46
10:GC:149:GLN:OE1	10:GC:149:GLN:N	2.42	0.46
1:GG:891:THR:OG1	1:GG:892:GLY:N	2.48	0.46
10:HC:60:GLU:OE1	10:HC:60:GLU:N	2.45	0.46
10:HC:242:ASP:OD1	10:IC:128:ASP:N	2.43	0.46
10:IC:136:GLN:HG2	10:IC:251:LEU:HD13	1.98	0.46
2:DH:288:PRO:HB3	2:DH:305:TRP:NE1	2.31	0.46
1:IG:878:ASN:HA	1:IG:1030:GLU:HA	1.97	0.46
1:KG:932:ALA:HB1	1:KG:1039:ILE:HG23	1.98	0.46
1:LG:891:THR:OG1	1:LG:892:GLY:N	2.49	0.46
4:EL:141:ASN:HD21	4:EL:143:ILE:HB	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:GF:243:MET:N	9:GF:257:SER:OG	2.38	0.46
4:GL:187:GLU:CD	11:GM:268:HIS:HD1	2.23	0.46
8:Gd:28:PRO:HB2	8:Gd:32:ASN:HD21	1.80	0.46
2:HH:198:ASP:OD2	2:HH:201:SER:OG	2.22	0.46
2:HH:199:PRO:HD2	1:XG:816:GLU:OE1	2.15	0.46
3:HK:112:ILE:O	3:HK:151:SER:OG	2.32	0.46
4:IL:91:VAL:HA	4:IL:94:VAL:HG12	1.97	0.46
4:IL:190:MET:HE2	4:IL:190:MET:HB2	1.89	0.46
11:IM:275:ASP:HA	11:IM:295:ASN:H	1.81	0.46
8:JD:24:LYS:NZ	8:JD:24:LYS:H	2.14	0.46
9:JF:219:ARG:HH21	9:JF:231:THR:HG23	1.81	0.46
2:AH:306:LEU:HD11	2:AH:309:GLU:HA	1.97	0.46
3:KK:107:LYS:HD3	3:KK:149:VAL:HA	1.98	0.46
3:KK:111:LYS:N	3:KK:111:LYS:HZ2	2.14	0.46
3:KK:120:SER:H	3:KK:160:GLY:C	2.24	0.46
11:KM:217:LYS:HZ3	11:KM:236:TRP:CD1	2.34	0.46
3:LK:76:ILE:HG13	3:LK:182:ILE:HB	1.98	0.46
3:AK:97:SER:O	3:AK:101:GLU:HG2	2.15	0.46
5:MN:62:ASN:OD1	5:MN:62:ASN:N	2.49	0.46
5:MN:102:VAL:HA	5:MN:108:VAL:HA	1.97	0.46
9:VF:268:ASP:OD1	2:VH:170:ARG:NH2	2.48	0.46
9:XF:207:ARG:HH11	9:XF:209:ILE:HD13	1.80	0.46
10:DC:242:ASP:OD1	10:DC:242:ASP:N	2.47	0.46
1:FG:1030:GLU:OE2	1:GG:941:ARG:NE	2.39	0.46
11:JM:292:MET:HE1	11:JM:298:VAL:HB	1.97	0.46
10:EC:179:TYR:HA	10:EC:182:ARG:HG2	1.98	0.46
10:FC:56:ARG:HH21	10:FC:166:LEU:HD21	1.81	0.46
10:IC:213:LYS:NZ	8:AD:55:MET:O	2.42	0.46
10:JC:122:ASP:N	10:JC:125:SER:OG	2.45	0.46
10:JC:179:ILE:O	10:JC:183:ARG:HG2	2.15	0.46
4:CL:109:LEU:HD12	4:CL:114:ILE:HB	1.98	0.46
9:Cf:248:ASP:OD1	9:Cf:249:SER:N	2.49	0.46
4:DL:55:ARG:O	4:DL:59:ARG:HG2	2.16	0.46
1:LG:931:SER:O	1:LG:1042:THR:OG1	2.34	0.46
1:MG:898:LYS:HE3	1:NG:866:GLY:HA3	1.97	0.46
1:MG:901:GLY:HA3	1:MG:916:PHE:HD1	1.81	0.46
1:Eg:801:MET:O	1:Eg:805:ALA:N	2.40	0.46
8:Fd:82:ARG:NH2	8:Fd:83:ALA:O	2.37	0.46
10:BC:32:LEU:HG	10:AC:185:TRP:CZ3	2.51	0.46
8:HD:52:MET:HB3	8:HD:52:MET:HE2	1.52	0.46
9:IF:263:LYS:HE2	9:IF:264:PHE:HB2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:JD:69:ASN:OD1	8:JD:69:ASN:N	2.49	0.46
10:CC:224:PRO:HB3	10:CC:253:PRO:HG3	1.98	0.46
2:KH:239:LEU:O	2:YH:250:TYR:OH	2.34	0.46
4:KL:124:THR:HG22	4:KL:232:GLN:HG2	1.98	0.46
4:KL:169:THR:OG1	4:KL:170:ASP:N	2.48	0.46
9:LF:241:TYR:HD2	9:LF:256:THR:HG21	1.81	0.46
3:LK:177:ASN:OD1	3:LK:178:ALA:N	2.49	0.46
9:XF:246:LEU:HB3	9:XF:255:LEU:HD12	1.97	0.46
11:EM:191:LEU:HD23	11:EM:192:ARG:N	2.31	0.46
11:FM:238:PHE:N	11:FM:258:LYS:O	2.44	0.46
11:GM:269:GLN:NE2	11:GM:290:ASP:OD1	2.30	0.46
5:AN:65:TYR:OH	4:BL:221:HIS:HB3	2.16	0.46
3:BK:49:CYS:O	3:BK:52:THR:OG1	2.22	0.46
10:KC:91:LEU:HD21	10:KC:148:TRP:CE3	2.51	0.46
2:CH:171:LEU:O	2:CH:244:GLY:N	2.48	0.46
11:CM:215:ARG:NH2	11:CM:232:ASP:OD2	2.48	0.46
11:CM:275:ASP:HA	11:CM:295:ASN:H	1.80	0.46
8:Cd:35:ASP:HB3	8:Cd:38:THR:HG23	1.98	0.46
8:DD:73:ILE:HA	8:DD:147:VAL:HG12	1.97	0.46
2:DH:302:ALA:O	2:DH:303:ARG:NH1	2.37	0.46
1:JG:1006:ILE:CD1	1:KG:968:PHE:HA	2.46	0.46
1:KG:876:SER:OG	1:KG:1031:VAL:O	2.21	0.46
1:AG:963:SER:HB2	1:PG:1011:VAL:HG12	1.98	0.45
2:GH:114:ASP:HA	2:GH:117:ARG:HG2	1.99	0.45
2:GH:321:SER:OG	2:GH:346:LEU:N	2.49	0.45
1:BG:867:ASP:OD1	1:BG:867:ASP:N	2.49	0.45
9:HF:214:ALA:HB3	9:HF:221:TRP:HB2	1.99	0.45
2:HH:233:LEU:HD11	2:HH:256:VAL:HG11	1.99	0.45
4:HL:145:TYR:CG	4:HL:146:PRO:HD3	2.51	0.45
3:IK:93:TRP:CD2	4:IL:45:PRO:HB2	2.51	0.45
11:IM:238:PHE:N	11:IM:258:LYS:O	2.38	0.45
5:IN:89:GLY:HA3	5:IN:104:ASN:HB2	1.98	0.45
8:KD:82:ARG:HD3	3:KK:138:ARG:HD2	1.98	0.45
2:KH:151:PRO:HA	2:KH:248:VAL:HG13	1.98	0.45
4:KL:124:THR:HA	4:KL:231:ILE:O	2.16	0.45
11:KM:242:LYS:HA	11:KM:262:GLU:HB2	1.99	0.45
2:LH:273:PRO:O	10:GC:126:ARG:NH1	2.47	0.45
4:LL:51:GLN:NE2	4:LL:52:PRO:O	2.49	0.45
2:MH:126:GLN:HA	2:MH:129:LYS:HE2	1.97	0.45
3:MK:78:ILE:O	3:MK:179:ARG:HB2	2.16	0.45
9:YF:238:ILE:HG23	9:YF:241:TYR:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:DC:232:VAL:HG12	10:DC:241:ILE:HA	1.98	0.45
1:ZG:817:THR:OG1	1:ZG:818:GLN:N	2.48	0.45
11:FM:300:ASP:OD2	11:FM:302:ARG:NH2	2.44	0.45
11:GM:145:ARG:HH21	11:GM:163:THR:HA	1.81	0.45
11:JM:161:GLY:O	11:JM:182:LYS:HD2	2.17	0.45
1:Cg:801:MET:HB2	2:DH:115:MET:HE3	1.97	0.45
10:GC:107:PRO:HG2	10:GC:209:MET:SD	2.56	0.45
3:CK:165:ILE:HG22	3:CK:177:ASN:HA	1.98	0.45
3:DK:46:ASP:OD1	3:DK:46:ASP:N	2.48	0.45
3:DK:114:ILE:HB	3:DK:154:ILE:HG12	1.98	0.45
1:JG:873:LEU:HB3	1:JG:1035:THR:O	2.16	0.45
1:LG:958:SER:O	1:LG:962:SER:OG	2.34	0.45
1:LG:1011:VAL:HG12	1:MG:963:SER:HB2	1.98	0.45
9:Ef:253:ARG:HB3	9:Ef:263:LYS:HE3	1.97	0.45
9:FF:238:ILE:HD12	9:FF:239:PRO:HD2	1.98	0.45
2:FH:189:TRP:CH2	2:FH:233:LEU:HB2	2.51	0.45
2:FH:288:PRO:HB3	2:FH:305:TRP:NE1	2.31	0.45
10:BC:41:SER:O	10:BC:44:THR:OG1	2.25	0.45
10:BC:176:ILE:HA	10:BC:179:ILE:HG12	1.98	0.45
8:GD:160:LYS:HA	8:GD:160:LYS:HD2	1.76	0.45
4:GL:49:ASN:HD22	11:GM:293:ALA:C	2.24	0.45
4:GL:174:SER:O	4:GL:178:LYS:HG3	2.16	0.45
5:GN:116:LYS:HD2	5:GN:116:LYS:HA	1.84	0.45
4:HL:125:LEU:HD23	4:HL:233:TRP:HH2	1.81	0.45
11:IM:229:ASN:OD1	11:IM:229:ASN:N	2.49	0.45
11:IM:292:MET:HE1	11:IM:298:VAL:H	1.81	0.45
8:Id:35:ASP:O	8:Id:38:THR:OG1	2.25	0.45
2:JH:170:ARG:HB2	2:JH:249:ASP:OD1	2.17	0.45
8:Kd:92:GLU:OE2	8:Kd:158:TYR:OH	2.35	0.45
2:LH:315:THR:OG1	2:LH:316:ASN:N	2.49	0.45
3:AK:177:ASN:O	3:AK:179:ARG:NH1	2.40	0.45
8:MD:60:LYS:O	8:MD:60:LYS:NZ	2.37	0.45
2:ZH:157:PHE:CZ	2:ZH:257:GLN:HG2	2.51	0.45
1:FG:878:ASN:OD1	1:FG:879:SER:N	2.49	0.45
11:BM:119:GLU:HG3	11:BM:139:ALA:HB3	1.98	0.45
11:FM:278:ASP:HB3	11:FM:280:TYR:CE1	2.51	0.45
1:Cg:807:GLN:NE2	1:Cg:811:ASP:OD2	2.49	0.45
4:BL:169:THR:OG1	4:BL:170:ASP:N	2.47	0.45
10:EC:72:LEU:HD12	10:EC:191:ALA:HB2	1.98	0.45
10:FC:122:ASP:OD1	10:FC:125:SER:OG	2.21	0.45
10:GC:222:SER:OG	10:GC:254:GLU:N	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:GC:236:ASP:OD1	10:GC:239:GLU:N	2.44	0.45
1:GG:876:SER:HB2	1:GG:1033:SER:N	2.31	0.45
10:LC:241:ILE:HB	10:MC:128:ASP:OD1	2.17	0.45
8:Cd:33:PRO:HB2	8:Cd:39:ILE:HG22	1.97	0.45
9:DF:221:TRP:CD1	9:DF:231:THR:HB	2.52	0.45
9:DF:261:VAL:HG12	9:DF:263:LYS:HD3	1.98	0.45
4:DL:145:TYR:CD1	4:DL:146:PRO:HD3	2.52	0.45
4:DL:145:TYR:CG	4:DL:146:PRO:HD3	2.50	0.45
1:IG:944:LEU:HD11	1:IG:1031:VAL:HG12	1.99	0.45
1:LG:919:MET:HG3	1:LG:930:ILE:HG23	1.98	0.45
1:OG:878:ASN:ND2	1:OG:1030:GLU:HB2	2.30	0.45
1:PG:973:GLN:O	1:PG:976:ASN:ND2	2.49	0.45
10:AC:95:TYR:HA	10:AC:207:PHE:HE2	1.80	0.45
10:AC:97:PHE:HE2	10:AC:210:MET:HE1	1.81	0.45
9:Ef:212:ILE:HD11	9:Ef:262:ILE:HG13	1.98	0.45
2:FH:282:HIS:ND1	2:FH:285:GLU:OE2	2.49	0.45
3:FK:66:LYS:NZ	3:FK:67:VAL:O	2.49	0.45
1:Gg:793:GLU:H	1:Gg:793:GLU:CD	2.24	0.45
1:BG:898:LYS:HE2	1:BG:898:LYS:HB2	1.83	0.45
3:HK:166:THR:HG22	3:HK:168:TYR:H	1.82	0.45
11:HM:262:GLU:HB3	11:HM:282:TYR:HE2	1.81	0.45
1:Jg:793:GLU:HA	1:Jg:796:GLN:NE2	2.32	0.45
5:JN:84:CYS:SG	5:JN:85:CYS:N	2.89	0.45
5:JN:89:GLY:O	5:JN:104:ASN:ND2	2.41	0.45
2:KH:171:LEU:HD21	2:KH:241:LEU:HB2	1.97	0.45
1:DG:958:SER:O	1:DG:962:SER:OG	2.34	0.45
11:LM:275:ASP:N	11:LM:275:ASP:OD1	2.49	0.45
8:Ld:97:ARG:HA	8:Ld:97:ARG:HH11	1.81	0.45
1:Mg:800:ASP:N	1:Mg:800:ASP:OD1	2.49	0.45
1:EG:1006:ILE:HG12	1:FG:967:GLY:O	2.16	0.45
2:VH:125:GLU:H	2:VH:125:GLU:CD	2.24	0.45
2:WH:151:PRO:HA	2:WH:248:VAL:HG13	1.98	0.45
5:AN:42:CYS:SG	5:AN:48:ILE:HG13	2.55	0.45
1:GG:967:GLY:HA2	1:GG:970:ASN:HD21	1.81	0.45
1:Dg:820:TYR:HB2	2:DH:205:GLN:HG2	1.97	0.45
2:DH:324:TRP:HB3	2:DH:339:MET:HB3	1.96	0.45
1:HG:886:LEU:HB3	1:HG:900:ILE:HG23	1.98	0.45
1:IG:931:SER:H	1:IG:1043:GLN:HE22	1.65	0.45
1:NG:946:SER:OG	1:NG:1030:GLU:O	2.34	0.45
5:EN:103:CYS:HB2	5:EN:105:ASP:OD1	2.16	0.45
8:Ed:138:GLN:NE2	8:ED:111:LYS:HG2	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:Ff:216:ILE:HD12	9:Ff:216:ILE:HA	1.78	0.45
3:GK:52:THR:O	3:GK:56:MET:HG2	2.17	0.45
1:BG:873:LEU:HB2	1:BG:1037:LEU:HD22	1.97	0.45
9:Gf:264:PHE:CE1	11:GM:247:ARG:HD2	2.52	0.45
11:HM:126:GLY:O	11:HM:146:LEU:HA	2.16	0.45
11:HM:257:ASP:OD1	11:HM:257:ASP:N	2.50	0.45
1:Bg:803:THR:O	1:Bg:806:THR:OG1	2.30	0.45
11:IM:306:GLN:CD	11:IM:306:GLN:H	2.24	0.45
2:AH:251:ARG:HB2	2:ZH:238:MET:HE1	1.98	0.45
10:CC:95:ASP:OD1	10:CC:96:PHE:N	2.49	0.45
2:KH:170:ARG:HG2	2:KH:245:GLN:HG3	1.99	0.45
3:KK:53:ILE:HD13	3:KK:109:PHE:HE1	1.81	0.45
3:KK:55:LYS:HE2	3:KK:55:LYS:HB3	1.76	0.45
3:KK:145:TRP:HE3	3:KK:154:ILE:HD12	1.79	0.45
4:KL:185:GLN:O	4:KL:188:THR:OG1	2.31	0.45
11:KM:190:ASN:HA	11:KM:209:SER:HB2	1.98	0.45
1:DG:862:ILE:HD13	1:DG:1046:THR:HA	1.98	0.45
2:LH:131:LYS:HD2	1:YG:812:TRP:CH2	2.51	0.45
3:LK:50:ASP:HB3	5:LN:45:MET:HE3	1.97	0.45
5:LN:63:GLY:HA3	8:MD:27:LYS:HB2	1.98	0.45
5:LN:69:TYR:CG	5:LN:76:MET:HE1	2.52	0.45
5:LN:102:VAL:HA	5:LN:108:VAL:HA	1.97	0.45
2:MH:106:VAL:HA	2:MH:109:LYS:HE2	1.97	0.45
2:MH:311:MET:HE3	2:MH:341:LYS:HA	1.97	0.45
11:MM:180:ASP:OD1	11:MM:199:LYS:HB2	2.17	0.45
5:MN:69:TYR:CE1	5:MN:76:MET:HE1	2.52	0.45
8:Md:146:HIS:ND1	8:Md:155:GLU:OE2	2.49	0.45
2:VH:151:PRO:HA	2:VH:248:VAL:HG13	1.98	0.45
2:VH:199:PRO:HD2	1:Dg:816:GLU:OE1	2.17	0.45
2:WH:297:VAL:HG12	2:WH:358:VAL:HG12	1.99	0.45
2:YH:191:ILE:HG13	2:YH:211:ASN:HA	1.97	0.45
2:YH:220:LEU:HB3	2:YH:221:TYR:CD2	2.52	0.45
2:YH:301:ASP:OD1	2:YH:301:ASP:N	2.49	0.45
10:DC:153:ASP:OD1	10:DC:153:ASP:N	2.47	0.45
2:ZH:330:SER:OG	2:ZH:332:ASP:OD1	2.21	0.45
11:BM:208:LYS:HZ3	11:BM:227:ILE:HG12	1.81	0.45
11:FM:275:ASP:HA	11:FM:295:ASN:H	1.81	0.45
11:JM:210:ASP:O	11:JM:230:ARG:N	2.39	0.45
9:BF:208:ILE:HD11	9:BF:224:GLY:HA3	1.99	0.45
2:BH:225:ASN:ND2	2:CH:176:VAL:O	2.50	0.45
10:FC:44:THR:O	10:FC:48:LYS:HG2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GG:878:ASN:OD1	1:GG:879:SER:N	2.50	0.45
1:GG:999:SER:HB2	1:HG:972:PHE:HZ	1.82	0.45
10:IC:162:VAL:HG12	10:IC:165:LEU:HD11	1.98	0.45
10:KC:122:ASP:N	10:KC:122:ASP:OD1	2.50	0.45
10:MC:213:LYS:NZ	8:ED:55:MET:HG2	2.32	0.45
2:CH:355:GLN:OE1	2:CH:355:GLN:N	2.50	0.45
9:Cf:264:PHE:O	9:Cf:266:GLN:NE2	2.48	0.45
1:Dg:793:GLU:HB3	1:Dg:796:GLN:HE21	1.80	0.45
3:DK:54:ILE:O	3:DK:58:THR:OG1	2.32	0.45
3:DK:93:TRP:CD2	4:DL:45:PRO:HB2	2.50	0.45
4:DL:169:THR:OG1	4:DL:170:ASP:N	2.49	0.45
1:JG:1019:ALA:O	1:JG:1023:PHE:HB2	2.15	0.45
1:KG:873:LEU:HB3	1:KG:1035:THR:O	2.16	0.45
1:LG:952:TYR:CE2	1:LG:1027:THR:HG21	2.51	0.45
1:MG:944:LEU:HD13	1:MG:945:ALA:N	2.32	0.45
1:NG:1010:THR:OG1	1:OG:967:GLY:HA3	2.17	0.45
1:OG:880:ASP:OD2	1:PG:911:LYS:HG2	2.16	0.45
8:Dd:94:LEU:HD23	8:Dd:119:ILE:HD11	1.98	0.45
8:FD:85:VAL:HG12	3:FK:153:ILE:HG23	1.99	0.45
4:FL:174:SER:O	4:FL:178:LYS:HG3	2.16	0.45
8:GD:148:TYR:O	8:GD:152:GLN:N	2.50	0.45
4:GL:44:HIS:N	4:GL:48:ASN:OD1	2.30	0.45
8:HD:106:PHE:HD1	8:HD:107:ARG:N	2.15	0.45
2:HH:189:TRP:HB3	2:HH:230:LEU:HD13	1.98	0.45
11:HM:229:ASN:HA	11:HM:249:GLN:HG2	1.98	0.45
2:IH:306:LEU:HD11	2:IH:309:GLU:HA	1.97	0.45
3:IK:133:THR:HG21	3:IK:160:GLY:H	1.82	0.45
11:IM:206:TRP:HZ3	9:If:214:ALA:HB3	1.81	0.45
5:IN:110:GLU:H	5:IN:110:GLU:CD	2.22	0.45
8:JD:123:THR:OG1	8:JD:126:GLU:OE1	2.27	0.45
8:Jd:131:ILE:O	8:Jd:135:ILE:HG12	2.16	0.45
8:KD:97:ARG:HH12	3:KK:112:ILE:HG21	1.80	0.45
3:KK:106:LEU:HD22	3:KK:106:LEU:HA	1.76	0.45
11:KM:202:LEU:O	11:KM:222:ILE:HA	2.17	0.45
11:KM:228:VAL:HG11	11:KM:231:LEU:HB2	1.98	0.45
3:LK:151:SER:OG	3:LK:152:ARG:N	2.49	0.45
2:VH:221:TYR:HE2	2:DH:138:GLU:HB3	1.80	0.45
2:VH:325:LEU:HG	2:VH:339:MET:HA	1.99	0.45
2:WH:296:VAL:HB	2:WH:359:GLU:HB3	1.98	0.45
11:AM:208:LYS:HE2	11:AM:227:ILE:HG12	1.97	0.45
11:BM:215:ARG:HG3	11:BM:234:GLU:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BK:120:SER:N	3:BK:160:GLY:O	2.36	0.45
3:BK:132:LEU:O	3:BK:136:ARG:HG3	2.15	0.45
10:EC:103:HIS:CD2	10:EC:226:VAL:HG21	2.51	0.45
10:GC:176:TRP:O	10:GC:180:THR:OG1	2.34	0.45
10:IC:116:LEU:HD11	10:IC:124:ILE:HG22	1.98	0.45
8:DD:87:TRP:CE3	8:DD:94:LEU:HD12	2.51	0.45
9:DF:241:TYR:HD2	9:DF:256:THR:HG21	1.81	0.45
1:Dg:795:GLN:OE1	1:Dg:795:GLN:N	2.50	0.45
1:HG:965:LEU:HD23	1:HG:1011:VAL:HG23	1.97	0.45
1:LG:924:ALA:HB3	1:LG:926:LYS:NZ	2.31	0.45
1:NG:875:THR:HA	1:OG:940:ALA:HB1	1.98	0.45
1:OG:924:ALA:HB3	1:OG:926:LYS:NZ	2.31	0.45
10:AC:50:GLN:HG3	10:AC:54:LYS:NZ	2.32	0.45
1:AG:1006:ILE:HG12	1:BG:968:PHE:HA	1.98	0.45
2:EH:189:TRP:CE2	2:EH:260:GLY:HA2	2.52	0.45
2:FH:326:ALA:HB3	2:FH:338:GLU:HB3	1.98	0.45
9:Ff:233:ARG:HB3	9:Ff:236:SER:HB3	1.98	0.45
9:Ff:263:LYS:HG3	9:Ff:264:PHE:H	1.82	0.45
2:GH:150:LYS:H	2:GH:247:ALA:HA	1.81	0.45
4:GL:165:VAL:HG23	4:GL:205:ALA:HA	1.99	0.45
9:Gf:216:ILE:HD12	9:Gf:216:ILE:HA	1.83	0.45
8:HD:87:TRP:CD2	8:HD:94:LEU:HD13	2.52	0.45
2:HH:296:VAL:HB	2:HH:359:GLU:HB2	1.99	0.45
2:HH:313:VAL:HG23	2:HH:337:TYR:HB2	1.97	0.45
3:HK:71:GLY:O	8:ID:27:LYS:NZ	2.50	0.45
1:Bg:792:GLN:NE2	1:Bg:793:GLU:OE2	2.49	0.45
2:IH:125:GLU:H	2:IH:125:GLU:CD	2.24	0.45
2:IH:169:ILE:HD12	2:IH:252:VAL:HG21	1.99	0.45
4:IL:45:PRO:N	4:IL:46:PRO:HD2	2.32	0.45
1:CG:891:THR:OG1	1:CG:892:GLY:N	2.49	0.45
1:CG:1011:VAL:HG12	1:DG:963:SER:HB3	1.97	0.45
8:Jd:92:GLU:OE1	8:Jd:93:GLU:N	2.50	0.45
2:AH:355:GLN:N	2:AH:355:GLN:OE1	2.50	0.45
8:KD:31:ASN:HD22	8:Kd:35:ASP:HA	1.81	0.45
10:CC:168:LYS:HG3	10:CC:169:THR:HG22	1.97	0.45
10:CC:178:ILE:O	10:CC:182:ARG:HG2	2.16	0.45
11:KM:314:ARG:HH22	8:Kd:46:VAL:HG11	1.82	0.45
9:Kf:245:LYS:HE3	9:Kf:257:SER:HA	1.98	0.45
2:LH:319:ILE:HD13	2:LH:337:TYR:CZ	2.52	0.45
9:Lf:246:LEU:HD23	9:Lf:255:LEU:HD21	1.98	0.45
8:MD:29:PRO:HG2	4:ML:225:GLN:HG2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Mg:818:GLN:NE2	2:MH:216:GLN:OE1	2.49	0.45
1:EG:899:LEU:HD21	1:EG:916:PHE:HB3	1.97	0.45
1:EG:961:ALA:O	1:EG:965:LEU:HD13	2.17	0.45
8:Md:104:PHE:CZ	8:Md:152:GLN:HB3	2.52	0.45
4:AL:159:PRO:O	4:AL:202:ARG:NH1	2.50	0.45
11:BM:118:TYR:CE2	11:BM:122:GLY:HA3	2.52	0.45
2:BH:282:HIS:HB3	2:BH:287:VAL:HG13	1.99	0.45
10:FC:92:ASP:OD1	10:FC:92:ASP:N	2.49	0.45
1:GG:972:PHE:HB3	1:GG:1005:VAL:CG2	2.47	0.45
8:Cd:67:LYS:HE2	8:Cd:67:LYS:HB3	1.76	0.45
4:DL:109:LEU:HD13	4:DL:109:LEU:HA	1.82	0.45
4:DL:136:SER:OG	11:DM:314:ARG:NH1	2.49	0.45
1:PG:898:LYS:HE2	1:PG:898:LYS:HB2	1.70	0.45
1:PG:911:LYS:HZ1	1:PG:913:VAL:HB	1.81	0.45
10:AC:260:SER:HA	10:AC:263:TRP:CE2	2.52	0.45
8:AD:161:ILE:HG13	8:AD:162:TYR:CD1	2.52	0.45
3:FK:119:TYR:HE2	3:FK:159:LEU:HD12	1.81	0.45
3:FK:152:ARG:HB2	3:FK:153:ILE:HD12	1.99	0.45
4:FL:59:ARG:HH12	4:FL:99:ARG:HD2	1.81	0.45
9:Ff:260:GLN:NE2	9:Ff:261:VAL:O	2.49	0.45
2:GH:203:ASN:HB3	2:GH:216:GLN:HB2	1.99	0.45
2:GH:299:GLY:HA3	2:GH:356:LEU:HD22	1.98	0.45
4:GL:170:ASP:OD2	4:GL:227:ARG:NH2	2.44	0.45
5:GN:82:MET:N	5:GN:82:MET:SD	2.90	0.45
2:HH:288:PRO:HB3	2:HH:305:TRP:NE1	2.32	0.45
9:IF:246:LEU:HD22	9:IF:255:LEU:HG	1.97	0.45
3:IK:109:PHE:HD1	3:IK:109:PHE:HA	1.67	0.45
11:IM:172:ASN:OD1	11:IM:173:LEU:N	2.50	0.45
1:CG:965:LEU:HD12	1:CG:1008:LEU:HD23	1.99	0.45
5:IN:115:GLN:OE1	5:IN:115:GLN:N	2.50	0.45
8:Jd:87:TRP:CD1	8:Jd:94:LEU:HD22	2.52	0.45
2:KH:180:VAL:HG13	2:KH:253:ASP:HA	1.97	0.45
11:KM:281:TYR:CE2	11:KM:300:ASP:HA	2.51	0.45
2:VH:249:ASP:OD1	2:VH:249:ASP:N	2.46	0.45
2:WH:206:TRP:CD1	2:WH:213:LEU:HD12	2.52	0.45
2:WH:249:ASP:N	2:WH:249:ASP:OD1	2.47	0.45
1:ZG:801:MET:HB2	2:BH:115:MET:HE3	1.98	0.45
1:ZG:810:GLN:HE21	1:ZG:810:GLN:HB3	1.60	0.45
1:FG:880:ASP:OD1	1:FG:881:GLU:N	2.50	0.45
1:FG:953:LEU:H	1:FG:953:LEU:HD22	1.82	0.45
11:BM:238:PHE:N	11:BM:258:LYS:O	2.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AN:89:GLY:HA3	5:AN:104:ASN:HB2	1.99	0.45
8:BD:73:ILE:HD12	8:BD:147:VAL:HG23	1.98	0.45
10:EC:179:TYR:HD1	10:EC:182:ARG:HH11	1.65	0.45
10:IC:183:TRP:CZ3	10:JC:31:SER:HB3	2.52	0.45
10:JC:231:ASP:OD1	10:JC:246:ARG:NE	2.49	0.45
9:Cf:210:TYR:CD2	9:Cf:224:GLY:HA2	2.52	0.45
1:LG:951:HIS:H	1:LG:1027:THR:HG22	1.80	0.45
2:EH:156:GLN:NE2	2:EH:157:PHE:O	2.50	0.45
2:EH:306:LEU:HD11	2:EH:309:GLU:HA	1.99	0.45
2:EH:315:THR:OG1	2:EH:316:ASN:N	2.49	0.45
8:Ed:36:ASP:N	8:Ed:36:ASP:OD1	2.49	0.45
3:FK:65:ILE:HG23	3:FK:78:ILE:HG13	1.99	0.45
4:FL:145:TYR:CD1	4:FL:146:PRO:HD3	2.51	0.45
2:GH:178:SER:HB3	2:GH:214:MET:HE1	1.99	0.45
1:BG:1006:ILE:HD13	1:CG:968:PHE:CD2	2.52	0.45
8:Gd:94:LEU:O	8:Gd:98:ILE:HG12	2.16	0.45
2:HH:184:SER:C	2:HH:255:ARG:HH21	2.25	0.45
2:HH:278:ASP:OD2	10:CC:133:LYS:NZ	2.44	0.45
11:HM:244:LYS:HD3	11:HM:282:TYR:CZ	2.52	0.45
11:HM:261:ALA:HB3	11:HM:279:ILE:HG23	1.98	0.45
8:Hd:92:GLU:OE1	8:Hd:92:GLU:N	2.43	0.45
8:ID:35:ASP:O	8:ID:39:ILE:HG12	2.17	0.45
4:IL:94:VAL:HA	4:IL:97:ILE:HG12	1.99	0.45
11:IM:205:TYR:HB3	11:IM:206:TRP:CD1	2.52	0.45
1:CG:897:SER:HA	1:CG:922:PRO:HD3	1.99	0.45
1:CG:967:GLY:HA2	1:CG:970:ASN:HD21	1.81	0.45
1:CG:1004:ALA:O	1:CG:1008:LEU:HD12	2.16	0.45
3:JK:49:CYS:O	3:JK:52:THR:OG1	2.22	0.45
8:Jd:57:LYS:HE2	8:Jd:57:LYS:HB2	1.73	0.45
10:CC:68:ALA:HA	10:CC:183:GLY:O	2.16	0.45
4:KL:217:ASN:O	4:KL:217:ASN:ND2	2.48	0.45
11:KM:306:GLN:HG3	11:KM:308:ASP:H	1.82	0.45
9:Kf:243:MET:HB2	9:Kf:257:SER:HB3	1.97	0.45
2:LH:281:LEU:H	2:LH:281:LEU:HG	1.65	0.45
5:LN:84:CYS:HA	10:GC:154:ASP:HB3	1.99	0.45
11:MM:120:GLY:H	11:MM:140:ASN:HB2	1.82	0.45
11:MM:265:ALA:O	11:MM:283:ASN:ND2	2.50	0.45
9:Mf:213:GLN:CD	9:Mf:223:ILE:HB	2.42	0.45
2:XH:324:TRP:HA	2:XH:339:MET:HB3	1.99	0.45
2:XH:355:GLN:NE2	2:XH:356:LEU:O	2.50	0.45
2:YH:105:GLU:CD	2:YH:105:GLU:H	2.25	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:GM:191:LEU:HD23	11:GM:192:ARG:N	2.32	0.45
8:Bd:127:SER:HB3	8:Bd:130:GLU:CD	2.42	0.45
10:IC:71:LEU:HD12	10:IC:190:ALA:HB2	1.98	0.45
10:JC:90:ASN:O	10:JC:94:ILE:HG12	2.17	0.45
10:KC:170:THR:OG1	10:KC:171:LYS:NZ	2.49	0.45
2:CH:302:ALA:O	2:CH:303:ARG:NH1	2.44	0.45
4:CL:49:ASN:OD1	4:CL:49:ASN:N	2.49	0.45
8:DD:36:ASP:N	8:DD:36:ASP:OD1	2.49	0.45
2:DH:207:ASP:OD1	2:DH:210:SER:OG	2.29	0.45
2:DH:262:ASN:OD1	2:DH:262:ASN:N	2.50	0.45
1:HG:958:SER:O	1:HG:962:SER:OG	2.35	0.45
1:PG:966:GLN:O	1:PG:970:ASN:ND2	2.50	0.45
2:EH:320:LEU:HB2	2:EH:346:LEU:HD23	1.99	0.45
3:EK:40:LYS:HB2	3:EK:40:LYS:HE3	1.77	0.45
1:Fg:807:GLN:NE2	1:Fg:811:ASP:OD1	2.50	0.45
2:FH:130:LEU:HA	2:FH:133:ILE:HG12	1.99	0.45
8:Fd:73:ILE:HG22	8:Fd:75:ASN:H	1.81	0.45
8:Fd:76:ALA:HB3	8:Fd:79:LEU:HD13	1.98	0.45
10:BC:127:ARG:NH2	10:AC:245:ASP:OD2	2.50	0.45
9:AF:211:TYR:CG	9:AF:265:SER:HB2	2.52	0.45
2:GH:212:THR:HG21	2:WH:236:PRO:HG3	1.98	0.45
3:HK:72:GLN:HB2	3:HK:186:ARG:HB3	1.98	0.45
1:Ig:800:ASP:O	1:Ig:803:THR:OG1	2.23	0.45
2:IH:180:VAL:HG13	2:IH:253:ASP:HA	1.99	0.45
11:IM:199:LYS:HA	11:IM:219:ALA:HB3	1.99	0.45
8:JD:55:MET:HE1	8:Jd:55:MET:HE1	1.99	0.45
2:AH:181:PHE:HE1	2:AH:254:LEU:HD23	1.82	0.45
8:KD:31:ASN:OD1	8:KD:31:ASN:N	2.50	0.45
4:KL:191:THR:HG21	11:KM:289:ALA:HB3	1.98	0.45
4:LL:210:ASP:OD1	4:LL:210:ASP:N	2.34	0.45
9:WF:245:LYS:N	9:WF:255:LEU:O	2.50	0.45
10:DC:166:PRO:HB2	10:DC:172:LYS:HG3	1.99	0.45
2:ZH:349:TRP:O	2:ZH:352:LYS:HG3	2.17	0.45
11:FM:121:ALA:HA	11:FM:141:GLU:HB3	1.99	0.45
1:Cg:791:GLN:N	1:Cg:793:GLU:OE1	2.50	0.45
3:BK:87:GLN:NE2	3:BK:173:ASP:OD1	2.49	0.45
3:BK:120:SER:H	3:BK:160:GLY:C	2.22	0.45
10:IC:156:LYS:HG3	10:IC:158:GLU:HG3	1.98	0.45
10:LC:104:ILE:HD12	10:LC:248:ILE:HD13	1.99	0.45
10:MC:145:THR:H	10:MC:148:GLN:CD	2.25	0.45
10:MC:185:ASN:HA	10:MC:188:ASP:OD2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:CM:191:LEU:HD12	11:CM:192:ARG:H	1.82	0.45
11:CM:267:ASN:O	11:CM:287:THR:OG1	2.34	0.45
1:KG:965:LEU:O	1:KG:1008:LEU:HB3	2.16	0.45
1:MG:1004:ALA:O	1:MG:1008:LEU:HD12	2.16	0.45
1:NG:880:ASP:OD1	1:NG:881:GLU:N	2.50	0.45
10:AC:122:ASP:OD1	10:AC:125:SER:OG	2.35	0.45
1:Gg:822:GLU:OE2	1:Gg:824:THR:OG1	2.34	0.45
1:BG:966:GLN:O	1:BG:970:ASN:ND2	2.50	0.45
2:HH:159:ASN:ND2	2:HH:257:GLN:OE1	2.49	0.45
2:HH:166:PRO:HG3	2:XH:151:PRO:HB2	1.99	0.45
4:HL:130:ASP:OD1	4:HL:130:ASP:N	2.47	0.45
11:HM:202:LEU:O	11:HM:222:ILE:HA	2.17	0.45
9:Hf:244:VAL:HA	9:Hf:256:THR:HA	1.98	0.45
1:Ig:797:ARG:HD3	2:JH:117:ARG:HH12	1.82	0.45
2:KH:319:ILE:HD12	2:KH:346:LEU:O	2.17	0.45
4:KL:109:LEU:HG	4:KL:114:ILE:HB	1.99	0.45
5:KN:81:LEU:HD11	2:LH:357:LYS:HB2	1.99	0.45
8:LD:162:TYR:O	10:GC:245:ARG:NH2	2.50	0.45
11:LM:244:LYS:NZ	11:LM:262:GLU:OE2	2.44	0.45
11:MM:205:TYR:HB3	11:MM:206:TRP:CD1	2.52	0.45
9:Mf:237:LYS:HZ3	9:Mf:243:MET:HB2	1.81	0.45
4:AL:224:ALA:HA	4:AL:227:ARG:HH12	1.82	0.45
2:YH:171:LEU:HD11	2:YH:241:LEU:HB2	1.99	0.45
2:ZH:107:ILE:H	2:ZH:107:ILE:HD12	1.82	0.45
1:FG:891:THR:OG1	1:FG:892:GLY:N	2.49	0.45
11:AM:219:ALA:HB1	11:AM:221:LYS:NZ	2.32	0.45
4:BL:212:ASN:N	4:BL:212:ASN:OD1	2.47	0.45
10:GC:168:LYS:N	10:GC:172:GLU:OE1	2.41	0.45
11:CM:163:THR:HB	11:CM:183:VAL:HG12	1.99	0.45
5:DN:47:GLY:O	5:DN:61:ASN:N	2.48	0.45
1:HG:948:THR:HG22	1:HG:1029:VAL:HG12	1.99	0.45
1:NG:972:PHE:HB3	1:NG:1005:VAL:HG22	1.99	0.45
1:Eg:800:ASP:O	1:Eg:803:THR:OG1	2.31	0.45
1:AG:973:GLN:HB2	1:AG:1005:VAL:HG11	1.99	0.44
2:FH:107:ILE:HD12	2:FH:107:ILE:H	1.82	0.44
3:FK:56:MET:O	3:FK:60:LEU:HG	2.16	0.44
8:Fd:93:GLU:O	8:Fd:97:ARG:HG2	2.17	0.44
4:HL:124:THR:HA	4:HL:231:ILE:O	2.17	0.44
8:ID:136:ASP:OD2	8:ID:145:ILE:N	2.42	0.44
2:IH:171:LEU:HD21	2:IH:241:LEU:HB3	1.99	0.44
1:Jg:805:ALA:HB3	2:YH:115:MET:HE1	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AH:150:LYS:HG3	9:ZF:219:ARG:HH22	1.82	0.44
2:AH:196:LEU:HD11	2:AH:202:PHE:HB2	1.99	0.44
8:KD:88:SER:HB2	10:FC:89:ARG:HH12	1.81	0.44
10:CC:249:ILE:HB	10:DC:122:GLN:HG2	1.99	0.44
2:KH:208:LYS:HD2	1:YG:824:THR:N	2.32	0.44
11:KM:153:GLN:NE2	11:KM:154:LYS:HG2	2.32	0.44
2:MH:170:ARG:H	2:MH:170:ARG:HG2	1.58	0.44
11:MM:158:VAL:HA	11:MM:178:LYS:HZ3	1.83	0.44
2:VH:157:PHE:HD1	2:VH:255:ARG:HB2	1.81	0.44
2:XH:284:LEU:HD22	2:XH:328:MET:HB2	1.97	0.44
1:FG:876:SER:N	1:GG:940:ALA:O	2.48	0.44
11:AM:149:ASN:OD1	11:AM:149:ASN:N	2.50	0.44
11:GM:159:GLY:HA2	11:GM:181:PRO:HG3	1.99	0.44
8:BD:39:ILE:HD12	4:BL:220:ILE:HG12	1.99	0.44
10:FC:249:ARG:NH1	10:FC:250:ILE:H	2.15	0.44
2:CH:183:ASP:OD1	2:CH:185:THR:OG1	2.25	0.44
9:DF:253:ARG:HB3	9:DF:263:LYS:HE3	1.99	0.44
4:DL:129:THR:HG22	4:DL:229:ILE:HG12	1.97	0.44
4:DL:174:SER:O	4:DL:178:LYS:HG3	2.17	0.44
1:NG:965:LEU:HD23	1:NG:1011:VAL:HG23	1.99	0.44
1:NG:967:GLY:HA2	1:NG:970:ASN:HD21	1.82	0.44
2:FH:183:ASP:OD1	2:FH:185:THR:OG1	2.31	0.44
8:Gd:151:SER:O	8:Gd:153:VAL:N	2.50	0.44
3:HK:96:TYR:CD2	8:Hd:26:LYS:HB2	2.52	0.44
9:IF:219:ARG:HG2	2:JH:148:PRO:HD2	2.00	0.44
1:CG:1014:ALA:HB1	1:DG:959:LEU:HD21	1.99	0.44
8:Id:35:ASP:HB3	8:Id:38:THR:HG23	1.99	0.44
8:Id:36:ASP:O	8:Id:39:ILE:HG12	2.16	0.44
9:If:233:ARG:HG3	9:If:235:GLY:H	1.82	0.44
2:JH:206:TRP:HE1	2:JH:210:SER:C	2.22	0.44
3:JK:52:THR:HA	3:JK:55:LYS:HG2	1.99	0.44
9:KF:232:VAL:HG21	9:KF:244:VAL:HG21	1.99	0.44
1:DG:951:HIS:H	1:DG:1027:THR:HG22	1.82	0.44
9:Kf:232:VAL:HG22	9:Kf:233:ARG:O	2.15	0.44
8:Ld:95:THR:HA	8:Ld:98:ILE:HG22	1.99	0.44
2:MH:275:SER:HA	10:HC:125:ARG:HD3	1.99	0.44
3:MK:116:VAL:HG13	3:MK:156:THR:HA	1.99	0.44
11:MM:238:PHE:N	11:MM:258:LYS:O	2.40	0.44
9:VF:215:VAL:H	2:VH:245:GLN:NE2	2.15	0.44
2:VH:130:LEU:HA	2:VH:133:ILE:HG12	2.00	0.44
11:EM:255:THR:HG21	11:EM:279:ILE:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:FM:141:GLU:OE2	11:FM:143:THR:OG1	2.35	0.44
11:JM:240:GLN:HB3	11:JM:242:LYS:HE3	2.00	0.44
2:BH:238:MET:HB2	2:CH:250:TYR:CZ	2.52	0.44
4:BL:145:TYR:CD1	4:BL:146:PRO:HD3	2.52	0.44
10:EC:258:ASN:OD1	10:EC:258:ASN:N	2.49	0.44
10:HC:108:VAL:HG23	10:HC:135:LYS:H	1.82	0.44
10:KC:67:VAL:HG23	10:KC:181:THR:HG23	1.98	0.44
2:CH:311:MET:SD	2:CH:341:LYS:HA	2.57	0.44
4:CL:124:THR:HG22	4:CL:232:GLN:HG2	1.99	0.44
4:CL:145:TYR:CG	4:CL:146:PRO:HD3	2.52	0.44
2:DH:214:MET:N	2:DH:214:MET:SD	2.90	0.44
4:DL:108:ASP:OD2	4:DL:150:ASN:ND2	2.50	0.44
1:KG:946:SER:OG	1:KG:1030:GLU:O	2.28	0.44
1:LG:869:MET:HB2	1:LG:1041:PHE:CE1	2.52	0.44
1:MG:1006:ILE:HG12	1:NG:968:PHE:HA	2.00	0.44
9:Df:218:GLY:N	9:Df:247:ILE:HD11	2.33	0.44
1:Eg:794:ILE:O	1:Eg:798:THR:N	2.50	0.44
10:BC:46:ALA:O	10:BC:49:LYS:HG3	2.17	0.44
9:GF:253:ARG:HH21	9:GF:255:LEU:H	1.65	0.44
1:Gg:791:GLN:N	1:Gg:793:GLU:OE2	2.51	0.44
4:HL:47:TYR:OH	4:HL:142:GLU:OE1	2.25	0.44
4:HL:98:TYR:O	4:HL:101:SER:OG	2.26	0.44
2:IH:301:ASP:OD1	2:IH:301:ASP:N	2.45	0.44
4:IL:145:TYR:CD1	4:IL:146:PRO:HD3	2.52	0.44
2:JH:203:ASN:ND2	2:JH:205:GLN:OE1	2.39	0.44
2:JH:289:PRO:HG2	2:JH:292:SER:HB3	1.99	0.44
3:JK:117:THR:HA	3:JK:157:GLN:O	2.18	0.44
4:JL:121:ASP:O	4:JL:235:THR:OG1	2.32	0.44
2:AH:238:MET:HB2	2:BH:250:TYR:CZ	2.52	0.44
11:KM:298:VAL:C	11:KM:299:LEU:HD22	2.43	0.44
1:Lg:800:ASP:OD1	1:Lg:800:ASP:N	2.49	0.44
2:LH:143:ALA:O	2:MH:131:LYS:NZ	2.40	0.44
2:LH:151:PRO:HA	2:LH:248:VAL:HG13	1.99	0.44
2:LH:179:LEU:O	2:LH:212:THR:HA	2.17	0.44
2:LH:235:THR:HG23	2:MH:251:ARG:NH2	2.32	0.44
1:FG:936:ASP:HB3	1:FG:939:THR:HB	1.99	0.44
11:EM:180:ASP:O	11:EM:182:LYS:NZ	2.44	0.44
11:FM:158:VAL:HA	11:FM:178:LYS:HZ3	1.82	0.44
11:JM:242:LYS:HA	11:JM:262:GLU:HG3	1.98	0.44
3:BK:46:ASP:N	3:BK:46:ASP:OD1	2.49	0.44
8:DD:106:PHE:HE1	8:DD:108:VAL:HG13	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:DH:123:ASN:OD1	2:DH:123:ASN:N	2.50	0.44
2:DH:315:THR:OG1	2:DH:316:ASN:N	2.49	0.44
11:DM:116:PHE:CE1	11:DM:118:TYR:HB2	2.52	0.44
1:JG:919:MET:HB2	1:JG:928:ILE:HG13	1.99	0.44
1:MG:885:ILE:HG13	1:MG:916:PHE:HE1	1.81	0.44
4:EL:189:MET:SD	4:EL:229:ILE:HG21	2.58	0.44
9:Ef:210:TYR:HB3	9:Ef:222:LEU:HD12	1.99	0.44
8:Fd:72:THR:OG1	8:Fd:73:ILE:N	2.49	0.44
3:GK:111:LYS:HZ2	3:GK:111:LYS:N	2.15	0.44
3:HK:111:LYS:HD2	3:HK:114:ILE:HD11	1.99	0.44
5:HN:85:CYS:N	10:CC:154:ASP:OD2	2.44	0.44
1:Bg:797:ARG:NH1	1:Bg:801:MET:HE1	2.33	0.44
2:IH:166:PRO:HA	2:IH:167:PRO:HD3	1.88	0.44
3:IK:49:CYS:O	3:IK:53:ILE:HG13	2.17	0.44
5:IN:92:TYR:HD2	5:IN:104:ASN:HA	1.82	0.44
9:If:216:ILE:HD12	9:If:216:ILE:HA	1.80	0.44
3:JK:48:ALA:HA	3:JK:108:GLN:HE22	1.82	0.44
10:CC:63:ALA:HA	10:CC:66:VAL:HG22	1.99	0.44
10:CC:71:GLY:HA2	10:CC:184:TRP:CD1	2.53	0.44
2:KH:198:ASP:OD1	2:KH:200:SER:OG	2.28	0.44
2:KH:321:SER:OG	2:KH:346:LEU:HB3	2.18	0.44
11:KM:154:LYS:HD3	11:KM:154:LYS:HA	1.82	0.44
1:DG:880:ASP:OD1	1:DG:881:GLU:N	2.48	0.44
8:CD:104:PHE:CD1	8:CD:152:GLN:HB3	2.53	0.44
9:Lf:209:ILE:HG22	9:Lf:225:SER:HB3	2.00	0.44
2:MH:195:ASP:OD1	2:MH:196:LEU:N	2.50	0.44
2:MH:315:THR:OG1	2:MH:316:ASN:N	2.50	0.44
8:Md:35:ASP:HB3	8:Md:38:THR:HG23	2.00	0.44
9:VF:215:VAL:HG12	9:VF:264:PHE:HE1	1.82	0.44
2:VH:121:PRO:O	1:Cg:797:ARG:NH2	2.51	0.44
1:WG:793:GLU:CD	1:WG:793:GLU:H	2.25	0.44
9:YF:221:TRP:CD1	9:YF:231:THR:HB	2.53	0.44
2:YH:176:VAL:HB	2:YH:216:GLN:HE21	1.83	0.44
11:JM:205:TYR:HD1	11:JM:205:TYR:HA	1.65	0.44
8:Ad:132:LEU:HD12	8:Ad:145:ILE:HD12	1.99	0.44
2:BH:281:LEU:HD13	10:JC:112:LEU:HB3	2.00	0.44
10:KC:91:LEU:HD21	10:KC:148:TRP:CD2	2.52	0.44
10:LC:113:ARG:N	2:DH:328:MET:HE1	2.32	0.44
10:MC:244:ARG:HB2	10:AC:128:ILE:HG12	2.00	0.44
9:DF:214:ALA:HB3	9:DF:221:TRP:HB2	2.00	0.44
1:LG:917:ASN:HA	1:LG:931:SER:HA	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:NG:898:LYS:HE3	1:OG:866:GLY:HA3	1.99	0.44
9:Df:213:GLN:OE1	9:Df:223:ILE:HB	2.17	0.44
8:ED:79:LEU:HG	8:ED:128:LEU:HB2	1.99	0.44
8:Ed:57:LYS:HG2	8:ED:137:TYR:CD2	2.52	0.44
8:FD:108:VAL:HG12	8:FD:156:LEU:HD21	1.99	0.44
8:FD:155:GLU:OE2	8:FD:157:ARG:NE	2.51	0.44
3:FK:72:GLN:HB2	3:FK:185:ARG:CZ	2.46	0.44
8:Fd:71:LEU:HD22	8:Fd:145:ILE:HG13	1.99	0.44
10:BC:78:LYS:HB2	10:BC:156:TYR:CE1	2.52	0.44
9:GF:243:MET:HB3	9:GF:257:SER:HB3	2.00	0.44
3:GK:81:SER:OG	3:GK:173:ASP:O	2.35	0.44
4:GL:94:VAL:HA	4:GL:97:ILE:HG12	2.00	0.44
5:IN:87:TRP:HB3	10:DC:147:ARG:HH11	1.82	0.44
2:JH:194:TYR:CZ	2:JH:204:ILE:HD13	2.52	0.44
4:JL:215:SER:OG	4:JL:216:ASP:N	2.49	0.44
5:JN:65:TYR:OH	4:KL:221:HIS:HB3	2.17	0.44
2:KH:315:THR:OG1	2:KH:316:ASN:N	2.50	0.44
3:KK:38:VAL:HA	3:KK:41:LEU:HD23	2.00	0.44
3:KK:150:ASP:OD1	3:KK:152:ARG:NH1	2.42	0.44
8:CD:36:ASP:OD1	8:CD:36:ASP:N	2.51	0.44
2:MH:346:LEU:HD11	10:GC:148:ARG:HG3	2.00	0.44
2:YH:192:ALA:HA	2:YH:231:ARG:NH1	2.33	0.44
9:ZF:222:LEU:HB2	9:ZF:230:LEU:HG	1.99	0.44
2:ZH:278:ASP:OD1	2:ZH:278:ASP:N	2.51	0.44
2:BH:275:SER:HA	10:JC:127:ARG:HD3	1.99	0.44
9:Bf:216:ILE:HG13	9:Bf:217:PRO:HD2	1.99	0.44
1:GG:897:SER:HA	1:GG:922:PRO:HD3	1.99	0.44
1:GG:966:GLN:HG2	1:GG:1012:GLY:HA3	1.99	0.44
10:HC:167:LYS:O	10:HC:172:LYS:NZ	2.49	0.44
2:CH:156:GLN:NE2	2:CH:157:PHE:O	2.50	0.44
4:CL:113:ASP:OD1	4:CL:128:PRO:HG3	2.18	0.44
4:CL:216:ASP:CG	4:CL:218:ALA:H	2.25	0.44
11:CM:118:TYR:OH	11:CM:122:GLY:HA3	2.18	0.44
3:DK:74:TYR:HB2	3:DK:184:PHE:CE1	2.52	0.44
3:DK:177:ASN:OD1	3:DK:178:ALA:N	2.50	0.44
1:KG:916:PHE:O	1:KG:932:ALA:N	2.47	0.44
1:OG:880:ASP:OD1	1:OG:881:GLU:N	2.48	0.44
1:PG:862:ILE:HD13	1:PG:1046:THR:HA	2.00	0.44
8:AD:93:GLU:H	8:AD:93:GLU:CD	2.20	0.44
1:AG:968:PHE:HA	1:PG:1006:ILE:HD13	2.00	0.44
1:AG:1011:VAL:HG12	1:BG:963:SER:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:EH:190:PRO:HB2	2:EH:231:ARG:HH12	1.82	0.44
3:EK:50:ASP:OD1	3:EK:50:ASP:N	2.49	0.44
5:EN:77:ASP:HA	2:FH:354:MET:SD	2.57	0.44
9:Ef:234:GLU:H	9:Ef:234:GLU:CD	2.24	0.44
3:FK:57:MET:HE2	3:FK:57:MET:HB2	1.90	0.44
1:BG:882:PRO:HA	1:BG:903:PHE:CE2	2.52	0.44
5:GN:110:GLU:H	5:GN:110:GLU:CD	2.24	0.44
1:Hg:818:GLN:NE2	2:HH:205:GLN:HE21	2.16	0.44
3:HK:81:SER:OG	3:HK:173:ASP:O	2.35	0.44
8:ID:44:ALA:O	8:ID:48:VAL:HG23	2.18	0.44
4:IL:109:LEU:HA	4:IL:109:LEU:HD13	1.88	0.44
8:Id:36:ASP:OD1	8:Id:36:ASP:N	2.50	0.44
9:If:219:ARG:HH11	9:If:233:ARG:NH1	2.16	0.44
9:If:243:MET:O	9:If:257:SER:N	2.51	0.44
5:JN:52:ASP:OD1	5:JN:54:SER:OG	2.33	0.44
8:Jd:35:ASP:HB3	8:Jd:38:THR:HG23	2.00	0.44
8:KD:52:MET:O	8:KD:55:MET:HG3	2.18	0.44
9:KF:207:ARG:NH2	9:KF:208:ILE:O	2.50	0.44
5:KN:62:ASN:OD1	5:KN:63:GLY:N	2.51	0.44
2:LH:263:ALA:HB1	2:LH:266:MET:HG3	2.00	0.44
3:LK:72:GLN:N	4:ML:215:SER:OG	2.51	0.44
3:MK:147:GLN:HA	8:Md:30:ILE:HD13	1.98	0.44
9:VF:237:LYS:NZ	9:VF:238:ILE:O	2.51	0.44
9:YF:207:ARG:NH2	9:YF:240:GLY:O	2.50	0.44
2:YH:278:ASP:OD1	2:YH:278:ASP:N	2.51	0.44
11:EM:212:LEU:HB3	11:EM:231:LEU:HD13	2.00	0.44
8:Ad:60:LYS:HZ3	8:AD:137:TYR:HA	1.83	0.44
8:Ad:147:VAL:HG22	8:Ad:154:VAL:HG12	1.99	0.44
9:Af:248:ASP:HB3	9:Af:253:ARG:H	1.82	0.44
10:EC:119:LEU:HB2	10:EC:125:ILE:HG22	2.00	0.44
10:EC:175:ILE:HA	10:EC:178:ILE:HG12	1.99	0.44
10:IC:214:LEU:HG	10:IC:219:MET:HB2	2.00	0.44
11:DM:255:THR:HB	11:DM:259:SER:OG	2.17	0.44
1:IG:882:PRO:HA	1:IG:903:PHE:CE2	2.52	0.44
1:KG:919:MET:HB2	1:KG:928:ILE:HG13	1.99	0.44
1:NG:1006:ILE:HD13	1:OG:968:PHE:CG	2.53	0.44
8:Dd:75:ASN:ND2	8:Dd:75:ASN:O	2.51	0.44
8:Dd:110:GLY:HA3	8:Dd:158:TYR:HB2	1.99	0.44
9:Df:216:ILE:HG13	9:Df:217:PRO:HD2	2.00	0.44
9:EF:246:LEU:HB3	9:EF:255:LEU:HD12	2.00	0.44
1:AG:1042:THR:OG1	1:AG:1043:GLN:OE1	2.23	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Ed:131:ILE:HG22	8:Ed:132:LEU:HD12	1.99	0.44
9:Ef:232:VAL:HG23	9:Ef:236:SER:HB2	1.99	0.44
2:FH:148:PRO:HD2	9:EF:218:GLY:HA3	1.99	0.44
6:FU:122:UNK:C	6:FU:124:UNK:H	2.31	0.44
10:BC:268:ALA:HA	8:GD:61:VAL:HG11	1.99	0.44
1:Gg:794:ILE:HA	1:Gg:797:ARG:HB2	2.00	0.44
4:GL:193:LEU:HD13	4:GL:193:LEU:HA	1.86	0.44
8:Gd:36:ASP:OD1	8:Gd:36:ASP:N	2.50	0.44
3:HK:87:GLN:N	3:HK:173:ASP:OD2	2.50	0.44
9:Hf:241:TYR:HB3	9:Hf:256:THR:HG21	2.00	0.44
3:IK:65:ILE:H	3:IK:65:ILE:HD12	1.82	0.44
4:IL:105:ILE:HG21	4:IL:154:LEU:HB2	1.99	0.44
11:IM:215:ARG:HD2	11:IM:234:GLU:HB3	2.00	0.44
8:JD:87:TRP:CD1	8:JD:94:LEU:HD22	2.53	0.44
8:JD:146:HIS:HB2	8:JD:155:GLU:HG2	1.99	0.44
1:DG:885:ILE:O	1:DG:900:ILE:HA	2.17	0.44
4:LL:169:THR:O	4:LL:226:ASN:ND2	2.51	0.44
11:LM:125:THR:HG23	11:LM:145:ARG:HB2	1.99	0.44
3:MK:87:GLN:N	3:MK:173:ASP:OD2	2.49	0.44
9:Mf:212:ILE:HD11	9:Mf:220:ALA:HB1	1.99	0.44
9:Mf:241:TYR:O	9:Mf:256:THR:OG1	2.31	0.44
9:VF:219:ARG:HD3	2:DH:148:PRO:O	2.18	0.44
9:XF:214:ALA:HB3	9:XF:221:TRP:HB2	1.99	0.44
2:XH:160:LEU:HG	2:XH:257:GLN:HG3	2.00	0.44
2:XH:279:LEU:HD11	2:XH:289:PRO:HB3	2.00	0.44
11:FM:255:THR:HB	11:FM:259:SER:OG	2.18	0.44
8:BD:34:SER:OG	8:Bd:35:ASP:OD1	2.34	0.44
8:BD:150:ASN:OD1	8:BD:150:ASN:N	2.48	0.44
2:BH:119:LEU:O	2:BH:121:PRO:HD3	2.18	0.44
2:CH:155:SER:HG	2:CH:255:ARG:NH1	2.15	0.44
11:CM:177:LEU:HD23	11:CM:181:PRO:HG2	2.00	0.44
9:DF:230:LEU:HD22	9:DF:230:LEU:HA	1.83	0.44
3:DK:48:ALA:HA	3:DK:108:GLN:HE22	1.81	0.44
1:HG:899:LEU:HD11	1:HG:916:PHE:HB3	1.99	0.44
1:JG:952:TYR:CE2	1:JG:1027:THR:HG21	2.51	0.44
1:AG:870:PHE:HB3	10:AC:56:ARG:NH2	2.32	0.44
1:AG:891:THR:OG1	1:AG:892:GLY:N	2.51	0.44
8:Ed:29:PRO:CD	8:Ed:32:ASN:HD21	2.30	0.44
2:FH:311:MET:HE3	2:FH:342:SER:H	1.83	0.44
3:FK:145:TRP:HE3	3:FK:154:ILE:HD12	1.83	0.44
2:GH:207:ASP:OD1	2:GH:210:SER:OG	2.27	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GH:311:MET:HE3	2:GH:341:LYS:HB2	1.99	0.44
1:BG:866:GLY:HA2	1:BG:1041:PHE:O	2.18	0.44
2:HH:207:ASP:N	2:HH:207:ASP:OD1	2.51	0.44
5:HN:92:TYR:HD1	5:HN:94:GLN:H	1.64	0.44
11:IM:244:LYS:HE2	11:IM:244:LYS:HB3	1.83	0.44
9:JF:221:TRP:CD1	9:JF:231:THR:HB	2.53	0.44
3:JK:132:LEU:HD11	3:JK:136:ARG:HE	1.82	0.44
9:Jf:220:ALA:HB3	9:Jf:232:VAL:HG13	1.99	0.44
8:KD:78:ASN:ND2	8:KD:78:ASN:O	2.51	0.44
10:CC:190:GLN:O	10:CC:194:ILE:HG12	2.18	0.44
3:KK:133:THR:HG21	3:KK:160:GLY:HA2	2.00	0.44
2:LH:122:LEU:HD21	1:YG:801:MET:HE2	1.99	0.44
9:Lf:216:ILE:HG13	9:Lf:217:PRO:HD2	2.00	0.44
1:VG:800:ASP:OD1	1:VG:801:MET:N	2.51	0.44
2:WH:110:LYS:HG2	2:WH:113:LYS:HZ3	1.82	0.44
2:WH:173:GLN:NE2	2:WH:218:THR:O	2.36	0.44
2:WH:202:PHE:HB3	2:WH:215:ILE:HD11	2.00	0.44
9:XF:212:ILE:HA	9:XF:222:LEU:HD13	1.99	0.44
4:AL:169:THR:OG1	4:AL:170:ASP:N	2.50	0.44
2:ZH:249:ASP:HB3	2:ZH:252:VAL:HG22	2.00	0.44
11:BM:284:LEU:HD22	11:BM:302:ARG:HH12	1.82	0.44
11:FM:171:ARG:CZ	11:FM:172:ASN:HB2	2.47	0.44
11:FM:186:SER:HA	11:FM:205:TYR:HB2	1.98	0.44
11:JM:153:GLN:O	11:JM:173:LEU:HD12	2.18	0.44
2:BH:342:SER:OG	2:BH:344:VAL:O	2.33	0.44
3:BK:56:MET:HE3	3:BK:105:PHE:HD1	1.83	0.44
5:BN:87:TRP:HD1	10:JC:150:GLN:HG2	1.82	0.44
10:HC:178:TYR:HD1	10:HC:181:ARG:HH11	1.66	0.44
10:IC:214:LEU:HD12	10:IC:214:LEU:HA	1.82	0.44
10:LC:108:VAL:HG13	10:LC:135:LYS:H	1.83	0.44
3:CK:48:ALA:HB1	5:CN:67:THR:HG21	2.00	0.44
2:DH:208:LYS:HE3	2:DH:208:LYS:HB3	1.87	0.44
3:DK:80:ALA:HB1	3:DK:136:ARG:NH2	2.33	0.44
1:IG:1044:ASP:N	1:IG:1044:ASP:OD1	2.48	0.44
1:JG:1006:ILE:CG1	1:KG:968:PHE:HA	2.48	0.44
1:KG:967:GLY:HA2	1:KG:970:ASN:HD21	1.83	0.44
1:MG:878:ASN:HA	1:MG:1030:GLU:HA	1.99	0.44
9:Df:216:ILE:HD12	9:Df:216:ILE:HA	1.82	0.44
8:AD:94:LEU:HD12	8:AD:94:LEU:HA	1.83	0.44
8:AD:148:TYR:HB2	8:AD:153:VAL:HG22	2.00	0.44
8:ED:150:ASN:OD1	8:ED:151:SER:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:968:PHE:HA	1:PG:1006:ILE:CD1	2.48	0.44
1:AG:1010:THR:OG1	1:BG:967:GLY:HA3	2.18	0.44
8:FD:29:PRO:HG2	4:FL:225:GLN:HG2	2.00	0.44
8:FD:94:LEU:O	8:FD:98:ILE:HG12	2.18	0.44
2:GH:315:THR:OG1	2:GH:316:ASN:N	2.51	0.44
4:GL:49:ASN:HB3	11:GM:293:ALA:HB1	1.99	0.44
4:HL:124:THR:HG22	4:HL:232:GLN:HG2	1.99	0.44
11:HM:313:ASP:HB2	11:HM:316:ASN:ND2	2.31	0.44
8:ID:84:SER:OG	3:IK:154:ILE:HB	2.18	0.44
4:IL:44:HIS:N	4:IL:48:ASN:OD1	2.49	0.44
11:IM:214:ILE:HB	11:IM:233:VAL:HG22	2.00	0.44
1:DG:1011:VAL:HG12	1:EG:963:SER:HB2	1.98	0.44
8:Kd:72:THR:OG1	8:Kd:73:ILE:N	2.51	0.44
5:LN:99:GLY:N	1:IG:893:LYS:HZ2	2.16	0.44
5:MN:46:GLY:C	5:MN:61:ASN:HB2	2.42	0.44
9:VF:208:ILE:HG13	9:VF:225:SER:H	1.82	0.44
2:WH:321:SER:HA	10:MC:224:TYR:HE1	1.83	0.44
2:XH:330:SER:OG	2:XH:334:THR:OG1	2.30	0.44
4:AL:133:PHE:HE1	4:AL:138:PRO:HA	1.82	0.44
2:YH:151:PRO:HA	2:YH:248:VAL:HG13	1.99	0.44
10:DC:224:TYR:HB2	10:DC:250:ALA:HB3	2.00	0.44
2:ZH:181:PHE:HD1	2:ZH:254:LEU:HB2	1.83	0.44
1:FG:966:GLN:O	1:FG:970:ASN:ND2	2.50	0.44
11:FM:210:ASP:OD1	11:FM:210:ASP:N	2.51	0.44
11:JM:306:GLN:HG3	11:JM:308:ASP:H	1.83	0.44
8:Ad:41:LEU:HD13	8:Ad:41:LEU:HA	1.79	0.44
9:Af:243:MET:O	9:Af:257:SER:N	2.50	0.44
5:BN:86:LEU:HB3	5:BN:87:TRP:CE3	2.50	0.44
1:GG:939:THR:HG22	1:GG:941:ARG:HD2	1.98	0.44
10:HC:156:LYS:HD2	10:HC:158:GLU:HG3	1.99	0.44
10:KC:241:ILE:CG1	10:LC:131:TYR:HB2	2.47	0.44
10:LC:235:ASP:CG	10:LC:237:SER:H	2.26	0.44
2:CH:183:ASP:HA	2:CH:256:VAL:HG22	2.00	0.44
1:IG:1030:GLU:CD	1:JG:941:ARG:HH21	2.26	0.44
1:KG:953:LEU:H	1:KG:953:LEU:HD22	1.82	0.44
1:PG:866:GLY:HA2	1:PG:1041:PHE:O	2.18	0.44
10:AC:216:LEU:HD12	10:AC:216:LEU:HA	1.77	0.44
8:AD:98:ILE:HG21	8:AD:132:LEU:HD21	2.00	0.44
8:FD:87:TRP:CD1	8:FD:89:GLY:H	2.35	0.43
4:FL:49:ASN:ND2	11:FM:293:ALA:O	2.51	0.43
8:Fd:82:ARG:CZ	8:Fd:82:ARG:HA	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GH:221:TYR:HE2	2:HH:138:GLU:HG2	1.82	0.43
3:GK:75:LEU:HG	3:GK:183:THR:HG22	2.00	0.43
1:BG:944:LEU:HD13	1:BG:945:ALA:N	2.33	0.43
1:Hg:797:ARG:HH12	2:XH:117:ARG:HB3	1.83	0.43
3:IK:111:LYS:HE3	3:IK:111:LYS:HB3	1.88	0.43
2:JH:107:ILE:HG13	1:XG:794:ILE:HG12	2.00	0.43
9:KF:210:TYR:HD1	9:KF:241:TYR:HE2	1.66	0.43
9:KF:250:LEU:HD12	9:KF:251:GLN:HG3	1.99	0.43
11:KM:180:ASP:O	11:KM:182:LYS:NZ	2.45	0.43
8:Kd:93:GLU:OE1	10:GC:264:ALA:N	2.50	0.43
5:LN:49:ASN:N	5:LN:59:VAL:O	2.40	0.43
8:MD:35:ASP:OD2	8:MD:38:THR:N	2.37	0.43
8:MD:73:ILE:HG21	8:MD:133:ARG:HG2	2.00	0.43
2:MH:282:HIS:HB3	2:MH:287:VAL:HG13	2.00	0.43
4:ML:174:SER:HB3	4:ML:177:HIS:HB3	2.00	0.43
4:ML:212:ASN:OD1	4:ML:212:ASN:N	2.51	0.43
8:Md:94:LEU:O	8:Md:98:ILE:HG12	2.17	0.43
2:XH:157:PHE:HZ	2:XH:257:GLN:HG2	1.83	0.43
10:DC:219:MET:HA	10:DC:255:ASN:HD21	1.83	0.43
1:FG:900:ILE:HD11	1:GG:866:GLY:HA3	2.00	0.43
11:FM:276:ALA:H	11:FM:295:ASN:HB2	1.83	0.43
11:JM:204:LEU:HD22	11:JM:204:LEU:HA	1.90	0.43
5:AN:78:LEU:HB3	2:BH:355:GLN:HB2	2.00	0.43
4:BL:98:TYR:CE1	4:BL:104:LYS:HE3	2.52	0.43
8:Bd:121:ILE:HD13	8:Bd:121:ILE:HA	1.86	0.43
10:GC:114:ARG:HG2	10:GC:130:ARG:HG2	1.99	0.43
1:GG:921:ILE:HB	1:GG:926:LYS:HD2	1.98	0.43
10:LC:165:LEU:HD13	10:LC:165:LEU:HA	1.88	0.43
10:MC:110:LEU:O	10:MC:131:TYR:HA	2.18	0.43
11:CM:174:GLN:HE22	11:CM:193:GLN:HB3	1.82	0.43
1:IG:931:SER:O	1:IG:1042:THR:OG1	2.36	0.43
1:MG:878:ASN:HD22	1:MG:1030:GLU:HB2	1.82	0.43
1:OG:898:LYS:HG2	1:PG:864:LYS:HE2	2.00	0.43
8:ED:77:TYR:CG	8:ED:78:ASN:N	2.86	0.43
8:ED:87:TRP:HD1	8:ED:89:GLY:H	1.64	0.43
1:Eg:813:LYS:HE2	1:Eg:813:LYS:HB2	1.67	0.43
2:EH:289:PRO:O	2:EH:292:SER:OG	2.26	0.43
4:EL:42:CYS:HB3	4:EL:58:LYS:HE2	1.99	0.43
4:EL:221:HIS:CE1	4:EL:225:GLN:HE21	2.36	0.43
4:EL:232:GLN:OE1	6:DU:129:UNK:N	2.51	0.43
8:FD:93:GLU:H	8:FD:93:GLU:CD	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:FF:267:GLU:O	2:FH:150:LYS:NZ	2.50	0.43
8:Fd:150:ASN:OD1	8:Fd:151:SER:N	2.44	0.43
10:BC:80:ILE:HD11	10:BC:196:LEU:HD13	2.00	0.43
1:BG:904:ASN:OD1	1:BG:913:VAL:HG12	2.18	0.43
9:HF:222:LEU:HB2	9:HF:230:LEU:HG	2.00	0.43
9:IF:264:PHE:HB3	9:IF:269:SER:HA	2.00	0.43
1:Ig:816:GLU:OE1	2:XH:199:PRO:HD2	2.19	0.43
2:IH:230:LEU:HB2	2:IH:233:LEU:HD13	1.99	0.43
2:AH:205:GLN:OE1	1:Ag:818:GLN:NE2	2.39	0.43
8:KD:35:ASP:OD2	8:KD:38:THR:OG1	2.30	0.43
3:KK:50:ASP:HA	3:KK:53:ILE:HD12	1.98	0.43
3:KK:66:LYS:HB3	3:KK:77:SER:OG	2.18	0.43
1:DG:916:PHE:HD1	1:DG:916:PHE:HA	1.67	0.43
3:LK:60:LEU:HD23	3:LK:60:LEU:HA	1.85	0.43
4:LL:149:ASN:HB3	4:LL:153:ARG:NH1	2.33	0.43
11:LM:183:VAL:HG23	11:LM:202:LEU:HA	1.99	0.43
11:LM:199:LYS:HA	11:LM:219:ALA:HB3	1.99	0.43
2:MH:171:LEU:HD11	2:MH:241:LEU:HB3	1.99	0.43
9:CF:265:SER:HB3	9:CF:268:ASP:HB2	1.99	0.43
4:AL:209:GLY:H	4:AL:211:LYS:NZ	2.14	0.43
2:YH:207:ASP:OD1	2:YH:210:SER:OG	2.30	0.43
11:EM:274:THR:HA	11:EM:293:ALA:HB3	2.00	0.43
11:FM:154:LYS:HD3	11:FM:154:LYS:HA	1.65	0.43
11:FM:180:ASP:CG	11:FM:199:LYS:HB2	2.43	0.43
11:FM:280:TYR:HE1	11:FM:299:LEU:HD23	1.83	0.43
11:JM:209:SER:OG	11:JM:210:ASP:N	2.51	0.43
8:Ad:109:LEU:HB2	8:Ad:155:GLU:OE2	2.18	0.43
5:BN:84:CYS:SG	5:BN:85:CYS:N	2.92	0.43
1:GG:965:LEU:HD23	1:GG:1011:VAL:HG23	1.99	0.43
10:HC:247:ARG:HA	10:IC:122:GLN:CD	2.43	0.43
10:IC:178:TYR:HA	10:IC:181:ARG:HG2	1.99	0.43
10:MC:174:ILE:HA	10:MC:177:ILE:HG12	2.00	0.43
11:CM:120:GLY:H	11:CM:140:ASN:HB2	1.83	0.43
8:Cd:139:ALA:O	8:Cd:142:LYS:NZ	2.43	0.43
8:DD:27:LYS:HD3	4:DL:115:GLN:NE2	2.33	0.43
8:DD:68:ASP:OD1	8:DD:137:TYR:OH	2.36	0.43
2:DH:194:TYR:CE1	2:DH:204:ILE:HG21	2.53	0.43
2:DH:284:LEU:O	2:DH:314:ARG:NE	2.41	0.43
8:AD:78:ASN:O	8:AD:78:ASN:ND2	2.51	0.43
2:EH:149:PRO:HA	2:EH:246:LYS:O	2.18	0.43
4:EL:174:SER:O	4:EL:178:LYS:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Fg:818:GLN:N	2:FH:216:GLN:OE1	2.46	0.43
4:FL:91:VAL:HA	4:FL:94:VAL:HG22	1.99	0.43
8:Fd:29:PRO:HB2	8:Fd:32:ASN:HB3	2.01	0.43
5:GN:113:SER:OG	5:GN:114:LEU:N	2.50	0.43
5:HN:52:ASP:O	5:HN:56:GLY:N	2.52	0.43
1:Jg:800:ASP:O	1:Jg:803:THR:OG1	2.35	0.43
3:JK:113:ALA:HA	3:JK:153:ILE:O	2.18	0.43
4:JL:164:TYR:CE1	4:JL:204:LYS:HE2	2.53	0.43
2:KH:325:LEU:HD21	2:KH:340:GLN:HE22	1.82	0.43
3:KK:169:THR:HG22	3:KK:177:ASN:HD22	1.83	0.43
4:KL:141:ASN:OD1	4:KL:142:GLU:N	2.51	0.43
11:KM:262:GLU:HA	11:KM:280:TYR:O	2.18	0.43
5:KN:63:GLY:HA3	8:LD:27:LYS:HB2	2.00	0.43
8:CD:82:ARG:HD3	8:CD:82:ARG:HA	1.57	0.43
9:MF:212:ILE:HG12	9:MF:222:LEU:HD12	2.00	0.43
9:MF:232:VAL:HG23	9:MF:247:ILE:HD11	2.00	0.43
3:MK:47:GLY:C	3:MK:108:GLN:HE22	2.25	0.43
2:VH:191:ILE:HG13	2:VH:211:ASN:HB2	2.00	0.43
2:VH:198:ASP:OD1	2:VH:200:SER:OG	2.32	0.43
2:WH:313:VAL:HG23	2:WH:337:TYR:HD1	1.82	0.43
2:XH:307:SER:HG	2:XH:308:ASN:CG	2.25	0.43
2:ZH:295:LEU:HD13	2:ZH:305:TRP:HA	2.00	0.43
11:JM:131:THR:HG21	11:JM:134:LEU:HD23	2.00	0.43
5:AN:110:GLU:H	5:AN:110:GLU:CD	2.26	0.43
7:AX:23:UNK:HA	7:AX:33:UNK:HA	2.00	0.43
4:BL:163:ILE:HD13	4:BL:233:TRP:HB2	2.01	0.43
8:Bd:131:ILE:HD13	8:Bd:131:ILE:HA	1.81	0.43
10:EC:236:ASP:CG	10:EC:238:SER:H	2.26	0.43
10:FC:97:PHE:CE2	10:FC:210:MET:HE1	2.52	0.43
10:FC:112:LEU:HD23	10:FC:112:LEU:HA	1.87	0.43
10:IC:100:LEU:HG	10:IC:106:PRO:HG3	2.01	0.43
10:IC:101:GLU:HG2	10:IC:102:HIS:CD2	2.52	0.43
4:CL:123:ARG:HB2	4:CL:233:TRP:CE2	2.54	0.43
4:CL:169:THR:OG1	4:CL:170:ASP:N	2.52	0.43
2:DH:321:SER:OG	2:DH:322:PRO:HD3	2.17	0.43
11:DM:214:ILE:C	11:DM:215:ARG:HD2	2.43	0.43
1:JG:931:SER:H	1:JG:1043:GLN:CD	2.27	0.43
10:AC:120:LEU:HD12	10:AC:126:ILE:HG23	2.01	0.43
8:AD:76:ALA:O	8:AD:79:LEU:HB2	2.18	0.43
2:EH:185:THR:HG21	2:EH:263:ALA:HA	2.00	0.43
3:EK:109:PHE:HE1	3:EK:186:ARG:HH11	1.64	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:FH:207:ASP:OD2	2:FH:210:SER:N	2.38	0.43
3:FK:96:TYR:CE2	8:Fd:26:LYS:HD3	2.53	0.43
4:FL:105:ILE:HG21	4:FL:154:LEU:HB2	1.99	0.43
4:FL:155:LEU:HD22	4:FL:155:LEU:HA	1.82	0.43
10:BC:103:GLU:O	8:GD:142:LYS:NZ	2.51	0.43
8:GD:95:THR:HG23	8:GD:106:PHE:HE2	1.84	0.43
1:Gg:792:GLN:NE2	1:Gg:793:GLU:HG3	2.33	0.43
2:IH:157:PHE:HA	2:IH:255:ARG:HB3	1.99	0.43
8:Id:94:LEU:O	8:Id:98:ILE:HG12	2.19	0.43
2:JH:162:PRO:HA	2:KH:153:ALA:HB3	2.00	0.43
2:JH:227:ALA:HA	2:JH:237:VAL:O	2.18	0.43
2:JH:229:ARG:HH12	2:KH:212:THR:HB	1.82	0.43
4:JL:94:VAL:HA	4:JL:97:ILE:HG12	2.01	0.43
8:KD:123:THR:HB	8:KD:126:GLU:CD	2.44	0.43
8:KD:162:TYR:O	10:FC:246:ARG:NH1	2.51	0.43
10:CC:184:TRP:O	10:CC:188:ILE:HG13	2.18	0.43
4:KL:168:PHE:O	4:KL:227:ARG:HA	2.19	0.43
8:CD:26:LYS:HA	5:BN:62:ASN:OD1	2.18	0.43
8:MD:73:ILE:O	8:MD:133:ARG:NH2	2.36	0.43
2:MH:105:GLU:H	2:MH:105:GLU:CD	2.25	0.43
1:FG:912:MET:HB3	1:FG:944:LEU:HB2	1.99	0.43
11:AM:301:MET:HE3	11:AM:301:MET:HB3	1.96	0.43
11:GM:210:ASP:O	11:GM:230:ARG:N	2.52	0.43
1:Cg:793:GLU:OE1	1:Cg:793:GLU:N	2.49	0.43
2:BH:335:HIS:HB3	2:BH:337:TYR:CE1	2.54	0.43
9:Bf:245:LYS:HZ2	9:Bf:257:SER:HA	1.84	0.43
10:EC:96:PHE:HA	10:EC:99:LEU:HD23	2.01	0.43
10:IC:89:LEU:HD13	10:IC:146:TRP:CE2	2.54	0.43
10:MC:179:THR:HB	10:AC:35:LEU:HD13	2.00	0.43
2:CH:320:LEU:N	2:CH:346:LEU:O	2.47	0.43
1:MG:874:ASP:OD1	1:MG:874:ASP:N	2.52	0.43
5:EN:101:VAL:HG12	5:EN:113:SER:HB2	2.00	0.43
8:Ed:55:MET:HE3	8:Ed:55:MET:HB3	1.95	0.43
2:FH:183:ASP:HA	2:FH:256:VAL:HG12	1.98	0.43
2:GH:288:PRO:HB3	2:GH:305:TRP:CE2	2.54	0.43
1:BG:899:LEU:HD21	1:BG:916:PHE:HB3	2.00	0.43
2:HH:182:LEU:HB2	2:HH:255:ARG:HD2	2.00	0.43
2:HH:242:ILE:HG12	2:HH:245:GLN:HE21	1.83	0.43
1:CG:947:ARG:HB2	1:CG:950:HIS:NE2	2.33	0.43
4:JL:190:MET:HE2	4:JL:190:MET:HB2	1.83	0.43
5:JN:92:TYR:HD1	5:JN:94:GLN:H	1.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AH:171:LEU:HB2	2:AH:243:PRO:HA	2.00	0.43
8:KD:29:PRO:HG2	4:KL:225:GLN:HA	2.01	0.43
3:KK:72:GLN:OE1	3:KK:72:GLN:N	2.51	0.43
11:KM:128:ASN:HB3	11:KM:130:ARG:HH12	1.84	0.43
1:DG:944:LEU:HD11	1:DG:1031:VAL:HG12	2.01	0.43
8:LD:151:SER:O	8:LD:153:VAL:HG23	2.19	0.43
4:LL:212:ASN:OD1	4:LL:212:ASN:N	2.51	0.43
11:LM:257:ASP:HA	11:LM:275:ASP:O	2.18	0.43
5:LN:100:LEU:HA	5:LN:113:SER:HB3	2.01	0.43
2:MH:207:ASP:HB3	2:MH:210:SER:HB3	2.00	0.43
2:VH:157:PHE:CZ	2:VH:257:GLN:HG2	2.53	0.43
9:ZF:241:TYR:CZ	9:ZF:262:ILE:HD11	2.54	0.43
1:FG:871:ALA:HB2	1:FG:889:ILE:HD13	2.00	0.43
11:BM:255:THR:HG21	11:BM:279:ILE:HD11	2.00	0.43
11:BM:256:HIS:O	11:BM:259:SER:OG	2.33	0.43
11:FM:250:ARG:HD2	11:FM:268:HIS:HB2	2.00	0.43
11:GM:185:ILE:HB	11:GM:204:LEU:HD22	1.99	0.43
10:FC:171:LYS:HA	10:FC:174:LYS:HE2	2.00	0.43
10:IC:89:LEU:HD13	10:IC:146:TRP:CZ2	2.53	0.43
10:LC:88:ASN:OD1	10:LC:88:ASN:N	2.50	0.43
11:CM:191:LEU:O	11:CM:209:SER:OG	2.21	0.43
2:DH:277:ASN:HB3	2:DH:280:LEU:HD13	2.00	0.43
4:DL:115:GLN:O	4:DL:125:LEU:HD13	2.19	0.43
1:IG:966:GLN:HG2	1:IG:1012:GLY:C	2.43	0.43
10:AC:73:LEU:HD12	10:AC:192:ALA:HB2	1.99	0.43
2:EH:108:ASP:N	2:EH:108:ASP:OD1	2.51	0.43
9:FF:213:GLN:HB2	9:FF:223:ILE:HG22	2.00	0.43
3:FK:76:ILE:HB	3:FK:182:ILE:HG13	2.00	0.43
3:FK:132:LEU:HD11	3:FK:136:ARG:HE	1.84	0.43
8:Fd:82:ARG:CZ	8:Fd:126:GLU:H	2.30	0.43
10:BC:89:ARG:NH1	10:BC:89:ARG:HA	2.34	0.43
10:BC:111:LEU:HD13	10:BC:111:LEU:HA	1.88	0.43
1:Gg:793:GLU:HB3	1:Gg:796:GLN:HE21	1.83	0.43
4:GL:167:GLY:HA2	4:GL:229:ILE:HD13	2.00	0.43
4:HL:63:ASP:O	4:HL:88:GLY:N	2.52	0.43
2:IH:117:ARG:CZ	1:XG:797:ARG:HH21	2.31	0.43
2:IH:157:PHE:CZ	2:IH:257:GLN:HG2	2.53	0.43
2:IH:207:ASP:OD1	2:IH:207:ASP:N	2.44	0.43
1:CG:898:LYS:HB2	1:CG:898:LYS:HE2	1.73	0.43
1:CG:1007:GLY:O	1:CG:1011:VAL:HG22	2.18	0.43
1:Jg:802:LEU:HD22	2:YH:115:MET:HB2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:JL:170:ASP:CG	4:JL:227:ARG:HH21	2.22	0.43
2:AH:280:LEU:HD22	2:AH:328:MET:HG2	2.01	0.43
2:AH:355:GLN:OE1	5:MN:79:GLN:NE2	2.51	0.43
8:CD:40:LYS:HE2	10:KC:197:GLU:HB2	2.00	0.43
4:LL:190:MET:HE3	4:LL:190:MET:HB3	1.87	0.43
4:LL:193:LEU:HD12	4:LL:193:LEU:HA	1.84	0.43
9:Lf:216:ILE:HD12	9:Lf:216:ILE:HA	1.80	0.43
1:EG:899:LEU:HB2	1:EG:919:MET:SD	2.59	0.43
1:EG:1006:ILE:HG22	1:EG:1007:GLY:N	2.34	0.43
2:YH:324:TRP:HA	2:YH:339:MET:HB3	2.00	0.43
11:BM:306:GLN:HB3	11:BM:309:LEU:HB2	2.00	0.43
11:EM:210:ASP:HA	11:EM:229:ASN:H	1.83	0.43
11:EM:244:LYS:HE3	11:EM:245:TYR:CZ	2.53	0.43
11:EM:278:ASP:HB3	11:EM:280:TYR:CE1	2.54	0.43
11:GM:306:GLN:HE21	11:GM:308:ASP:H	1.67	0.43
8:BD:31:ASN:HD22	8:Bd:35:ASP:HA	1.83	0.43
8:BD:69:ASN:HD21	8:BD:133:ARG:HB3	1.83	0.43
8:BD:83:ALA:HA	3:BK:154:ILE:O	2.19	0.43
9:BF:243:MET:H	9:BF:257:SER:HG	1.58	0.43
4:BL:174:SER:O	4:BL:178:LYS:HG3	2.19	0.43
4:BL:224:ALA:HA	4:BL:227:ARG:NH1	2.33	0.43
8:Bd:71:LEU:HD12	8:Bd:71:LEU:HA	1.78	0.43
1:GG:874:ASP:O	1:GG:1033:SER:HB2	2.19	0.43
10:KC:41:SER:HG	10:KC:44:THR:HG1	1.57	0.43
10:KC:243:ILE:HG13	10:LC:129:ARG:HB2	2.01	0.43
10:MC:147:ARG:NH1	10:MC:148:GLN:HA	2.33	0.43
2:CH:332:ASP:N	2:CH:332:ASP:OD1	2.50	0.43
3:CK:91:LEU:HD13	3:CK:91:LEU:HA	1.84	0.43
4:CL:141:ASN:ND2	4:CL:144:CYS:H	2.16	0.43
8:Cd:107:ARG:O	8:Cd:155:GLU:HA	2.18	0.43
2:DH:183:ASP:HB2	2:DH:259:TYR:HA	1.99	0.43
1:HG:882:PRO:HA	1:HG:903:PHE:CE2	2.54	0.43
1:IG:867:ASP:OD1	1:IG:867:ASP:N	2.48	0.43
1:JG:946:SER:OG	1:JG:1030:GLU:O	2.33	0.43
1:KG:910:ASP:OD1	1:KG:910:ASP:N	2.50	0.43
1:MG:881:GLU:OE2	1:NG:907:SER:N	2.48	0.43
1:MG:969:GLY:O	1:MG:1005:VAL:HG13	2.18	0.43
1:MG:1006:ILE:HD13	1:NG:968:PHE:HA	2.01	0.43
1:NG:965:LEU:O	1:NG:1008:LEU:HB3	2.18	0.43
1:OG:970:ASN:OD1	1:OG:971:ALA:N	2.51	0.43
9:Df:210:TYR:CD1	9:Df:224:GLY:HA2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:EL:169:THR:OG1	4:EL:170:ASP:N	2.52	0.43
4:EL:220:ILE:HG13	8:ED:39:ILE:HD12	1.99	0.43
5:EN:42:CYS:SG	5:EN:48:ILE:HD13	2.59	0.43
9:Ff:213:GLN:CD	9:Ff:223:ILE:HB	2.42	0.43
9:AF:219:ARG:HH21	2:BH:151:PRO:HD2	1.84	0.43
1:BG:1006:ILE:CG1	1:CG:968:PHE:HA	2.49	0.43
1:Bg:795:GLN:CD	1:Bg:795:GLN:H	2.25	0.43
8:ID:68:ASP:OD1	8:ID:69:ASN:N	2.51	0.43
2:IH:115:MET:SD	2:IH:116:THR:N	2.92	0.43
3:IK:62:LYS:HE3	3:IK:62:LYS:HB2	1.87	0.43
4:IL:125:LEU:HG	4:IL:233:TRP:HZ3	1.83	0.43
1:CG:1017:GLN:HE22	1:DG:1020:GLN:NE2	2.15	0.43
9:If:216:ILE:HG22	9:If:219:ARG:O	2.19	0.43
9:If:242:GLY:HA3	9:If:257:SER:OG	2.19	0.43
2:JH:214:MET:SD	2:JH:214:MET:N	2.92	0.43
2:AH:108:ASP:OD1	2:AH:108:ASP:N	2.52	0.43
8:KD:114:SER:HA	10:GC:115:ASN:HD21	1.84	0.43
11:KM:276:ALA:H	11:KM:295:ASN:HB2	1.84	0.43
5:KN:87:TRP:O	5:KN:88:HIS:ND1	2.52	0.43
2:LH:149:PRO:HB2	2:LH:248:VAL:HG12	2.01	0.43
2:LH:189:TRP:CH2	2:LH:233:LEU:HG	2.53	0.43
4:LL:104:LYS:HA	4:LL:104:LYS:HD2	1.90	0.43
2:MH:346:LEU:HD23	2:MH:346:LEU:HA	1.87	0.43
3:MK:74:TYR:HB2	3:MK:184:PHE:CE1	2.53	0.43
1:EG:1042:THR:OG1	1:EG:1043:GLN:OE1	2.37	0.43
1:XG:797:ARG:HA	1:XG:800:ASP:OD2	2.18	0.43
2:XH:280:LEU:HD12	2:XH:280:LEU:HA	1.91	0.43
2:YH:325:LEU:N	2:YH:338:GLU:O	2.50	0.43
2:BH:115:MET:HE2	2:BH:115:MET:HB2	1.65	0.43
2:BH:153:ALA:HB1	2:BH:251:ARG:HB3	2.01	0.43
3:BK:92:ASN:O	3:BK:95:SER:OG	2.22	0.43
8:Bd:87:TRP:CG	8:Bd:88:SER:N	2.86	0.43
10:FC:46:ALA:O	10:FC:49:LYS:HG3	2.18	0.43
10:GC:108:PRO:HD2	10:GC:212:TYR:CE2	2.54	0.43
10:IC:149:TYR:CG	10:IC:201:ILE:HD13	2.53	0.43
10:LC:102:HIS:CE1	8:DD:162:TYR:HE1	2.37	0.43
11:CM:278:ASP:HB3	11:CM:280:TYR:CE1	2.54	0.43
5:CN:56:GLY:HA2	5:CN:71:THR:HG23	2.00	0.43
8:Cd:105:ARG:HH22	8:Cd:151:SER:HB2	1.83	0.43
9:Cf:221:TRP:HD1	9:Cf:230:LEU:O	2.02	0.43
1:HG:969:GLY:HA2	1:HG:1005:VAL:HA	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:KG:916:PHE:HD1	1:KG:916:PHE:HA	1.72	0.43
1:MG:1006:ILE:CD1	1:NG:968:PHE:HA	2.48	0.43
1:NG:897:SER:HA	1:NG:922:PRO:HD3	2.00	0.43
1:OG:969:GLY:HA3	1:OG:1009:ALA:N	2.33	0.43
10:AC:80:ILE:HD11	10:AC:196:LEU:HD22	1.99	0.43
1:Eg:810:GLN:HE21	1:Eg:810:GLN:HB3	1.58	0.43
8:Ed:81:ALA:HB3	8:Ed:128:LEU:HD11	2.01	0.43
2:GH:170:ARG:HH11	2:GH:247:ALA:HB3	1.84	0.43
3:GK:162:ASP:N	3:GK:162:ASP:OD1	2.51	0.43
2:HH:184:SER:OG	2:HH:257:GLN:O	2.35	0.43
11:HM:168:VAL:H	11:HM:187:GLY:HA3	1.83	0.43
9:Hf:213:GLN:HB2	9:Hf:221:TRP:CD1	2.54	0.43
1:Bg:797:ARG:NH1	2:VH:108:ASP:HA	2.34	0.43
3:IK:99:LEU:HD13	3:IK:99:LEU:HA	1.84	0.43
1:CG:931:SER:H	1:CG:1043:GLN:HE22	1.65	0.43
9:If:241:TYR:HD2	9:If:260:GLN:HG3	1.82	0.43
2:JH:179:LEU:HD11	2:JH:213:LEU:HD12	2.01	0.43
10:CC:249:ILE:HG13	10:DC:122:GLN:HA	2.01	0.43
1:DG:920:SER:HB2	1:EG:865:THR:HB	2.00	0.43
1:DG:1040:LEU:HD23	1:DG:1040:LEU:H	1.83	0.43
9:Kf:241:TYR:HB3	9:Kf:256:THR:HG21	2.00	0.43
4:LL:145:TYR:CG	4:LL:146:PRO:HD3	2.53	0.43
9:Lf:243:MET:O	9:Lf:257:SER:N	2.51	0.43
3:MK:126:VAL:HA	3:MK:129:GLU:OE2	2.18	0.43
4:ML:124:THR:HG22	4:ML:232:GLN:HG2	2.00	0.43
1:EG:965:LEU:HD23	1:EG:1011:VAL:HG23	2.01	0.43
2:WH:288:PRO:HG3	2:WH:305:TRP:CH2	2.54	0.43
4:AL:94:VAL:HA	4:AL:97:ILE:HG12	2.01	0.43
4:AL:183:GLN:NE2	4:AL:207:GLY:H	2.16	0.43
10:DC:178:TYR:HA	10:DC:181:ARG:CD	2.49	0.43
1:FG:866:GLY:HA2	1:FG:1041:PHE:O	2.19	0.43
11:AM:306:GLN:HG3	11:AM:308:ASP:H	1.83	0.43
11:BM:300:ASP:OD1	11:BM:302:ARG:HG3	2.19	0.43
11:GM:302:ARG:NH1	11:GM:309:LEU:HD11	2.34	0.43
11:JM:229:ASN:OD1	11:JM:229:ASN:N	2.50	0.43
5:BN:74:ALA:HB3	5:BN:76:MET:HE3	2.01	0.43
10:LC:149:TYR:O	10:LC:197:ASN:HB3	2.19	0.43
2:CH:184:SER:HB2	2:CH:259:TYR:CE1	2.51	0.43
11:CM:209:SER:HB3	11:CM:212:LEU:HD21	2.00	0.43
5:CN:47:GLY:O	5:CN:61:ASN:N	2.38	0.43
8:DD:34:SER:OG	8:Dd:36:ASP:OD1	2.29	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HG:944:LEU:HD11	1:HG:1031:VAL:HA	2.01	0.43
1:IG:899:LEU:HD13	1:IG:919:MET:HB2	2.00	0.43
1:PG:969:GLY:O	1:PG:1005:VAL:HG13	2.19	0.43
1:AG:899:LEU:HB2	1:AG:919:MET:SD	2.58	0.43
3:EK:154:ILE:HB	8:ED:84:SER:OG	2.18	0.43
8:Ed:126:GLU:CD	8:Ed:131:ILE:HG13	2.44	0.43
1:Fg:797:ARG:HA	1:Fg:797:ARG:HD2	1.86	0.43
10:BC:112:LEU:HD23	10:BC:112:LEU:HA	1.88	0.43
8:Hd:33:PRO:HB2	8:Hd:39:ILE:HG22	2.00	0.43
11:IM:271:SER:OG	11:IM:290:ASP:OD1	2.35	0.43
1:CG:952:TYR:CE2	1:CG:1027:THR:HG21	2.54	0.43
8:JD:28:PRO:HG2	8:JD:29:PRO:HD3	2.00	0.43
9:JF:263:LYS:HD3	9:JF:264:PHE:O	2.17	0.43
8:Jd:36:ASP:O	8:Jd:39:ILE:HG12	2.18	0.43
2:KH:194:TYR:CE2	2:KH:204:ILE:HG21	2.54	0.43
3:KK:90:ARG:NH2	11:KM:293:ALA:O	2.52	0.43
8:LD:88:SER:HA	8:LD:120:SER:HA	2.00	0.43
3:LK:91:LEU:HD21	3:LK:139:VAL:HG11	2.01	0.43
4:LL:133:PHE:HD1	4:LL:133:PHE:HA	1.68	0.43
11:LM:171:ARG:NH2	11:LM:172:ASN:HB2	2.34	0.43
1:VG:793:GLU:H	1:VG:793:GLU:HG3	1.58	0.43
9:CF:248:ASP:HB3	9:CF:253:ARG:O	2.19	0.43
2:WH:189:TRP:CG	2:WH:230:LEU:HD13	2.54	0.43
10:DC:197:ASN:OD1	10:DC:200:ARG:NH1	2.52	0.43
1:ZG:800:ASP:OD1	1:ZG:801:MET:N	2.52	0.43
2:ZH:157:PHE:CD1	2:ZH:255:ARG:HB2	2.54	0.43
2:ZH:283:VAL:O	2:ZH:314:ARG:HD2	2.19	0.43
11:AM:177:LEU:HD12	11:AM:196:MET:HE1	2.00	0.43
11:EM:174:GLN:HE22	11:EM:192:ARG:HB3	1.82	0.43
11:EM:275:ASP:OD1	11:EM:275:ASP:N	2.52	0.43
11:JM:177:LEU:HD13	11:JM:181:PRO:HG2	1.99	0.43
5:AN:71:THR:OG1	5:AN:72:ARG:N	2.52	0.43
8:Ad:92:GLU:OE1	8:Ad:92:GLU:N	2.31	0.43
2:BH:168:VAL:HG12	2:BH:240:THR:OG1	2.19	0.43
4:BL:127:ILE:HD13	4:BL:127:ILE:HA	1.84	0.43
8:Bd:118:LEU:HD23	10:JC:243:ILE:HG22	2.00	0.43
10:EC:188:ILE:HG22	10:EC:192:ASN:HD21	1.83	0.43
10:JC:112:LEU:HD13	10:JC:112:LEU:HA	1.91	0.43
10:JC:227:VAL:HA	10:JC:250:ILE:HA	2.01	0.43
2:CH:341:LYS:HB2	2:CH:361:LEU:HD11	2.00	0.43
9:DF:248:ASP:HB3	9:DF:253:ARG:HG3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:DH:174:GLY:N	2:DH:216:GLN:OE1	2.46	0.43
1:IG:931:SER:H	1:IG:1043:GLN:NE2	2.17	0.43
1:KG:899:LEU:HB2	1:KG:919:MET:SD	2.59	0.43
1:KG:966:GLN:O	1:KG:970:ASN:ND2	2.52	0.43
1:KG:1024:ASN:OD1	1:KG:1024:ASN:N	2.51	0.43
1:LG:902:SER:O	1:LG:915:THR:N	2.51	0.43
1:LG:936:ASP:OD2	1:LG:939:THR:OG1	2.27	0.43
1:OG:949:ASN:HA	1:OG:952:TYR:HE2	1.84	0.43
10:AC:100:LEU:HA	10:AC:100:LEU:HD13	1.87	0.43
8:FD:109:LEU:HD23	8:FD:155:GLU:HG3	2.00	0.43
2:FH:110:LYS:HA	2:FH:113:LYS:HG2	2.00	0.43
2:FH:111:ALA:HB1	1:Dg:801:MET:HE1	2.00	0.43
4:FL:54:ARG:O	4:FL:57:VAL:HG22	2.19	0.43
8:Fd:87:TRP:CG	8:Fd:88:SER:N	2.87	0.43
2:GH:143:ALA:O	2:HH:131:LYS:NZ	2.41	0.43
3:GK:96:TYR:CE2	8:Gd:26:LYS:HE2	2.54	0.43
3:GK:177:ASN:OD1	3:GK:178:ALA:N	2.52	0.43
1:BG:891:THR:OG1	1:BG:892:GLY:N	2.50	0.43
1:BG:1006:ILE:HD13	1:CG:968:PHE:CG	2.54	0.43
4:GL:145:TYR:CD1	4:GL:146:PRO:HD3	2.54	0.43
4:GL:187:GLU:OE2	11:GM:250:ARG:NH2	2.52	0.43
2:HH:324:TRP:HA	2:HH:339:MET:HB3	2.00	0.43
5:HN:66:SER:OG	5:HN:67:THR:N	2.51	0.43
9:Hf:210:TYR:CG	9:Hf:222:LEU:HD21	2.54	0.43
9:IF:231:THR:O	9:IF:233:ARG:NH1	2.52	0.43
3:IK:72:GLN:HB2	4:JL:215:SER:HA	2.00	0.43
4:IL:224:ALA:HA	4:IL:227:ARG:NH1	2.33	0.43
1:CG:1019:ALA:O	1:CG:1023:PHE:HB2	2.18	0.43
1:Jg:800:ASP:OD1	1:Jg:801:MET:N	2.50	0.43
2:JH:126:GLN:HB3	2:KH:112:PHE:CE1	2.54	0.43
5:JN:72:ARG:HG3	5:JN:73:HIS:ND1	2.34	0.43
9:Kf:216:ILE:HD12	9:Kf:216:ILE:HA	1.84	0.43
4:LL:54:ARG:NH2	4:LL:57:VAL:HG13	2.33	0.43
5:LN:47:GLY:O	5:LN:61:ASN:N	2.43	0.43
3:MK:121:SER:OG	3:MK:122:LYS:N	2.52	0.43
4:ML:139:ARG:NH2	11:MM:319:PHE:HB2	2.34	0.43
1:EG:969:GLY:HA2	1:EG:1005:VAL:HA	2.00	0.43
8:Md:48:VAL:HG11	10:HC:92:ILE:HA	2.01	0.43
2:VH:182:LEU:O	2:VH:256:VAL:HG23	2.19	0.43
2:WH:207:ASP:OD1	2:WH:208:LYS:N	2.50	0.43
9:XF:247:ILE:HG12	9:XF:254:ILE:HD12	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AL:174:SER:O	4:AL:178:LYS:HG3	2.19	0.43
2:YH:315:THR:OG1	2:YH:316:ASN:N	2.51	0.43
10:DC:156:LYS:HG3	10:DC:158:GLU:HG3	2.00	0.43
1:FG:873:LEU:HB2	1:FG:1037:LEU:HD22	2.00	0.43
11:AM:242:LYS:HA	11:AM:262:GLU:HG2	2.00	0.43
11:BM:220:ALA:HB1	11:BM:222:ILE:HD13	2.01	0.43
11:EM:163:THR:HB	11:EM:183:VAL:HG12	2.01	0.43
11:FM:222:ILE:HG22	11:FM:224:LEU:HD21	2.01	0.43
11:GM:137:TYR:HA	11:GM:156:GLU:O	2.18	0.43
8:Ad:85:VAL:HG22	10:JC:267:VAL:HA	1.99	0.43
4:BL:145:TYR:CG	4:BL:146:PRO:HD3	2.53	0.43
8:Bd:135:ILE:HD13	8:Bd:135:ILE:HA	1.90	0.43
10:HC:147:ARG:HH11	10:HC:148:GLN:HA	1.84	0.43
10:HC:235:ASP:CG	10:HC:237:SER:H	2.27	0.43
10:IC:107:PRO:HD3	10:IC:137:ALA:HB2	2.00	0.43
10:JC:143:THR:HG22	10:JC:144:THR:HG23	2.01	0.43
3:CK:73:ASN:N	3:CK:73:ASN:OD1	2.51	0.43
3:CK:111:LYS:H	3:CK:111:LYS:HZ1	1.67	0.43
4:DL:113:ASP:OD1	4:DL:113:ASP:N	2.40	0.43
11:DM:214:ILE:O	11:DM:215:ARG:HD2	2.18	0.43
1:IG:1006:ILE:CD1	1:JG:968:PHE:HA	2.49	0.43
1:LG:946:SER:HB3	1:LG:1029:VAL:HB	2.00	0.43
1:NG:1017:GLN:NE2	1:NG:1018:GLN:HG2	2.34	0.43
1:OG:911:LYS:HZ1	1:OG:913:VAL:HB	1.83	0.43
1:Ag:811:ASP:O	1:Ag:814:GLN:NE2	2.50	0.43
9:Df:233:ARG:HG3	9:Df:234:GLU:H	1.83	0.43
1:Eg:809:VAL:HA	1:Eg:812:TRP:CD1	2.53	0.43
2:EH:161:SER:O	2:EH:164:SER:OG	2.35	0.42
2:EH:208:LYS:HD3	1:Fg:824:THR:N	2.34	0.42
4:EL:170:ASP:CG	4:EL:227:ARG:HH21	2.27	0.42
8:Ed:36:ASP:O	8:Ed:39:ILE:HG12	2.19	0.42
9:Ef:255:LEU:HA	9:Ef:261:VAL:HG22	2.01	0.42
3:FK:123:TYR:CD2	3:FK:124:VAL:HG23	2.54	0.42
8:GD:82:ARG:HB2	3:GK:156:THR:OG1	2.19	0.42
3:GK:72:GLN:NE2	4:HL:215:SER:HB3	2.34	0.42
4:GL:91:VAL:HA	4:GL:94:VAL:HG12	2.00	0.42
4:GL:124:THR:HA	4:GL:231:ILE:O	2.19	0.42
4:GL:190:MET:HE3	4:GL:190:MET:HB3	1.86	0.42
4:HL:229:ILE:HD13	4:HL:229:ILE:HA	1.94	0.42
11:HM:153:GLN:O	11:HM:174:GLN:N	2.46	0.42
8:Hd:55:MET:HE2	8:Hd:59:GLU:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:Hf:216:ILE:HG13	9:Hf:217:PRO:HD2	2.01	0.42
8:ID:125:ASP:OD1	3:IK:138:ARG:NH2	2.51	0.42
1:Ig:801:MET:HB2	2:JH:122:LEU:HG	2.01	0.42
2:IH:176:VAL:HG22	2:IH:216:GLN:HB2	2.01	0.42
4:IL:102:LYS:O	4:IL:106:ILE:HG12	2.19	0.42
4:IL:113:ASP:OD1	4:IL:113:ASP:N	2.47	0.42
1:CG:901:GLY:HA3	1:CG:916:PHE:HD1	1.84	0.42
5:IN:76:MET:N	5:IN:76:MET:SD	2.92	0.42
9:If:254:ILE:O	9:If:261:VAL:HA	2.19	0.42
2:JH:206:TRP:NE1	2:JH:210:SER:O	2.38	0.42
2:AH:225:ASN:ND2	2:BH:175:PHE:HB3	2.33	0.42
10:CC:150:TYR:O	10:CC:198:ASN:HB3	2.19	0.42
9:KF:243:MET:O	9:KF:257:SER:N	2.39	0.42
4:KL:141:ASN:ND2	4:KL:144:CYS:SG	2.92	0.42
11:KM:145:ARG:HH21	11:KM:163:THR:HA	1.84	0.42
9:Kf:209:ILE:N	9:Kf:225:SER:OG	2.50	0.42
1:Lg:819:VAL:HG12	2:YH:199:PRO:HG2	2.01	0.42
8:CD:95:THR:HA	8:CD:98:ILE:HG22	2.01	0.42
2:LH:277:ASN:OD1	2:LH:278:ASP:N	2.52	0.42
2:MH:225:ASN:HB2	2:ZH:250:TYR:OH	2.18	0.42
3:MK:166:THR:HG22	3:MK:168:TYR:H	1.84	0.42
2:XH:189:TRP:HZ2	2:XH:232:GLY:H	1.66	0.42
9:YF:263:LYS:HD2	9:YF:264:PHE:N	2.34	0.42
4:AL:124:THR:HA	4:AL:231:ILE:O	2.19	0.42
1:YG:792:GLN:NE2	1:YG:793:GLU:OE2	2.52	0.42
1:FG:1006:ILE:HG12	1:GG:967:GLY:O	2.19	0.42
11:BM:278:ASP:HB3	11:BM:280:TYR:CZ	2.54	0.42
11:GM:168:VAL:HG21	11:GM:185:ILE:HG23	2.01	0.42
11:GM:194:LEU:HD23	11:GM:194:LEU:HA	1.91	0.42
11:JM:154:LYS:HD3	11:JM:154:LYS:HA	1.87	0.42
10:EC:147:TRP:HB2	10:EC:151:LEU:HD23	2.00	0.42
10:FC:148:TRP:CZ3	10:FC:149:ARG:HG2	2.54	0.42
10:JC:145:PRO:HA	10:JC:146:PRO:HD3	1.93	0.42
10:MC:149:TYR:HB3	10:MC:201:ILE:HB	2.01	0.42
10:MC:180:GLU:OE1	10:MC:181:ARG:N	2.52	0.42
3:CK:61:ASN:HD21	3:CK:67:VAL:H	1.65	0.42
8:DD:136:ASP:OD1	8:DD:145:ILE:N	2.52	0.42
2:DH:194:TYR:HE2	2:DH:206:TRP:CD2	2.37	0.42
1:HG:931:SER:H	1:HG:1043:GLN:HE22	1.67	0.42
8:GD:78:ASN:O	8:GD:78:ASN:ND2	2.52	0.42
8:GD:111:LYS:HD3	8:GD:111:LYS:HA	1.90	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:HF:215:VAL:H	2:HH:245:GLN:HE22	1.67	0.42
2:HH:359:GLU:N	2:HH:359:GLU:OE1	2.52	0.42
5:HN:65:TYR:OH	4:IL:221:HIS:HB3	2.19	0.42
8:Hd:74:PRO:HG3	8:Hd:147:VAL:HG11	2.01	0.42
2:IH:340:GLN:OE1	2:IH:340:GLN:N	2.53	0.42
1:CG:969:GLY:CA	1:CG:1009:ALA:HB2	2.48	0.42
9:If:251:GLN:NE2	9:If:253:ARG:HE	2.17	0.42
3:JK:66:LYS:HB3	3:JK:77:SER:HB3	2.00	0.42
4:JL:165:VAL:HG12	4:JL:231:ILE:HG13	2.01	0.42
8:Jd:100:LYS:HE3	8:Jd:100:LYS:HB2	1.78	0.42
2:AH:288:PRO:HB3	2:AH:305:TRP:CD1	2.54	0.42
2:KH:201:SER:HA	2:KH:219:LYS:HG3	2.00	0.42
3:KK:143:TYR:HE1	8:Kd:26:LYS:HE3	1.83	0.42
4:KL:159:PRO:HG2	4:KL:160:GLN:HE22	1.83	0.42
5:KN:86:LEU:HB3	5:KN:87:TRP:CE3	2.54	0.42
8:Kd:86:ASP:OD1	8:Kd:122:SER:OG	2.25	0.42
9:LF:250:LEU:HD23	9:LF:250:LEU:H	1.83	0.42
2:LH:157:PHE:HD1	2:LH:255:ARG:HB3	1.84	0.42
4:LL:98:TYR:HD1	4:LL:98:TYR:HA	1.70	0.42
3:MK:90:ARG:NH2	11:MM:293:ALA:O	2.52	0.42
5:MN:89:GLY:O	5:MN:104:ASN:ND2	2.36	0.42
1:EG:951:HIS:O	1:EG:955:ARG:NE	2.48	0.42
8:Md:150:ASN:OD1	8:Md:151:SER:N	2.48	0.42
1:VG:820:TYR:CG	2:VH:205:GLN:HB3	2.54	0.42
9:CF:210:TYR:HA	9:CF:224:GLY:HA2	2.00	0.42
9:CF:258:SER:OG	9:CF:260:GLN:OE1	2.30	0.42
9:WF:253:ARG:HH12	9:WF:255:LEU:HD21	1.84	0.42
2:YH:295:LEU:HD11	2:YH:304:ALA:HB3	1.99	0.42
9:Bf:241:TYR:HD1	9:Bf:260:GLN:HE22	1.67	0.42
10:GC:63:ALA:HA	10:GC:66:VAL:HG22	2.02	0.42
10:HC:145:THR:H	10:HC:148:GLN:CD	2.27	0.42
10:IC:138:HIS:ND1	10:IC:139:PHE:O	2.49	0.42
10:JC:47:GLN:HA	10:JC:50:GLN:HG2	2.01	0.42
10:KC:152:LEU:HD21	10:KC:203:ILE:HG21	2.00	0.42
2:CH:279:LEU:HD21	2:CH:289:PRO:HB3	2.01	0.42
3:CK:132:LEU:HD11	3:CK:136:ARG:HE	1.85	0.42
11:CM:116:PHE:CE1	11:CM:118:TYR:HB2	2.52	0.42
11:CM:156:GLU:OE1	11:CM:178:LYS:NZ	2.48	0.42
8:Cd:94:LEU:O	8:Cd:98:ILE:HG12	2.19	0.42
1:MG:917:ASN:OD1	1:MG:917:ASN:N	2.52	0.42
1:OG:866:GLY:HA2	1:OG:1041:PHE:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:OG:1006:ILE:HG22	1:OG:1007:GLY:N	2.34	0.42
2:EH:168:VAL:HA	2:EH:240:THR:HG23	2.02	0.42
2:EH:201:SER:O	2:EH:218:THR:N	2.38	0.42
8:FD:136:ASP:OD2	8:Fd:60:LYS:HE2	2.19	0.42
4:FL:169:THR:HG1	4:FL:170:ASP:H	1.66	0.42
4:FL:186:ALA:HB1	4:FL:205:ALA:HB1	2.02	0.42
2:GH:340:GLN:OE1	2:GH:341:LYS:HG2	2.20	0.42
1:BG:1010:THR:OG1	1:CG:967:GLY:HA3	2.19	0.42
9:Gf:236:SER:N	9:Gf:243:MET:SD	2.92	0.42
8:HD:52:MET:SD	8:Hd:48:VAL:HG23	2.59	0.42
9:HF:219:ARG:HB3	9:HF:221:TRP:HZ3	1.85	0.42
3:HK:143:TYR:O	3:HK:147:GLN:HG2	2.20	0.42
2:IH:309:GLU:HB2	2:IH:341:LYS:HE3	2.02	0.42
5:JN:77:ASP:HA	2:KH:354:MET:SD	2.58	0.42
8:Jd:36:ASP:OD1	8:Jd:36:ASP:N	2.51	0.42
8:Jd:50:ASP:O	8:Jd:54:GLU:HG2	2.19	0.42
9:Jf:223:ILE:HD12	9:Jf:223:ILE:HA	1.89	0.42
2:KH:296:VAL:HB	2:KH:359:GLU:HB2	2.01	0.42
2:KH:340:GLN:OE1	2:KH:340:GLN:N	2.49	0.42
3:KK:87:GLN:HB3	3:KK:128:ARG:HH22	1.85	0.42
11:KM:299:LEU:HD13	11:KM:299:LEU:HA	1.88	0.42
11:LM:172:ASN:HA	11:LM:192:ARG:HH22	1.83	0.42
3:AK:177:ASN:OD1	3:AK:178:ALA:N	2.51	0.42
8:MD:55:MET:HE3	8:MD:55:MET:HB3	1.92	0.42
8:MD:121:ILE:HD13	8:MD:121:ILE:HA	1.84	0.42
1:EG:972:PHE:HB3	1:EG:1005:VAL:CG2	2.49	0.42
7:MX:25:UNK:N	7:MX:71:UNK:O	2.52	0.42
1:VG:807:GLN:HA	1:VG:810:GLN:HG3	2.01	0.42
1:FG:962:SER:HB3	1:FG:1015:TRP:HB3	2.00	0.42
11:AM:298:VAL:C	11:AM:299:LEU:HD22	2.45	0.42
11:BM:208:LYS:NZ	11:BM:227:ILE:HG12	2.34	0.42
11:BM:268:HIS:ND1	4:BL:187:GLU:OE1	2.50	0.42
11:EM:235:LEU:HD23	11:EM:255:THR:HG22	2.02	0.42
2:BH:127:VAL:O	2:BH:130:LEU:HG	2.19	0.42
8:Bd:78:ASN:OD1	8:Bd:78:ASN:N	2.52	0.42
10:FC:97:PHE:O	10:FC:101:VAL:HG23	2.19	0.42
10:GC:71:GLY:HA2	10:GC:184:TRP:CD1	2.53	0.42
10:KC:237:ASP:CG	10:KC:239:SER:H	2.28	0.42
10:MC:149:TYR:CG	10:MC:201:ILE:HD13	2.53	0.42
4:CL:165:VAL:HG23	4:CL:205:ALA:HA	2.01	0.42
9:Cf:223:ILE:HD11	9:Cf:227:GLY:HA2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Dg:794:ILE:O	1:Dg:798:THR:OG1	2.27	0.42
2:DH:208:LYS:HD3	1:Eg:824:THR:N	2.28	0.42
2:DH:228:VAL:HB	2:DH:237:VAL:HB	2.00	0.42
11:DM:125:THR:HG23	11:DM:145:ARG:HB2	2.02	0.42
1:IG:878:ASN:OD1	1:IG:879:SER:N	2.52	0.42
1:IG:937:PRO:HG3	1:IG:1036:GLY:O	2.20	0.42
1:OG:885:ILE:HG13	1:OG:916:PHE:HE1	1.84	0.42
1:OG:947:ARG:O	1:OG:950:HIS:NE2	2.52	0.42
1:OG:966:GLN:HG2	1:OG:1012:GLY:C	2.45	0.42
8:Dd:142:LYS:HE2	8:Dd:142:LYS:HB2	1.91	0.42
1:AG:966:GLN:OE1	1:AG:1013:LYS:N	2.52	0.42
1:AG:967:GLY:HA2	1:AG:970:ASN:HD21	1.84	0.42
2:FH:320:LEU:N	2:FH:346:LEU:O	2.47	0.42
5:FN:90:GLY:O	5:FN:104:ASN:ND2	2.50	0.42
8:Fd:77:TYR:HA	8:Fd:80:GLN:HG2	2.02	0.42
9:AF:216:ILE:HD11	9:AF:219:ARG:HB2	2.01	0.42
8:GD:55:MET:HE2	8:GD:55:MET:HB2	1.87	0.42
3:GK:56:MET:HG3	3:GK:105:PHE:HD2	1.83	0.42
3:HK:159:LEU:HD13	3:HK:159:LEU:HA	1.91	0.42
4:HL:187:GLU:O	4:HL:190:MET:HG3	2.19	0.42
11:HM:302:ARG:NH1	11:HM:309:LEU:HD11	2.35	0.42
8:Hd:85:VAL:HG22	10:DC:265:VAL:HA	2.01	0.42
8:ID:161:ILE:HG23	8:ID:162:TYR:CG	2.54	0.42
3:IK:114:ILE:HB	3:IK:154:ILE:HG12	2.01	0.42
8:Id:104:PHE:CZ	8:Id:152:GLN:HB3	2.55	0.42
8:KD:135:ILE:HD13	8:KD:135:ILE:HA	1.93	0.42
3:KK:123:TYR:CD2	3:KK:124:VAL:HG23	2.55	0.42
1:DG:973:GLN:HB2	1:DG:1005:VAL:CG1	2.50	0.42
8:LD:124:LYS:HZ1	3:LK:145:TRP:CG	2.37	0.42
5:LN:81:LEU:HD13	5:LN:81:LEU:HA	1.91	0.42
3:MK:111:LYS:HG3	3:MK:114:ILE:HD11	2.02	0.42
4:ML:59:ARG:HH22	4:ML:99:ARG:HE	1.66	0.42
1:EG:967:GLY:HA2	1:EG:970:ASN:HD21	1.85	0.42
7:WX:21:UNK:N	7:WX:78:UNK:O	2.53	0.42
1:XG:792:GLN:O	1:XG:795:GLN:HG2	2.18	0.42
4:AL:48:ASN:HD22	4:AL:53:ASP:HB2	1.83	0.42
1:YG:800:ASP:O	1:YG:803:THR:OG1	2.27	0.42
11:BM:137:TYR:HA	11:BM:156:GLU:O	2.19	0.42
11:BM:317:LYS:HB2	11:BM:317:LYS:HE3	1.79	0.42
11:JM:288:ARG:NH2	11:JM:318:GLN:H	2.17	0.42
7:AX:18:UNK:HA	7:AX:38:UNK:C	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:FC:249:ARG:NH1	10:FC:249:ARG:HA	2.33	0.42
5:CN:69:TYR:CD2	5:CN:76:MET:HE1	2.54	0.42
2:DH:203:ASN:N	2:DH:216:GLN:O	2.52	0.42
4:DL:97:ILE:HA	4:DL:100:ASP:OD1	2.19	0.42
1:IG:1025:THR:HA	1:IG:1026:PRO:HD3	1.88	0.42
1:AG:961:ALA:O	1:AG:965:LEU:HD13	2.20	0.42
9:Ef:216:ILE:HG13	9:Ef:217:PRO:HD2	2.00	0.42
8:FD:44:ALA:O	8:FD:48:VAL:HG23	2.20	0.42
1:Fg:800:ASP:OD1	1:Fg:801:MET:N	2.48	0.42
3:FK:50:ASP:HB2	5:FN:45:MET:HE3	2.01	0.42
5:FN:84:CYS:HB3	10:AC:157:VAL:HG23	2.01	0.42
9:AF:237:LYS:HD3	9:AF:237:LYS:HA	1.92	0.42
4:GL:187:GLU:O	4:GL:191:THR:HG23	2.19	0.42
1:Hg:807:GLN:OE1	1:Hg:810:GLN:NE2	2.53	0.42
11:HM:131:THR:HG21	11:HM:134:LEU:HD21	2.01	0.42
11:HM:275:ASP:HA	11:HM:296:GLY:N	2.34	0.42
8:Hd:100:LYS:HE2	8:Hd:100:LYS:HB2	1.83	0.42
8:Id:79:LEU:O	8:Id:127:SER:OG	2.37	0.42
8:JD:162:TYR:O	10:EC:245:ARG:NH1	2.53	0.42
9:JF:207:ARG:NH1	9:JF:240:GLY:O	2.49	0.42
4:JL:186:ALA:HB1	4:JL:205:ALA:HB1	2.00	0.42
2:AH:183:ASP:OD1	2:AH:186:GLY:N	2.53	0.42
10:CC:150:TYR:CG	10:CC:202:ILE:HD13	2.54	0.42
10:CC:221:VAL:HA	10:CC:255:LEU:HA	2.01	0.42
9:KF:245:LYS:HG3	9:KF:257:SER:HA	2.00	0.42
11:KM:275:ASP:OD1	11:KM:275:ASP:N	2.53	0.42
1:DG:952:TYR:CE2	1:DG:1027:THR:HG21	2.54	0.42
4:LL:124:THR:HG22	4:LL:232:GLN:HG2	2.00	0.42
8:MD:45:ALA:HA	8:MD:48:VAL:HG12	2.02	0.42
3:MK:117:THR:HG22	3:MK:157:GLN:HG2	2.01	0.42
11:MM:268:HIS:ND1	11:MM:287:THR:OG1	2.48	0.42
1:VG:793:GLU:OE1	1:VG:794:ILE:N	2.53	0.42
1:WG:792:GLN:O	1:WG:795:GLN:HG2	2.19	0.42
1:YG:797:ARG:HA	1:YG:800:ASP:OD2	2.19	0.42
2:ZH:254:LEU:HD13	2:ZH:254:LEU:HA	1.91	0.42
2:ZH:317:LEU:HB3	2:ZH:347:VAL:HG11	2.01	0.42
11:GM:188:PHE:HD1	11:GM:206:TRP:HB2	1.85	0.42
10:FC:241:ILE:CG1	10:GC:132:TYR:HB2	2.49	0.42
10:IC:73:TRP:O	10:IC:77:ILE:HG12	2.20	0.42
10:IC:120:ASP:H	10:IC:123:SER:HG	1.61	0.42
10:JC:147:THR:HG23	10:JC:150:GLN:HG3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:KC:61:LYS:O	10:KC:65:LEU:HG	2.18	0.42
10:KC:182:GLU:O	10:KC:186:LYS:HG3	2.19	0.42
10:MC:140:ILE:HD11	10:MC:143:PRO:HA	2.01	0.42
3:DK:111:LYS:HE3	3:DK:111:LYS:HB3	1.88	0.42
4:DL:221:HIS:ND1	4:DL:225:GLN:OE1	2.52	0.42
1:LG:869:MET:HB2	1:LG:1041:PHE:HE1	1.84	0.42
1:LG:1006:ILE:CD1	1:MG:968:PHE:HA	2.49	0.42
1:MG:899:LEU:HD21	1:MG:916:PHE:HB3	2.01	0.42
1:OG:877:VAL:O	1:OG:1030:GLU:HG3	2.20	0.42
1:OG:1006:ILE:CD1	1:PG:968:PHE:HA	2.50	0.42
8:Dd:128:LEU:HA	8:Dd:131:ILE:HD12	2.00	0.42
1:Ag:793:GLU:H	1:Ag:793:GLU:CD	2.27	0.42
8:AD:82:ARG:NE	8:AD:125:ASP:OD1	2.34	0.42
1:AG:968:PHE:HA	1:PG:1006:ILE:HG12	2.01	0.42
2:EH:225:ASN:HD21	2:FH:175:PHE:HA	1.83	0.42
4:EL:166:ALA:HB3	4:EL:230:GLU:HG2	2.00	0.42
5:EN:88:HIS:C	5:EN:90:GLY:H	2.28	0.42
3:FK:86:ASP:N	3:FK:86:ASP:OD1	2.52	0.42
8:GD:73:ILE:HD13	8:GD:133:ARG:HG3	2.00	0.42
2:GH:208:LYS:NZ	1:Hg:823:GLY:HA2	2.34	0.42
4:GL:115:GLN:HB2	4:GL:126:ILE:HB	2.02	0.42
8:Gd:100:LYS:HB2	8:Gd:100:LYS:HE3	1.79	0.42
8:HD:150:ASN:N	8:HD:150:ASN:OD1	2.52	0.42
2:HH:115:MET:HE3	2:HH:115:MET:HB3	1.85	0.42
8:ID:26:LYS:HE2	4:IL:110:GLN:O	2.20	0.42
1:Ig:816:GLU:H	1:Ig:816:GLU:HG3	1.74	0.42
8:Id:84:SER:H	10:EC:267:ALA:HB3	1.84	0.42
8:JD:162:TYR:OH	10:EC:103:HIS:HA	2.19	0.42
2:JH:315:THR:OG1	2:JH:316:ASN:N	2.52	0.42
5:JN:115:GLN:N	5:JN:115:GLN:OE1	2.53	0.42
2:AH:233:LEU:HD22	2:AH:235:THR:H	1.83	0.42
10:CC:231:LEU:HB2	10:CC:244:ASP:HB2	2.02	0.42
2:KH:320:LEU:HB2	2:KH:346:LEU:HD23	2.01	0.42
4:KL:165:VAL:HG12	4:KL:231:ILE:HG13	2.01	0.42
1:DG:1006:ILE:CG1	1:EG:968:PHE:HA	2.50	0.42
9:LF:212:ILE:HB	9:LF:264:PHE:CD1	2.54	0.42
8:CD:34:SER:OG	8:Cd:36:ASP:OD1	2.30	0.42
3:LK:143:TYR:O	3:LK:146:SER:OG	2.24	0.42
9:Lf:219:ARG:HA	9:Lf:232:VAL:O	2.19	0.42
11:MM:181:PRO:HD2	11:MM:200:GLY:HA2	2.01	0.42
2:XH:311:MET:HE3	2:XH:341:LYS:HA	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:DC:178:TYR:O	10:DC:181:ARG:HG2	2.20	0.42
1:FG:966:GLN:HG2	1:FG:1012:GLY:C	2.45	0.42
11:EM:219:ALA:HB1	11:EM:221:LYS:HZ1	1.84	0.42
11:FM:209:SER:HB3	11:FM:212:LEU:HD21	2.02	0.42
11:GM:279:ILE:HB	11:GM:298:VAL:HG22	2.02	0.42
11:JM:275:ASP:HA	11:JM:295:ASN:H	1.84	0.42
5:AN:90:GLY:O	5:AN:104:ASN:ND2	2.52	0.42
3:BK:48:ALA:HB1	5:BN:67:THR:HG21	2.01	0.42
4:BL:54:ARG:NH2	4:BL:56:ALA:HB3	2.35	0.42
10:HC:149:TYR:CG	10:HC:201:ILE:HD13	2.55	0.42
10:HC:185:ASN:HA	10:HC:188:ASP:OD2	2.20	0.42
10:IC:109:LEU:HD13	10:IC:109:LEU:HA	1.91	0.42
10:JC:78:LYS:HB2	10:JC:156:TYR:CE2	2.55	0.42
10:JC:171:LYS:HA	10:JC:174:LYS:HE2	2.01	0.42
10:KC:171:LYS:H	10:KC:171:LYS:HG3	1.56	0.42
10:MC:62:ALA:HB2	10:MC:175:TRP:CD1	2.54	0.42
10:MC:145:THR:HG23	10:MC:148:GLN:HE22	1.85	0.42
11:CM:172:ASN:OD1	11:CM:173:LEU:N	2.53	0.42
8:Cd:72:THR:OG1	8:Cd:73:ILE:N	2.52	0.42
8:DD:76:ALA:N	8:DD:79:LEU:HD12	2.32	0.42
4:DL:127:ILE:HB	4:DL:229:ILE:HB	2.02	0.42
11:DM:306:GLN:HG3	11:DM:309:LEU:HB2	2.02	0.42
1:HG:878:ASN:OD1	1:HG:879:SER:N	2.53	0.42
1:HG:903:PHE:CG	1:HG:912:MET:HE1	2.55	0.42
1:KG:871:ALA:HB2	1:KG:889:ILE:HD13	2.02	0.42
1:LG:949:ASN:HA	1:LG:952:TYR:CE2	2.54	0.42
1:NG:915:THR:HG23	1:NG:933:TYR:HE1	1.83	0.42
1:NG:937:PRO:HD3	1:NG:1037:LEU:HA	2.01	0.42
1:OG:920:SER:HB2	1:PG:865:THR:HB	2.00	0.42
1:AG:878:ASN:OD1	1:AG:879:SER:N	2.53	0.42
2:EH:183:ASP:HA	2:EH:256:VAL:HB	2.01	0.42
5:EN:104:ASN:OD1	5:EN:104:ASN:N	2.53	0.42
8:Ed:86:ASP:OD1	10:AC:131:ARG:NH2	2.53	0.42
10:BC:44:THR:HG21	10:AC:167:LEU:HG	2.01	0.42
8:GD:79:LEU:HD13	8:GD:79:LEU:HA	1.93	0.42
9:GF:214:ALA:H	9:GF:221:TRP:HB2	1.84	0.42
2:GH:332:ASP:OD1	2:GH:332:ASP:N	2.52	0.42
4:GL:166:ALA:HB3	4:GL:230:GLU:HG2	2.02	0.42
5:GN:89:GLY:HA3	5:GN:104:ASN:HB2	2.02	0.42
8:HD:28:PRO:CG	8:HD:29:PRO:HD3	2.50	0.42
2:HH:225:ASN:OD1	2:HH:225:ASN:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:HM:136:LEU:HD23	11:HM:152:LEU:HD13	2.02	0.42
5:HN:44:LYS:HE2	5:HN:44:LYS:HB3	1.86	0.42
8:ID:137:TYR:CE1	8:Id:57:LYS:HA	2.55	0.42
2:IH:295:LEU:HB2	2:IH:304:ALA:HB3	2.01	0.42
3:IK:83:LEU:HD13	3:IK:83:LEU:HA	1.88	0.42
5:JN:87:TRP:CD1	2:KH:344:VAL:HG21	2.52	0.42
2:AH:203:ASN:O	2:AH:216:GLN:NE2	2.52	0.42
2:AH:335:HIS:HB3	2:AH:337:TYR:HE1	1.84	0.42
10:CC:172:GLU:HA	10:CC:175:ILE:HG12	2.02	0.42
4:KL:174:SER:O	4:KL:178:LYS:HG3	2.19	0.42
4:KL:176:SER:HB2	4:KL:180:LYS:NZ	2.34	0.42
11:KM:257:ASP:HA	11:KM:275:ASP:O	2.20	0.42
11:KM:313:ASP:N	11:KM:316:ASN:OD1	2.37	0.42
1:DG:1006:ILE:CD1	1:EG:968:PHE:HA	2.49	0.42
1:Mg:820:TYR:HB2	2:MH:205:GLN:OE1	2.20	0.42
2:MH:225:ASN:HD21	2:ZH:176:VAL:N	2.17	0.42
1:EG:917:ASN:OD1	1:EG:917:ASN:N	2.52	0.42
2:VH:253:ASP:N	2:VH:253:ASP:OD1	2.52	0.42
1:XG:811:ASP:O	1:XG:814:GLN:NE2	2.53	0.42
2:YH:115:MET:HG3	2:YH:116:THR:N	2.33	0.42
10:DC:114:ASN:N	10:DC:128:ASP:O	2.41	0.42
10:DC:146:TRP:HB2	10:DC:150:LEU:HD23	2.02	0.42
10:DC:235:ASP:CG	10:DC:237:SER:H	2.27	0.42
2:ZH:238:MET:HE3	2:ZH:238:MET:HB2	1.68	0.42
11:AM:262:GLU:HB2	11:AM:282:TYR:CE1	2.55	0.42
11:BM:220:ALA:C	11:BM:221:LYS:HE3	2.45	0.42
11:EM:300:ASP:CG	11:EM:302:ARG:HE	2.27	0.42
5:AN:49:ASN:OD1	5:AN:49:ASN:N	2.53	0.42
9:Af:254:ILE:O	9:Af:261:VAL:HA	2.19	0.42
2:BH:349:TRP:CE3	2:BH:350:HIS:HB2	2.54	0.42
10:FC:100:LEU:HD22	10:FC:100:LEU:HA	1.89	0.42
10:GC:240:ILE:CG1	10:HC:131:TYR:HB2	2.50	0.42
1:JG:874:ASP:OD1	1:JG:874:ASP:N	2.51	0.42
1:KG:969:GLY:O	1:KG:1005:VAL:HG13	2.19	0.42
1:MG:1007:GLY:O	1:MG:1011:VAL:HG22	2.19	0.42
1:NG:866:GLY:HA2	1:NG:1041:PHE:O	2.20	0.42
10:AC:151:TYR:CG	10:AC:203:ILE:HD13	2.55	0.42
1:Eg:797:ARG:HE	1:Eg:801:MET:HE3	1.84	0.42
1:AG:895:LYS:HD3	1:AG:895:LYS:HA	1.86	0.42
2:EH:296:VAL:HG13	2:EH:359:GLU:HB2	2.01	0.42
3:EK:48:ALA:HA	3:EK:108:GLN:HE22	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:EL:155:LEU:HD23	4:EL:155:LEU:HA	1.88	0.42
1:Fg:818:GLN:CD	2:FH:216:GLN:HB2	2.44	0.42
2:FH:249:ASP:OD1	2:FH:249:ASP:N	2.51	0.42
4:GL:108:ASP:OD2	4:GL:150:ASN:ND2	2.53	0.42
4:GL:226:ASN:O	4:GL:228:ARG:NH1	2.46	0.42
2:HH:174:GLY:N	2:HH:217:ALA:O	2.41	0.42
4:HL:212:ASN:OD1	4:HL:212:ASN:N	2.51	0.42
8:ID:160:LYS:HD2	8:ID:160:LYS:HA	1.80	0.42
11:IM:276:ALA:H	11:IM:295:ASN:HB2	1.85	0.42
1:CG:961:ALA:O	1:CG:965:LEU:HD13	2.20	0.42
8:JD:35:ASP:O	8:JD:38:THR:OG1	2.30	0.42
2:JH:207:ASP:OD1	2:JH:210:SER:OG	2.29	0.42
5:JN:90:GLY:O	5:JN:104:ASN:ND2	2.52	0.42
3:KK:106:LEU:HD12	3:KK:149:VAL:HG21	2.02	0.42
9:Kf:243:MET:O	9:Kf:257:SER:N	2.52	0.42
9:MF:219:ARG:HG2	2:ZH:148:PRO:HD2	2.00	0.42
5:MN:75:VAL:C	5:MN:76:MET:HE2	2.45	0.42
1:EG:1006:ILE:HD13	1:FG:968:PHE:HA	2.02	0.42
9:VF:219:ARG:HH21	9:VF:231:THR:HG1	1.63	0.42
9:CF:214:ALA:HB3	9:CF:221:TRP:CG	2.55	0.42
10:DC:120:ASP:OD1	10:DC:123:SER:OG	2.21	0.42
2:ZH:206:TRP:HH2	1:Ag:823:GLY:HA3	1.85	0.42
7:ZX:21:UNK:N	7:ZX:78:UNK:O	2.53	0.42
11:EM:219:ALA:HB1	11:EM:221:LYS:NZ	2.35	0.42
1:Cg:792:GLN:H	1:Cg:792:GLN:CD	2.26	0.42
2:BH:173:GLN:HA	2:BH:217:ALA:HB3	2.02	0.42
10:FC:122:ASP:N	10:FC:125:SER:OG	2.50	0.42
1:GG:882:PRO:HA	1:GG:903:PHE:CE2	2.55	0.42
1:GG:1010:THR:OG1	1:HG:967:GLY:HA3	2.20	0.42
10:JC:174:LYS:HG2	10:KC:39:ALA:HB1	2.02	0.42
10:MC:111:GLU:HB2	10:MC:131:TYR:CE1	2.55	0.42
9:Cf:209:ILE:O	9:Cf:225:SER:OG	2.36	0.42
4:DL:224:ALA:HA	4:DL:227:ARG:HH11	1.85	0.42
1:HG:1006:ILE:HG12	1:IG:967:GLY:O	2.20	0.42
1:IG:965:LEU:HD23	1:IG:1011:VAL:HG23	2.01	0.42
1:NG:1006:ILE:CD1	1:OG:968:PHE:HA	2.50	0.42
8:AD:93:GLU:OE1	8:AD:93:GLU:N	2.36	0.42
8:ED:28:PRO:HG2	8:ED:29:PRO:HD3	2.02	0.42
1:AG:882:PRO:HA	1:AG:903:PHE:CE2	2.55	0.42
1:AG:1007:GLY:O	1:AG:1011:VAL:HG22	2.19	0.42
2:EH:206:TRP:CZ2	2:EH:208:LYS:HA	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:EK:104:ALA:HA	3:EK:107:LYS:HE2	2.02	0.42
5:EN:79:GLN:NE2	2:FH:355:GLN:HG3	2.35	0.42
1:Fg:793:GLU:HA	1:Fg:796:GLN:NE2	2.34	0.42
8:GD:67:LYS:HD2	8:GD:68:ASP:N	2.34	0.42
8:HD:124:LYS:HE2	8:HD:124:LYS:HB3	1.88	0.42
4:HL:48:ASN:ND2	4:HL:51:GLN:HB2	2.35	0.42
4:HL:174:SER:HB3	4:HL:177:HIS:HB3	2.02	0.42
8:Hd:87:TRP:HZ2	8:Hd:90:PRO:HD2	1.83	0.42
2:IH:208:LYS:HD2	1:Jg:823:GLY:HA2	2.02	0.42
2:IH:223:TYR:HB2	2:IH:242:ILE:HD13	2.02	0.42
1:CG:947:ARG:O	1:CG:950:HIS:NE2	2.53	0.42
1:CG:973:GLN:HB2	1:CG:1005:VAL:HG11	2.02	0.42
5:IN:65:TYR:HD1	5:IN:65:TYR:HA	1.74	0.42
9:If:212:ILE:HG12	9:If:263:LYS:C	2.45	0.42
9:If:260:GLN:HE21	9:If:260:GLN:HB3	1.52	0.42
4:JL:191:THR:HG21	11:JM:289:ALA:HB3	2.02	0.42
2:AH:298:SER:OG	5:MN:72:ARG:NH2	2.53	0.42
8:KD:130:GLU:OE2	8:KD:133:ARG:NH1	2.53	0.42
1:DG:899:LEU:HB2	1:DG:919:MET:SD	2.60	0.42
8:Kd:29:PRO:HD2	8:Kd:32:ASN:HD21	1.85	0.42
8:CD:161:ILE:HG12	8:CD:162:TYR:N	2.31	0.42
4:LL:134:MET:HB3	4:LL:137:SER:OG	2.19	0.42
4:LL:159:PRO:HG2	4:LL:160:GLN:NE2	2.35	0.42
11:LM:317:LYS:HE3	11:LM:317:LYS:HB2	1.73	0.42
5:LN:65:TYR:OH	4:ML:221:HIS:HB3	2.20	0.42
8:Ld:97:ARG:HG3	10:HC:265:VAL:HG12	2.01	0.42
11:MM:173:LEU:HD11	11:MM:175:ILE:HD11	2.02	0.42
2:VH:323:GLY:N	10:JC:228:SER:OG	2.53	0.42
1:WG:796:GLN:O	1:WG:799:SER:OG	2.37	0.42
2:XH:225:ASN:N	2:XH:225:ASN:OD1	2.53	0.42
2:XH:341:LYS:HZ3	2:XH:341:LYS:N	2.13	0.42
2:YH:106:VAL:HA	2:YH:109:LYS:HE2	2.01	0.42
10:DC:88:ASN:O	10:DC:92:ILE:HG12	2.20	0.42
10:DC:110:LEU:HD13	10:DC:110:LEU:HA	1.91	0.42
2:ZH:206:TRP:NE1	2:ZH:210:SER:O	2.44	0.42
1:FG:917:ASN:HA	1:FG:930:ILE:O	2.20	0.42
11:FM:206:TRP:HB3	11:FM:208:LYS:NZ	2.35	0.42
11:GM:158:VAL:HA	11:GM:178:LYS:HZ3	1.83	0.42
11:JM:228:VAL:O	11:JM:248:ALA:HA	2.20	0.42
8:Bd:27:LYS:HE3	8:Bd:27:LYS:HB3	1.93	0.42
9:Bf:212:ILE:HG13	9:Bf:264:PHE:CD1	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:GC:153:MET:HE3	10:GC:153:MET:HB3	1.89	0.42
10:KC:94:ILE:HG22	8:Cd:45:ALA:HA	2.02	0.42
10:KC:222:VAL:HA	10:KC:256:LEU:HA	2.02	0.42
10:MC:120:ASP:N	10:MC:120:ASP:OD1	2.53	0.42
2:CH:182:LEU:HA	2:CH:188:PRO:HA	2.02	0.42
5:CN:50:TYR:HB3	8:DD:33:PRO:HB3	2.02	0.42
8:Cd:111:LYS:HE2	8:Cd:111:LYS:HB2	1.91	0.42
8:DD:87:TRP:CD2	8:DD:94:LEU:HD12	2.55	0.42
8:DD:106:PHE:HA	8:DD:154:VAL:HG23	2.00	0.42
1:Dg:814:GLN:NE2	1:Dg:814:GLN:O	2.52	0.42
1:KG:886:LEU:HB3	1:KG:900:ILE:HG22	2.02	0.42
1:LG:966:GLN:OE1	1:LG:1013:LYS:N	2.53	0.42
1:NG:898:LYS:HE2	1:NG:898:LYS:HB2	1.82	0.42
1:OG:898:LYS:HE2	1:OG:898:LYS:HB2	1.75	0.42
1:PG:944:LEU:HD13	1:PG:945:ALA:N	2.35	0.42
1:AG:1006:ILE:HD13	1:BG:968:PHE:HA	2.02	0.42
2:EH:196:LEU:HD13	2:EH:204:ILE:HG12	2.02	0.42
4:EL:138:PRO:HB3	4:EL:184:ALA:HB1	2.00	0.42
8:FD:28:PRO:HG2	8:FD:29:PRO:HD3	2.01	0.42
8:Fd:55:MET:HE2	10:AC:214:ARG:HH11	1.85	0.42
10:BC:256:LEU:HG	10:AC:241:ILE:HG12	2.01	0.42
9:AF:214:ALA:HB3	9:AF:221:TRP:HB2	2.01	0.42
2:GH:289:PRO:O	2:GH:292:SER:OG	2.33	0.42
3:GK:60:LEU:HG	3:GK:65:ILE:HD11	2.02	0.42
3:GK:70:VAL:HG12	4:HL:214:ILE:HD12	2.02	0.42
3:HK:61:ASN:OD1	3:HK:66:LYS:NZ	2.48	0.42
11:HM:208:LYS:HA	11:HM:208:LYS:HD3	1.84	0.42
9:Hf:233:ARG:HG2	9:Hf:234:GLU:N	2.35	0.42
2:IH:111:ALA:HA	2:IH:114:ASP:OD2	2.20	0.42
3:IK:46:ASP:OD1	3:IK:46:ASP:N	2.51	0.42
2:JH:266:MET:HA	2:JH:267:PRO:HD3	1.89	0.42
2:JH:302:ALA:O	2:JH:303:ARG:NH1	2.40	0.42
8:KD:39:ILE:HG23	4:KL:220:ILE:HG13	2.01	0.42
2:KH:230:LEU:HD12	2:KH:233:LEU:HB3	2.00	0.42
4:KL:191:THR:HG22	11:KM:270:SER:HB2	2.01	0.42
11:KM:284:LEU:HD21	11:KM:302:ARG:HD3	2.02	0.42
5:KN:66:SER:OG	5:KN:67:THR:N	2.52	0.42
1:DG:902:SER:O	1:DG:915:THR:N	2.53	0.42
1:Lg:798:THR:HG23	2:ZH:115:MET:HB3	2.02	0.42
2:LH:122:LEU:HA	2:LH:122:LEU:HD23	1.81	0.42
2:LH:283:VAL:O	2:LH:314:ARG:HD2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:LK:168:TYR:CZ	3:LK:170:LEU:HB2	2.55	0.42
11:LM:117:ARG:HE	11:LM:117:ARG:HB3	1.62	0.42
11:LM:222:ILE:HG22	11:LM:224:LEU:HG	2.01	0.42
3:MK:132:LEU:O	3:MK:136:ARG:HG3	2.19	0.42
9:VF:254:ILE:O	9:VF:261:VAL:HA	2.19	0.42
9:CF:243:MET:HB2	9:CF:257:SER:HB3	2.01	0.42
2:XH:180:VAL:HG13	2:XH:253:ASP:HA	2.02	0.42
1:YG:817:THR:HG22	1:YG:818:GLN:H	1.85	0.42
10:DC:111:GLU:HG3	10:DC:131:TYR:CE2	2.55	0.42
10:DC:147:ARG:H	10:DC:147:ARG:HG3	1.64	0.42
2:ZH:112:PHE:O	2:ZH:115:MET:HG3	2.19	0.42
11:AM:208:LYS:HA	11:AM:208:LYS:HD3	1.83	0.42
11:GM:154:LYS:HA	11:GM:154:LYS:HD3	1.78	0.42
8:Bd:35:ASP:O	8:Bd:38:THR:OG1	2.33	0.42
10:EC:114:ARG:HD3	10:EC:130:ARG:HD3	2.02	0.42
10:HC:78:ILE:HD11	10:HC:194:LEU:HD22	2.02	0.42
5:CN:69:TYR:CG	5:CN:76:MET:HE1	2.54	0.42
1:MG:900:ILE:HD11	1:NG:866:GLY:HA3	2.02	0.42
1:OG:915:THR:HG23	1:OG:933:TYR:HE1	1.84	0.42
1:OG:919:MET:HE3	1:OG:919:MET:HB3	1.95	0.42
8:ED:91:ILE:O	8:ED:95:THR:HG22	2.18	0.42
1:AG:967:GLY:O	1:PG:1006:ILE:HG12	2.20	0.41
1:AG:1006:ILE:CD1	1:BG:968:PHE:HA	2.50	0.41
2:EH:146:GLY:N	7:DX:70:UNK:H2	2.17	0.41
2:EH:216:GLN:CD	1:Eg:818:GLN:HG2	2.45	0.41
2:EH:321:SER:OG	2:EH:322:PRO:HD3	2.20	0.41
9:FF:233:ARG:HG2	9:FF:236:SER:HB2	2.01	0.41
2:FH:184:SER:OG	2:FH:256:VAL:O	2.28	0.41
8:Fd:76:ALA:O	8:Fd:80:GLN:NE2	2.31	0.41
4:GL:145:TYR:CG	4:GL:146:PRO:HD3	2.55	0.41
4:GL:177:HIS:HE1	4:GL:181:LEU:HD12	1.85	0.41
9:Gf:241:TYR:HB3	9:Gf:256:THR:HG21	2.01	0.41
2:HH:283:VAL:O	2:HH:314:ARG:HD2	2.20	0.41
4:HL:102:LYS:HE3	4:HL:102:LYS:HB2	1.84	0.41
8:Hd:71:LEU:HD22	8:Hd:145:ILE:HG23	2.01	0.41
9:JF:219:ARG:NH1	9:JF:233:ARG:HH11	2.16	0.41
2:KH:176:VAL:HG22	2:KH:216:GLN:HB2	2.02	0.41
11:KM:180:ASP:CG	11:KM:199:LYS:HB2	2.45	0.41
11:KM:255:THR:HB	11:KM:259:SER:OG	2.20	0.41
1:DG:917:ASN:HA	1:DG:931:SER:HA	2.01	0.41
1:DG:969:GLY:HA2	1:DG:1005:VAL:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Kd:136:ASP:HB2	8:Kd:145:ILE:HD11	2.02	0.41
9:Kf:241:TYR:HD2	9:Kf:256:THR:HG21	1.84	0.41
8:LD:109:LEU:HB3	8:Ld:137:TYR:CD2	2.54	0.41
2:LH:110:LYS:HA	2:LH:113:LYS:HD2	2.02	0.41
2:MH:166:PRO:HA	2:MH:167:PRO:HD3	1.83	0.41
2:MH:223:TYR:HB2	2:MH:242:ILE:HD13	2.02	0.41
3:MK:102:ILE:HD13	3:MK:102:ILE:HA	1.90	0.41
9:XF:243:MET:HB3	9:XF:257:SER:HB3	2.02	0.41
2:XH:312:TYR:CZ	2:XH:338:GLU:HG3	2.54	0.41
11:BM:145:ARG:HH21	11:BM:163:THR:HA	1.84	0.41
8:Ad:84:SER:N	10:JC:268:ALA:HB3	2.35	0.41
8:Ad:136:ASP:HB2	8:Ad:145:ILE:HD11	2.01	0.41
10:GC:96:PHE:O	10:GC:100:VAL:HG23	2.20	0.41
10:GC:236:ASP:CG	10:GC:238:SER:H	2.28	0.41
10:HC:181:ARG:HA	10:HC:184:LYS:HG2	2.02	0.41
10:KC:231:ASP:OD1	10:KC:231:ASP:N	2.49	0.41
10:MC:94:ASP:OD2	10:MC:97:SER:OG	2.31	0.41
3:CK:143:TYR:O	3:CK:146:SER:OG	2.27	0.41
3:DK:47:GLY:O	3:DK:108:GLN:NE2	2.52	0.41
1:NG:935:ILE:HG22	1:NG:942:THR:HG22	2.01	0.41
10:AC:97:PHE:CE2	10:AC:210:MET:HE1	2.53	0.41
8:AD:68:ASP:OD1	8:AD:69:ASN:N	2.53	0.41
2:EH:339:MET:HB2	2:EH:339:MET:HE3	1.80	0.41
9:Ef:244:VAL:HA	9:Ef:245:LYS:HZ1	1.85	0.41
8:FD:58:VAL:O	8:FD:61:VAL:HG12	2.20	0.41
8:FD:109:LEU:HD13	8:FD:109:LEU:HA	1.93	0.41
2:FH:184:SER:OG	2:FH:258:GLY:O	2.37	0.41
9:Ff:208:ILE:HD11	9:Ff:226:ASN:H	1.85	0.41
10:BC:35:LEU:HB3	10:AC:177:TRP:CH2	2.55	0.41
2:GH:112:PHE:CE1	2:WH:126:GLN:HB3	2.56	0.41
4:GL:55:ARG:O	4:GL:59:ARG:HG2	2.20	0.41
4:GL:113:ASP:OD1	4:GL:113:ASP:N	2.47	0.41
4:GL:191:THR:HG22	11:GM:270:SER:HB2	2.03	0.41
8:HD:35:ASP:OD2	8:HD:38:THR:N	2.40	0.41
8:HD:56:ALA:HA	8:HD:59:GLU:HG2	2.02	0.41
3:HK:142:GLU:CD	4:HL:139:ARG:HH12	2.28	0.41
8:ID:69:ASN:H	8:ID:69:ASN:HD22	1.68	0.41
9:IF:241:TYR:HA	9:IF:260:GLN:HE22	1.83	0.41
3:IK:121:SER:OG	3:IK:122:LYS:N	2.54	0.41
3:IK:168:TYR:CE1	3:IK:170:LEU:HB2	2.55	0.41
1:CG:886:LEU:HA	1:CG:899:LEU:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Jg:803:THR:HA	1:Jg:806:THR:HG22	2.02	0.41
2:AH:251:ARG:HH22	2:ZH:236:PRO:HD2	1.85	0.41
10:CC:215:LEU:HD12	10:CC:215:LEU:HA	1.75	0.41
4:KL:133:PHE:CE2	4:KL:185:GLN:HG2	2.55	0.41
8:CD:162:TYR:HB2	10:KC:246:ARG:NH2	2.35	0.41
2:LH:250:TYR:HD2	2:YH:238:MET:HE2	1.85	0.41
3:LK:66:LYS:HA	3:LK:66:LYS:HD2	1.92	0.41
11:LM:154:LYS:HD3	11:LM:154:LYS:HA	1.88	0.41
8:MD:36:ASP:OD1	8:MD:37:ALA:N	2.53	0.41
3:MK:46:ASP:OD1	3:MK:46:ASP:N	2.51	0.41
3:MK:53:ILE:HG13	3:MK:108:GLN:HG2	2.03	0.41
3:MK:134:LEU:O	3:MK:138:ARG:HG3	2.21	0.41
11:MM:144:THR:O	11:MM:145:ARG:NE	2.51	0.41
8:Md:36:ASP:N	8:Md:36:ASP:OD1	2.51	0.41
8:Md:127:SER:HB3	8:Md:130:GLU:CD	2.45	0.41
9:Mf:208:ILE:HD12	9:Mf:225:SER:H	1.86	0.41
2:VH:145:PRO:HG3	2:DH:128:VAL:HG13	2.02	0.41
10:DC:258:SER:HA	10:DC:261:TRP:CD2	2.55	0.41
1:ZG:793:GLU:CD	1:ZG:793:GLU:H	2.27	0.41
11:BM:149:ASN:OD1	11:BM:149:ASN:N	2.51	0.41
11:FM:161:GLY:O	11:FM:182:LYS:HD2	2.20	0.41
11:GM:211:THR:HA	11:GM:230:ARG:O	2.20	0.41
8:BD:51:SER:O	8:BD:54:GLU:HG3	2.19	0.41
10:GC:164:THR:OG1	10:GC:165:LEU:N	2.53	0.41
10:HC:84:LYS:O	10:HC:84:LYS:NZ	2.48	0.41
10:IC:90:ASP:OD1	10:IC:90:ASP:N	2.48	0.41
10:JC:185:TRP:CZ3	10:KC:31:SER:HB2	2.55	0.41
10:KC:256:LEU:H	10:KC:256:LEU:HG	1.40	0.41
8:DD:127:SER:HG	8:DD:130:GLU:CD	2.24	0.41
9:DF:251:GLN:HB2	9:DF:253:ARG:HE	1.85	0.41
4:DL:43:PHE:CE1	4:DL:48:ASN:HB2	2.55	0.41
11:DM:244:LYS:HD3	11:DM:282:TYR:CD2	2.56	0.41
1:OG:965:LEU:HD23	1:OG:1011:VAL:HG23	2.02	0.41
10:AC:191:GLN:O	10:AC:195:ILE:HG12	2.20	0.41
8:ED:105:ARG:HB2	8:ED:153:VAL:HG22	2.02	0.41
1:AG:966:GLN:O	1:AG:970:ASN:ND2	2.53	0.41
2:EH:181:PHE:CE1	2:EH:254:LEU:HD23	2.55	0.41
9:Ef:219:ARG:HG2	9:Ef:233:ARG:HD2	2.02	0.41
8:Fd:104:PHE:CZ	8:Fd:152:GLN:HB3	2.54	0.41
8:GD:31:ASN:OD1	8:GD:32:ASN:N	2.42	0.41
4:GL:210:ASP:OD1	4:GL:210:ASP:N	2.37	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Gd:26:LYS:HB2	8:Gd:26:LYS:HE3	1.78	0.41
2:HH:207:ASP:HB2	2:HH:210:SER:HB3	2.03	0.41
8:ID:77:TYR:OH	3:IK:130:ARG:NH1	2.52	0.41
2:IH:254:LEU:HD23	2:IH:254:LEU:HA	1.91	0.41
1:CG:1006:ILE:CG1	1:DG:968:PHE:HA	2.51	0.41
5:IN:84:CYS:SG	5:IN:85:CYS:N	2.93	0.41
9:If:238:ILE:HG23	9:If:241:TYR:HB2	2.02	0.41
2:JH:183:ASP:OD1	2:JH:186:GLY:N	2.53	0.41
9:Jf:246:LEU:HD21	9:Jf:255:LEU:HD23	2.02	0.41
2:AH:339:MET:HE1	2:AH:345:LEU:HD11	2.03	0.41
8:KD:36:ASP:HA	8:KD:39:ILE:HD12	2.02	0.41
10:CC:240:ILE:CG1	10:DC:131:TYR:HB2	2.49	0.41
4:KL:224:ALA:HA	4:KL:227:ARG:NH1	2.34	0.41
11:KM:191:LEU:HB3	11:KM:212:LEU:HD11	2.01	0.41
8:LD:83:ALA:HA	3:LK:154:ILE:O	2.20	0.41
4:ML:168:PHE:HB2	4:ML:228:ARG:HG2	2.02	0.41
5:MN:52:ASP:O	5:MN:56:GLY:N	2.54	0.41
8:Md:151:SER:O	8:Md:153:VAL:N	2.53	0.41
2:VH:219:LYS:HE3	2:VH:221:TYR:H	1.85	0.41
2:WH:354:MET:HE3	2:WH:354:MET:HB3	1.96	0.41
2:XH:282:HIS:HB3	2:XH:287:VAL:HB	2.02	0.41
11:AM:302:ARG:NH1	11:AM:309:LEU:HD11	2.35	0.41
11:EM:208:LYS:HD3	11:EM:208:LYS:HA	1.90	0.41
11:JM:160:ASN:H	11:JM:180:ASP:N	2.15	0.41
11:JM:179:GLY:C	11:JM:181:PRO:HD3	2.45	0.41
8:BD:162:TYR:OH	10:JC:104:HIS:HA	2.20	0.41
3:BK:93:TRP:HE3	4:BL:46:PRO:HG3	1.85	0.41
4:BL:176:SER:HB2	4:BL:180:LYS:NZ	2.35	0.41
5:BN:85:CYS:N	10:JC:155:ASP:OD2	2.49	0.41
8:Bd:68:ASP:N	8:Bd:68:ASP:OD1	2.52	0.41
10:FC:60:LEU:HD21	10:FC:166:LEU:HD22	2.01	0.41
10:FC:250:ILE:HG13	10:GC:123:GLN:NE2	2.35	0.41
1:GG:903:PHE:CD1	1:GG:912:MET:HE1	2.55	0.41
10:HC:198:ILE:HA	10:HC:201:ILE:HG22	2.01	0.41
10:KC:119:ASN:OD1	10:KC:120:LEU:N	2.53	0.41
10:KC:173:GLU:HA	10:KC:176:ILE:HG12	2.02	0.41
10:MC:156:LYS:NZ	10:MC:158:GLU:HG3	2.36	0.41
8:DD:42:ALA:HB2	8:Dd:41:LEU:HD22	2.02	0.41
11:DM:292:MET:HE1	11:DM:298:VAL:HB	2.01	0.41
1:JG:871:ALA:HB3	1:JG:1037:LEU:HG	2.03	0.41
1:KG:891:THR:OG1	1:KG:892:GLY:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MG:864:LYS:HD3	1:MG:865:THR:N	2.35	0.41
1:MG:1044:ASP:OD1	1:MG:1044:ASP:N	2.53	0.41
1:OG:924:ALA:HB3	1:OG:926:LYS:HZ2	1.85	0.41
1:OG:1001:LEU:O	1:OG:1005:VAL:HG23	2.20	0.41
1:PG:886:LEU:HA	1:PG:899:LEU:O	2.20	0.41
10:AC:122:ASP:OD1	10:AC:122:ASP:N	2.51	0.41
8:Dd:136:ASP:OD2	8:Dd:145:ILE:HG12	2.20	0.41
8:ED:161:ILE:HG23	8:ED:162:TYR:CG	2.55	0.41
3:EK:98:LEU:HD22	3:EK:98:LEU:H	1.86	0.41
4:EL:211:LYS:HE3	4:EL:211:LYS:HB3	1.90	0.41
8:Ed:142:LYS:H	8:Ed:142:LYS:HE2	1.85	0.41
2:FH:187:ALA:HB1	2:FH:262:ASN:HB2	2.01	0.41
2:FH:280:LEU:HB3	2:FH:328:MET:HG3	2.02	0.41
3:FK:66:LYS:HA	3:FK:66:LYS:HD2	1.92	0.41
3:FK:119:TYR:CE2	3:FK:159:LEU:HD12	2.55	0.41
5:FN:86:LEU:HB3	5:FN:87:TRP:HE3	1.83	0.41
10:BC:205:GLU:HG3	10:BC:206:ASP:N	2.34	0.41
3:GK:111:LYS:HD3	3:GK:114:ILE:HD11	2.02	0.41
8:HD:30:ILE:HD11	4:HL:113:ASP:HB3	2.01	0.41
2:HH:233:LEU:HD23	2:HH:233:LEU:HA	1.87	0.41
8:Hd:151:SER:O	8:Hd:153:VAL:N	2.52	0.41
9:IF:241:TYR:HA	9:IF:260:GLN:NE2	2.35	0.41
4:IL:60:VAL:HG12	4:IL:92:GLY:HA3	2.03	0.41
11:IM:246:LEU:O	11:IM:264:SER:HB3	2.20	0.41
2:JH:131:LYS:HG2	2:JH:135:GLU:OE1	2.20	0.41
2:JH:250:TYR:CE2	2:JH:251:ARG:HB2	2.55	0.41
4:JL:59:ARG:HA	4:JL:59:ARG:HD3	1.92	0.41
2:AH:131:LYS:HD2	1:ZG:812:TRP:CH2	2.55	0.41
2:AH:166:PRO:HG3	2:BH:151:PRO:HB2	2.02	0.41
2:KH:167:PRO:HD2	2:KH:239:LEU:HD12	2.00	0.41
4:KL:202:ARG:HB2	4:KL:203:LEU:HD12	2.02	0.41
5:KN:115:GLN:OE1	5:KN:115:GLN:N	2.53	0.41
9:LF:215:VAL:HG13	2:LH:245:GLN:HE22	1.85	0.41
8:CD:70:THR:HG23	8:CD:133:ARG:NH2	2.35	0.41
3:LK:102:ILE:HD13	3:LK:102:ILE:HA	1.95	0.41
11:LM:166:ASN:HA	11:LM:186:SER:HB3	2.01	0.41
8:MD:60:LYS:HE2	8:MD:65:PRO:HD3	2.01	0.41
9:MF:263:LYS:HE2	9:MF:263:LYS:HB2	1.93	0.41
4:ML:91:VAL:HA	4:ML:94:VAL:HG22	2.03	0.41
4:AL:193:LEU:HD13	4:AL:193:LEU:HA	1.91	0.41
2:ZH:105:GLU:O	2:ZH:109:LYS:HE2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:BM:180:ASP:OD1	11:BM:199:LYS:HB2	2.20	0.41
11:BM:235:LEU:HD23	11:BM:255:THR:HG22	2.02	0.41
11:FM:195:ASP:OD1	11:FM:215:ARG:HB2	2.20	0.41
11:JM:298:VAL:C	11:JM:299:LEU:HD22	2.45	0.41
2:BH:183:ASP:C	2:BH:256:VAL:H	2.28	0.41
10:EC:117:LEU:HD13	10:EC:127:ILE:HB	2.01	0.41
10:EC:210:ILE:HD13	10:EC:210:ILE:HA	1.87	0.41
10:GC:247:LEU:HB2	10:HC:124:ILE:HG13	2.01	0.41
10:LC:92:ILE:HG13	10:LC:93:TYR:CD1	2.55	0.41
10:LC:129:ARG:HH22	8:CD:86:ASP:CG	2.28	0.41
10:LC:168:THR:O	10:LC:172:LYS:HG3	2.20	0.41
11:CM:117:ARG:HE	11:CM:117:ARG:HB3	1.70	0.41
11:CM:193:GLN:O	11:CM:194:LEU:HD13	2.20	0.41
1:Dg:820:TYR:CD2	2:DH:205:GLN:HB3	2.56	0.41
1:HG:890:VAL:O	1:HG:895:LYS:HE2	2.21	0.41
1:IG:969:GLY:HA2	1:IG:1005:VAL:HA	2.02	0.41
1:KG:875:THR:HA	1:LG:940:ALA:HB1	2.00	0.41
1:MG:1001:LEU:O	1:MG:1005:VAL:HG23	2.21	0.41
8:AD:37:ALA:O	8:AD:41:LEU:HG	2.20	0.41
3:EK:186:ARG:NH2	5:EN:65:TYR:HB2	2.34	0.41
4:EL:94:VAL:HA	4:EL:97:ILE:HG12	2.02	0.41
8:FD:108:VAL:O	8:FD:109:LEU:HD22	2.20	0.41
9:FF:252:GLY:HA3	9:FF:264:PHE:CE1	2.54	0.41
3:FK:47:GLY:O	3:FK:108:GLN:NE2	2.51	0.41
3:FK:148:GLY:N	8:Fd:30:ILE:HD13	2.36	0.41
8:Fd:74:PRO:HD2	8:Fd:129:ALA:HB1	2.01	0.41
9:Ff:210:TYR:HA	9:Ff:224:GLY:HA2	2.03	0.41
2:GH:215:ILE:HD13	2:GH:215:ILE:HA	1.91	0.41
2:GH:230:LEU:HB2	2:GH:233:LEU:HB2	2.02	0.41
2:GH:320:LEU:N	2:GH:346:LEU:O	2.44	0.41
3:GK:57:MET:HE2	3:GK:57:MET:HB3	1.89	0.41
4:GL:54:ARG:NH2	4:GL:56:ALA:HB3	2.36	0.41
4:GL:186:ALA:HB1	4:GL:205:ALA:HB1	2.02	0.41
8:HD:94:LEU:HD12	8:HD:94:LEU:HA	1.95	0.41
2:HH:111:ALA:HA	2:HH:114:ASP:OD2	2.20	0.41
8:Hd:87:TRP:O	8:Hd:120:SER:HA	2.21	0.41
8:Hd:93:GLU:OE2	10:DC:263:ALA:N	2.42	0.41
8:ID:26:LYS:HG3	4:IL:110:GLN:NE2	2.35	0.41
2:IH:125:GLU:C	2:IH:129:LYS:HZ2	2.28	0.41
2:IH:151:PRO:HB2	2:XH:166:PRO:HG3	2.01	0.41
2:IH:253:ASP:OD1	2:IH:253:ASP:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:IL:176:SER:HA	4:IL:179:ARG:HG2	2.02	0.41
11:IM:141:GLU:HB3	11:IM:160:ASN:O	2.20	0.41
8:Id:57:LYS:HE2	8:Id:57:LYS:HB2	1.94	0.41
2:JH:168:VAL:HA	2:JH:240:THR:HG23	2.03	0.41
2:JH:245:GLN:HE21	2:JH:245:GLN:HB2	1.74	0.41
9:KF:233:ARG:NH2	9:YF:266:GLN:OE1	2.53	0.41
3:KK:152:ARG:HD2	2:LH:352:LYS:HB2	2.01	0.41
4:KL:109:LEU:HD12	4:KL:109:LEU:HA	1.86	0.41
1:DG:924:ALA:HB3	1:DG:926:LYS:NZ	2.35	0.41
9:Kf:209:ILE:HD12	9:Kf:209:ILE:HA	1.93	0.41
8:LD:91:ILE:O	8:LD:95:THR:OG1	2.35	0.41
8:LD:93:GLU:CD	8:LD:93:GLU:H	2.27	0.41
4:LL:54:ARG:HE	4:LL:57:VAL:HG13	1.86	0.41
9:Lf:212:ILE:HG13	9:Lf:262:ILE:HG12	2.03	0.41
1:Mg:797:ARG:HA	1:Mg:797:ARG:HD2	1.86	0.41
2:MH:106:VAL:HG23	2:MH:107:ILE:HD12	2.01	0.41
2:MH:151:PRO:HA	2:MH:248:VAL:HG23	2.02	0.41
2:MH:280:LEU:HD12	2:MH:280:LEU:HA	1.93	0.41
7:MX:20:UNK:O	7:MX:37:UNK:N	2.54	0.41
2:VH:189:TRP:O	2:VH:211:ASN:ND2	2.53	0.41
9:WF:210:TYR:CD2	9:WF:238:ILE:HD11	2.56	0.41
2:XH:317:LEU:HD22	2:XH:349:TRP:HB2	2.02	0.41
10:DC:198:ILE:HA	10:DC:201:ILE:HG22	2.03	0.41
1:ZG:801:MET:HE3	2:BH:115:MET:HE3	2.01	0.41
1:FG:865:THR:OG1	1:FG:1044:ASP:OD2	2.35	0.41
11:BM:146:LEU:HD13	11:BM:146:LEU:HA	1.90	0.41
11:BM:170:SER:HB3	11:BM:189:VAL:HG22	2.01	0.41
11:EM:205:TYR:HD1	11:EM:205:TYR:HA	1.63	0.41
11:GM:193:GLN:HG2	11:GM:213:THR:HB	2.03	0.41
11:JM:194:LEU:HD23	11:JM:194:LEU:HA	1.84	0.41
8:BD:119:ILE:HD13	8:BD:119:ILE:HA	1.92	0.41
4:BL:94:VAL:HA	4:BL:97:ILE:HG12	2.02	0.41
10:FC:227:VAL:HB	10:FC:250:ILE:HG22	2.02	0.41
10:GC:121:ASP:N	10:GC:124:SER:OG	2.52	0.41
10:GC:214:LYS:HA	10:GC:214:LYS:HD3	1.85	0.41
10:IC:87:ARG:NH2	8:AD:122:SER:HB2	2.35	0.41
10:JC:80:ILE:HD11	10:JC:196:LEU:HD22	2.02	0.41
4:CL:193:LEU:HD13	4:CL:193:LEU:HA	1.91	0.41
11:CM:274:THR:HA	11:CM:293:ALA:HB3	2.02	0.41
11:DM:244:LYS:HE3	11:DM:245:TYR:CE2	2.55	0.41
8:Dd:112:SER:HA	8:Dd:158:TYR:CE2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AD:68:ASP:OD1	8:AD:70:THR:N	2.44	0.41
8:FD:118:LEU:O	10:AC:98:ASN:ND2	2.52	0.41
9:FF:253:ARG:NH2	9:FF:263:LYS:HB3	2.36	0.41
3:FK:38:VAL:N	3:FK:39:PRO:HD2	2.36	0.41
4:FL:57:VAL:HA	4:FL:60:VAL:HG22	2.02	0.41
10:BC:80:ILE:HD11	10:BC:196:LEU:HD22	2.02	0.41
3:GK:152:ARG:C	3:GK:153:ILE:HD12	2.45	0.41
4:GL:121:ASP:OD1	4:GL:122:THR:N	2.51	0.41
3:HK:66:LYS:NZ	3:HK:67:VAL:H	2.19	0.41
3:IK:99:LEU:HB3	3:IK:143:TYR:CE2	2.56	0.41
11:IM:196:MET:HE2	11:IM:196:MET:HA	2.01	0.41
8:Id:107:ARG:O	8:Id:155:GLU:HA	2.21	0.41
9:If:219:ARG:HA	9:If:232:VAL:O	2.20	0.41
8:JD:98:ILE:HG21	8:JD:132:LEU:HD21	2.03	0.41
3:JK:157:GLN:OE1	3:JK:158:GLY:N	2.53	0.41
8:Jd:128:LEU:HA	8:Jd:131:ILE:HB	2.02	0.41
2:AH:150:LYS:H	2:AH:247:ALA:HA	1.85	0.41
10:CC:95:ASP:OD1	10:CC:98:SER:N	2.41	0.41
10:CC:101:LEU:HD23	10:CC:101:LEU:HA	1.93	0.41
2:KH:309:GLU:OE1	2:KH:309:GLU:N	2.54	0.41
11:KM:150:ILE:HG22	11:KM:152:LEU:HD22	2.01	0.41
8:Kd:98:ILE:HG21	8:Kd:132:LEU:HD21	2.02	0.41
1:Lg:815:VAL:HG23	2:LH:218:THR:HG22	2.02	0.41
3:LK:168:TYR:CE1	3:LK:170:LEU:HB2	2.55	0.41
3:AK:66:LYS:HB3	3:AK:77:SER:HB3	2.03	0.41
3:AK:132:LEU:O	3:AK:136:ARG:HG3	2.21	0.41
8:MD:160:LYS:HA	8:MD:160:LYS:HD2	1.85	0.41
2:VH:183:ASP:OD1	2:VH:186:GLY:N	2.53	0.41
1:WG:792:GLN:HA	1:WG:795:GLN:NE2	2.35	0.41
2:YH:170:ARG:HG3	2:YH:245:GLN:HG3	2.02	0.41
10:DC:189:GLN:O	10:DC:193:ILE:HG12	2.21	0.41
1:FG:939:THR:HG22	1:FG:941:ARG:HG3	2.01	0.41
11:BM:195:ASP:HB3	11:BM:197:TYR:HE1	1.86	0.41
11:EM:177:LEU:HD12	11:EM:196:MET:HE1	2.02	0.41
11:GM:301:MET:HE3	11:GM:301:MET:HB3	1.98	0.41
5:AN:97:SER:OG	1:KG:923:GLY:HA2	2.20	0.41
8:BD:31:ASN:OD1	8:BD:31:ASN:N	2.54	0.41
2:BH:311:MET:SD	2:BH:341:LYS:HA	2.61	0.41
10:GC:139:HIS:ND1	10:GC:140:PHE:O	2.37	0.41
10:GC:209:MET:HE2	10:GC:209:MET:HB2	1.95	0.41
1:GG:898:LYS:HZ2	1:HG:864:LYS:CE	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:HC:178:TYR:HA	10:HC:181:ARG:HG2	2.03	0.41
10:JC:61:LYS:HE3	10:JC:61:LYS:HB3	1.90	0.41
10:JC:94:ILE:HG13	10:JC:95:TYR:CD2	2.55	0.41
10:LC:147:ARG:HG3	5:DN:87:TRP:CZ3	2.55	0.41
2:CH:201:SER:HA	2:CH:218:THR:HB	2.03	0.41
4:CL:155:LEU:HD22	4:CL:155:LEU:HA	1.89	0.41
8:Cd:92:GLU:H	8:Cd:92:GLU:CD	2.25	0.41
1:IG:961:ALA:O	1:IG:965:LEU:HD13	2.20	0.41
1:JG:874:ASP:O	1:JG:1033:SER:HB2	2.21	0.41
1:JG:969:GLY:O	1:JG:1005:VAL:HG13	2.20	0.41
1:NG:886:LEU:HB3	1:NG:900:ILE:HG22	2.01	0.41
9:Df:234:GLU:H	9:Df:234:GLU:CD	2.29	0.41
1:AG:911:LYS:NZ	1:AG:913:VAL:HB	2.35	0.41
3:EK:56:MET:HE2	3:EK:56:MET:HB3	1.92	0.41
4:EL:221:HIS:HB3	5:DN:65:TYR:OH	2.21	0.41
8:Ed:73:ILE:HD12	8:Ed:129:ALA:HB1	2.01	0.41
8:Fd:115:VAL:HA	8:Fd:116:PRO:HD3	1.94	0.41
10:BC:221:MET:HA	10:BC:257:ASN:HD21	1.85	0.41
5:GN:76:MET:O	5:GN:78:LEU:HD12	2.20	0.41
2:IH:185:THR:HB	2:IH:265:SER:OG	2.21	0.41
11:IM:257:ASP:HA	11:IM:275:ASP:O	2.20	0.41
5:IN:77:ASP:HA	2:JH:354:MET:SD	2.61	0.41
2:JH:115:MET:HE2	2:JH:115:MET:HB2	1.94	0.41
2:JH:135:GLU:HA	2:JH:138:GLU:OE2	2.20	0.41
2:JH:171:LEU:HB2	2:JH:243:PRO:HB3	2.03	0.41
8:Jd:94:LEU:O	8:Jd:98:ILE:HG12	2.20	0.41
2:AH:125:GLU:OE1	2:AH:125:GLU:N	2.39	0.41
1:Kg:797:ARG:HD2	1:Kg:797:ARG:HA	1.87	0.41
4:KL:43:PHE:CE1	4:KL:48:ASN:HB2	2.56	0.41
11:KM:254:LYS:HG3	11:KM:272:LEU:HD23	2.01	0.41
1:DG:969:GLY:CA	1:DG:1009:ALA:HB2	2.49	0.41
8:LD:24:LYS:HE3	8:LD:24:LYS:HB2	1.92	0.41
9:Lf:209:ILE:HD12	9:Lf:209:ILE:HA	1.92	0.41
8:MD:27:LYS:HA	8:MD:27:LYS:HD2	1.82	0.41
11:MM:212:LEU:HD13	11:MM:212:LEU:HA	1.96	0.41
2:VH:207:ASP:OD2	2:VH:209:THR:OG1	2.38	0.41
4:AL:54:ARG:NH2	4:AL:57:VAL:HG23	2.33	0.41
2:YH:181:PHE:HA	2:YH:254:LEU:HG	2.03	0.41
10:DC:195:GLU:HA	10:DC:198:ILE:HG22	2.03	0.41
11:AM:262:GLU:HB2	11:AM:282:TYR:HE1	1.85	0.41
11:AM:299:LEU:HD13	11:AM:299:LEU:HA	1.93	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:FM:306:GLN:HB3	11:FM:309:LEU:HB2	2.02	0.41
11:JM:257:ASP:HA	11:JM:275:ASP:O	2.21	0.41
2:BH:140:ALA:HB2	2:CH:124:PRO:HB3	2.03	0.41
10:EC:93:ILE:HG23	10:EC:94:TYR:HD1	1.85	0.41
1:GG:1025:THR:HA	1:GG:1026:PRO:HD3	1.93	0.41
10:IC:105:LEU:HD12	10:IC:106:PRO:HD2	2.03	0.41
10:JC:122:ASP:N	10:JC:122:ASP:OD1	2.54	0.41
2:CH:157:PHE:HD1	2:CH:255:ARG:HB2	1.85	0.41
8:DD:91:ILE:O	8:DD:95:THR:HG22	2.21	0.41
1:KG:882:PRO:HA	1:KG:903:PHE:CE2	2.56	0.41
1:MG:898:LYS:HE2	1:MG:898:LYS:HB2	1.83	0.41
1:NG:1007:GLY:O	1:NG:1011:VAL:HG22	2.21	0.41
10:AC:51:LYS:O	10:AC:55:ILE:HG13	2.21	0.41
8:Dd:93:GLU:O	8:Dd:97:ARG:HG2	2.20	0.41
1:AG:966:GLN:HG2	1:AG:1012:GLY:HA3	2.03	0.41
8:Ed:35:ASP:O	8:Ed:38:THR:OG1	2.38	0.41
8:Ed:80:GLN:OE1	8:Ed:80:GLN:N	2.53	0.41
3:FK:98:LEU:HD13	3:FK:98:LEU:HA	1.94	0.41
4:FL:187:GLU:OE2	11:FM:268:HIS:ND1	2.54	0.41
10:BC:249:ARG:HH21	2:HH:273:PRO:HD3	1.86	0.41
2:GH:198:ASP:HA	1:Hg:816:GLU:HG3	2.02	0.41
3:GK:123:TYR:CD2	3:GK:124:VAL:HG23	2.56	0.41
3:GK:152:ARG:HD2	2:HH:352:LYS:HB2	2.01	0.41
1:BG:1024:ASN:OD1	1:BG:1024:ASN:N	2.49	0.41
2:HH:112:PHE:HA	1:WG:797:ARG:HH22	1.85	0.41
2:IH:153:ALA:HB1	2:IH:251:ARG:HB3	2.02	0.41
4:IL:118:GLU:OE2	4:IL:123:ARG:NH2	2.54	0.41
8:Id:48:VAL:HG11	10:DC:92:ILE:HD13	2.03	0.41
5:JN:95:LEU:HD23	5:JN:95:LEU:H	1.85	0.41
2:AH:157:PHE:HA	2:AH:255:ARG:HB2	2.03	0.41
10:CC:230:ASP:OD1	10:CC:245:ARG:HG3	2.20	0.41
4:KL:155:LEU:HD22	4:KL:155:LEU:HA	1.82	0.41
11:KM:273:ALA:HB2	11:KM:279:ILE:HD11	2.02	0.41
11:MM:224:LEU:HB2	11:MM:246:LEU:HD12	2.02	0.41
1:EG:1014:ALA:HB1	1:FG:959:LEU:HD21	2.02	0.41
2:VH:150:LYS:N	2:VH:247:ALA:HA	2.36	0.41
2:VH:226:LEU:HD23	2:VH:241:LEU:HD22	2.03	0.41
2:XH:183:ASP:HB2	2:XH:260:GLY:H	1.86	0.41
4:AL:224:ALA:HA	4:AL:227:ARG:NH1	2.36	0.41
11:AM:114:ASN:O	11:AM:134:LEU:HA	2.21	0.41
11:BM:257:ASP:OD1	11:BM:257:ASP:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:FM:231:LEU:HD11	11:FM:233:VAL:HG13	2.02	0.41
2:BH:238:MET:H	2:BH:238:MET:HG2	1.76	0.41
3:BK:111:LYS:HG3	3:BK:114:ILE:HD11	2.02	0.41
4:BL:59:ARG:HD2	4:BL:59:ARG:HA	1.86	0.41
1:GG:876:SER:O	1:HG:941:ARG:HA	2.21	0.41
1:GG:973:GLN:O	1:GG:976:ASN:ND2	2.53	0.41
1:GG:1006:ILE:HG12	1:HG:968:PHE:HA	2.01	0.41
10:KC:95:TYR:HD1	10:KC:95:TYR:HA	1.75	0.41
10:MC:114:ASN:N	10:MC:128:ASP:O	2.28	0.41
2:CH:319:ILE:HG22	2:CH:347:VAL:HG12	2.03	0.41
3:CK:84:PHE:CE2	3:CK:136:ARG:HD3	2.56	0.41
4:CL:44:HIS:HB2	4:CL:48:ASN:HA	2.02	0.41
9:Cf:210:TYR:HD2	9:Cf:224:GLY:HA2	1.86	0.41
11:DM:145:ARG:NE	11:DM:164:GLN:HB3	2.36	0.41
1:IG:969:GLY:HA3	1:IG:1009:ALA:N	2.36	0.41
1:KG:1032:TYR:HA	1:LG:941:ARG:NH2	2.36	0.41
1:MG:886:LEU:HA	1:MG:899:LEU:O	2.21	0.41
1:MG:1006:ILE:HG12	1:NG:967:GLY:O	2.21	0.41
1:NG:944:LEU:HA	1:NG:944:LEU:HD22	1.87	0.41
1:NG:961:ALA:O	1:NG:965:LEU:HD13	2.21	0.41
1:OG:1006:ILE:HD13	1:PG:968:PHE:HA	2.02	0.41
10:AC:46:ALA:O	10:AC:49:LYS:HG2	2.20	0.41
8:Dd:127:SER:HB3	8:Dd:130:GLU:OE1	2.20	0.41
8:AD:36:ASP:OD1	8:AD:36:ASP:N	2.54	0.41
8:AD:92:GLU:OE1	8:AD:92:GLU:N	2.51	0.41
1:Eg:797:ARG:O	1:Eg:797:ARG:NE	2.48	0.41
1:Eg:800:ASP:OD1	1:Eg:801:MET:N	2.53	0.41
1:AG:968:PHE:CG	1:AG:1008:LEU:HD13	2.55	0.41
1:AG:972:PHE:HB3	1:AG:1005:VAL:CG2	2.51	0.41
2:EH:264:LYS:HA	2:EH:266:MET:HE1	2.01	0.41
4:EL:148:LEU:H	4:EL:148:LEU:HD12	1.86	0.41
4:EL:187:GLU:OE1	11:EM:268:HIS:ND1	2.54	0.41
4:EL:216:ASP:H	3:DK:72:GLN:NE2	2.19	0.41
9:Ef:233:ARG:HE	9:Ef:233:ARG:HB3	1.68	0.41
2:FH:123:ASN:HB3	2:FH:125:GLU:OE1	2.21	0.41
2:FH:280:LEU:HD23	2:FH:280:LEU:HA	1.80	0.41
3:FK:134:LEU:O	3:FK:138:ARG:HG3	2.21	0.41
8:Fd:41:LEU:HD13	8:Fd:41:LEU:HA	1.84	0.41
8:GD:62:ILE:HD12	8:GD:62:ILE:HA	1.88	0.41
9:GF:207:ARG:NH1	9:GF:240:GLY:O	2.53	0.41
2:GH:184:SER:HB2	2:GH:259:TYR:CE2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:GK:120:SER:N	3:GK:160:GLY:O	2.33	0.41
3:GK:143:TYR:O	3:GK:146:SER:OG	2.26	0.41
1:BG:967:GLY:HA2	1:BG:970:ASN:HD21	1.86	0.41
4:GL:177:HIS:CE1	4:GL:181:LEU:HD12	2.56	0.41
4:GL:216:ASP:OD1	4:GL:218:ALA:N	2.38	0.41
4:GL:224:ALA:HA	4:GL:227:ARG:NH1	2.36	0.41
3:HK:117:THR:OG1	3:HK:181:GLU:OE2	2.26	0.41
3:HK:151:SER:OG	3:HK:152:ARG:N	2.53	0.41
4:HL:141:ASN:CG	4:HL:143:ILE:H	2.28	0.41
11:HM:275:ASP:HA	11:HM:296:GLY:H	1.86	0.41
5:HN:103:CYS:N	5:HN:107:TYR:O	2.45	0.41
1:Ig:800:ASP:N	1:Ig:800:ASP:OD1	2.53	0.41
2:IH:117:ARG:HH22	2:IH:108:ASP:CG	2.28	0.41
2:IH:135:GLU:O	2:IH:138:GLU:HG2	2.20	0.41
3:IK:40:LYS:HE2	3:IK:40:LYS:HB2	1.86	0.41
3:IK:123:TYR:CD2	3:IK:124:VAL:HG23	2.55	0.41
11:IM:158:VAL:HA	11:IM:178:LYS:HE2	2.03	0.41
11:IM:177:LEU:HD12	11:IM:196:MET:HE1	2.03	0.41
11:IM:206:TRP:CZ3	9:If:221:TRP:HB2	2.56	0.41
1:CG:874:ASP:OD1	1:CG:874:ASP:N	2.52	0.41
1:CG:910:ASP:OD1	1:CG:910:ASP:N	2.47	0.41
1:Jg:794:ILE:O	1:Jg:798:THR:N	2.54	0.41
3:JK:143:TYR:O	3:JK:147:GLN:HG2	2.21	0.41
5:JN:76:MET:HB3	5:JN:78:LEU:HD23	2.01	0.41
5:JN:113:SER:OG	5:JN:114:LEU:N	2.54	0.41
9:Jf:216:ILE:HD12	9:Jf:216:ILE:HA	1.91	0.41
1:DG:970:ASN:OD1	1:DG:971:ALA:N	2.54	0.41
2:LH:210:SER:HB2	2:YH:229:ARG:HH22	1.86	0.41
11:LM:135:ASP:OD1	11:LM:136:LEU:N	2.54	0.41
8:Ld:36:ASP:O	8:Ld:39:ILE:HG12	2.21	0.41
8:Ld:106:PHE:CZ	8:Ld:108:VAL:HG13	2.56	0.41
8:Ld:127:SER:HB3	8:Ld:130:GLU:OE2	2.21	0.41
9:Lf:210:TYR:HB3	9:Lf:222:LEU:HD12	2.03	0.41
2:MH:200:SER:HB3	1:ZG:816:GLU:CD	2.45	0.41
3:MK:80:ALA:HB1	3:MK:136:ARG:HH12	1.85	0.41
3:MK:168:TYR:CE2	3:MK:170:LEU:HB3	2.56	0.41
11:MM:209:SER:OG	11:MM:210:ASP:N	2.52	0.41
11:MM:214:ILE:C	11:MM:215:ARG:HD2	2.46	0.41
11:MM:298:VAL:O	11:MM:299:LEU:HD13	2.21	0.41
1:EG:911:LYS:HB2	1:EG:943:ALA:HA	2.03	0.41
1:EG:944:LEU:HD13	1:EG:945:ALA:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:VH:112:PHE:CE1	2:CH:126:GLN:HB3	2.55	0.41
2:VH:330:SER:OG	2:VH:332:ASP:OD1	2.32	0.41
2:WH:329:THR:HB	2:WH:335:HIS:CE1	2.55	0.41
1:YG:820:TYR:CZ	1:YG:822:GLU:HG2	2.56	0.41
2:YH:168:VAL:HG13	2:YH:240:THR:HG23	2.03	0.41
1:FG:899:LEU:HB2	1:FG:919:MET:HG2	2.02	0.41
11:AM:255:THR:HG21	11:AM:279:ILE:HD11	2.03	0.41
11:AM:302:ARG:HH11	11:AM:309:LEU:HD11	1.85	0.41
11:JM:183:VAL:HG23	11:JM:202:LEU:HA	2.02	0.41
11:JM:256:HIS:O	11:JM:277:SER:OG	2.34	0.41
11:JM:303:GLU:C	11:JM:305:GLY:H	2.28	0.41
5:AN:96:ASN:OD1	5:AN:98:SER:OG	2.28	0.41
9:BF:250:LEU:HD13	9:BF:251:GLN:HG3	2.03	0.41
2:BH:133:ILE:HD12	2:BH:133:ILE:HA	1.93	0.41
8:Bd:24:LYS:HG2	8:Bd:25:PHE:CD1	2.56	0.41
10:EC:228:HIS:HA	10:EC:246:VAL:O	2.21	0.41
10:FC:50:GLN:HG3	10:FC:54:LYS:NZ	2.35	0.41
10:FC:60:LEU:HD11	10:FC:166:LEU:HD22	2.03	0.41
10:FC:231:ASP:OD1	10:FC:231:ASP:N	2.54	0.41
10:IC:106:PRO:HB3	10:IC:211:TYR:CE2	2.56	0.41
10:IC:235:ASP:CG	10:IC:237:SER:H	2.29	0.41
10:JC:243:ILE:HG13	10:KC:131:ARG:HB2	2.02	0.41
10:KC:90:ASN:O	10:KC:94:ILE:HG23	2.20	0.41
10:KC:170:THR:O	10:KC:173:GLU:HG2	2.21	0.41
10:LC:62:ALA:HA	10:LC:65:VAL:HG22	2.02	0.41
10:LC:165:LEU:O	10:LC:167:LYS:NZ	2.47	0.41
10:LC:241:ILE:HG12	10:MC:129:ARG:O	2.21	0.41
11:CM:206:TRP:HB3	11:CM:208:LYS:NZ	2.35	0.41
8:Cd:32:ASN:HA	8:Cd:33:PRO:HD3	1.95	0.41
2:DH:306:LEU:HD11	2:DH:309:GLU:HA	2.02	0.41
3:DK:55:LYS:HB3	3:DK:55:LYS:HE2	1.81	0.41
3:DK:92:ASN:OD1	3:DK:92:ASN:N	2.54	0.41
1:HG:1025:THR:HA	1:HG:1026:PRO:HD3	1.94	0.41
1:IG:876:SER:OG	1:IG:1031:VAL:O	2.25	0.41
1:IG:970:ASN:OD1	1:IG:971:ALA:N	2.54	0.41
1:KG:899:LEU:HD21	1:KG:916:PHE:HB3	2.01	0.41
1:MG:949:ASN:HA	1:MG:952:TYR:CE2	2.55	0.41
1:OG:899:LEU:HD11	1:OG:916:PHE:HB3	2.03	0.41
1:PG:882:PRO:HA	1:PG:903:PHE:CE2	2.56	0.41
1:PG:962:SER:HG	1:PG:1015:TRP:CG	2.39	0.41
1:PG:1019:ALA:HA	1:PG:1022:LEU:HG	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:AC:91:LEU:HA	10:AC:94:ILE:HG22	2.02	0.41
8:AD:51:SER:O	8:AD:54:GLU:HG3	2.20	0.41
1:AG:865:THR:HG21	1:PG:927:THR:HG21	2.02	0.41
2:FH:340:GLN:OE1	2:FH:340:GLN:N	2.54	0.41
4:FL:190:MET:HG3	4:FL:191:THR:N	2.35	0.41
2:GH:126:GLN:O	2:GH:130:LEU:HG	2.21	0.41
1:BG:863:ILE:HB	1:BG:1045:VAL:HG22	2.03	0.41
1:Hg:798:THR:O	1:Hg:802:LEU:HG	2.20	0.41
1:CG:969:GLY:HA2	1:CG:1005:VAL:HA	2.03	0.41
5:IN:62:ASN:OD1	5:IN:62:ASN:N	2.54	0.41
8:Id:87:TRP:CD1	8:Id:94:LEU:HD22	2.56	0.41
4:JL:181:LEU:O	4:JL:185:GLN:HG3	2.21	0.41
3:KK:83:LEU:HD12	3:KK:84:PHE:CZ	2.56	0.41
5:KN:76:MET:HE2	2:LH:299:GLY:HA2	2.02	0.41
11:LM:298:VAL:C	11:LM:299:LEU:HD22	2.45	0.41
1:Mg:793:GLU:OE1	1:Mg:793:GLU:N	2.54	0.41
2:VH:229:ARG:HG2	2:VH:236:PRO:HB3	2.03	0.41
2:VH:278:ASP:N	2:VH:278:ASP:OD1	2.53	0.41
9:WF:264:PHE:HB2	2:WH:246:LYS:HZ2	1.86	0.41
1:XG:793:GLU:H	1:XG:793:GLU:CD	2.29	0.41
9:YF:209:ILE:O	9:YF:225:SER:N	2.54	0.41
4:AL:130:ASP:OD1	4:AL:130:ASP:N	2.54	0.41
11:BM:299:LEU:HD13	11:BM:299:LEU:HA	1.92	0.41
11:JM:306:GLN:HE21	11:JM:308:ASP:H	1.69	0.41
8:Ad:111:LYS:HB2	8:Ad:111:LYS:HE2	1.80	0.41
8:Ad:142:LYS:HB2	8:Ad:142:LYS:HE2	1.81	0.41
8:BD:119:ILE:HG23	8:BD:138:GLN:CD	2.46	0.41
2:BH:107:ILE:HA	2:BH:110:LYS:HG2	2.03	0.41
3:BK:38:VAL:N	3:BK:39:PRO:HD2	2.36	0.41
8:Bd:85:VAL:HG12	10:KC:267:VAL:HA	2.03	0.41
10:GC:75:ARG:HB2	10:GC:188:ILE:HG12	2.03	0.41
10:GC:146:THR:OG1	10:GC:147:TRP:N	2.54	0.41
10:HC:165:LEU:HD13	10:HC:166:PRO:HD2	2.02	0.41
10:KC:149:ARG:HB3	10:KC:149:ARG:NH1	2.35	0.41
10:LC:63:LEU:HD22	10:LC:178:TYR:HB3	2.02	0.41
10:MC:107:PRO:HD3	10:MC:137:ALA:HB2	2.02	0.41
10:MC:169:LYS:HA	10:MC:169:LYS:HD3	1.95	0.41
2:CH:325:LEU:HD13	2:CH:339:MET:HA	2.02	0.41
8:DD:161:ILE:HG13	8:DD:162:TYR:CE2	2.56	0.41
4:DL:44:HIS:N	4:DL:48:ASN:OD1	2.54	0.41
5:DN:66:SER:OG	5:DN:67:THR:N	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JG:930:ILE:HA	1:JG:1043:GLN:NE2	2.36	0.41
1:KG:949:ASN:HA	1:KG:952:TYR:CE2	2.55	0.41
1:NG:869:MET:HG2	1:NG:870:PHE:H	1.86	0.41
1:NG:899:LEU:HB2	1:NG:919:MET:SD	2.61	0.41
1:NG:1006:ILE:CG1	1:OG:968:PHE:HA	2.49	0.41
1:OG:1006:ILE:CG1	1:PG:968:PHE:HA	2.51	0.41
8:Dd:151:SER:O	8:Dd:153:VAL:N	2.54	0.41
8:AD:35:ASP:O	8:AD:38:THR:OG1	2.32	0.41
8:ED:92:GLU:OE1	8:ED:92:GLU:N	2.54	0.41
1:AG:872:VAL:HA	1:AG:1036:GLY:HA2	2.03	0.40
4:EL:139:ARG:HD2	11:EM:319:PHE:HD2	1.86	0.40
4:FL:58:LYS:HD2	4:FL:59:ARG:HG2	2.03	0.40
8:Fd:82:ARG:HA	8:Fd:82:ARG:NH1	2.36	0.40
10:BC:48:LYS:O	10:BC:52:MET:HG3	2.20	0.40
9:AF:250:LEU:HD13	9:AF:251:GLN:HG3	2.03	0.40
3:GK:121:SER:OG	3:GK:122:LYS:N	2.54	0.40
8:Gd:109:LEU:HB2	8:Gd:155:GLU:OE2	2.21	0.40
8:Gd:111:LYS:HE3	8:Gd:111:LYS:HB3	1.95	0.40
2:HH:115:MET:HB2	1:WG:798:THR:HG23	2.03	0.40
3:HK:65:ILE:HG23	3:HK:78:ILE:HG12	2.02	0.40
3:HK:99:LEU:HA	3:HK:102:ILE:HG22	2.03	0.40
11:HM:238:PHE:N	11:HM:258:LYS:O	2.54	0.40
8:ID:107:ARG:HE	8:ID:155:GLU:HG2	1.85	0.40
3:IK:72:GLN:HB3	3:IK:185:ARG:HG3	2.03	0.40
11:IM:205:TYR:HD1	11:IM:205:TYR:HA	1.71	0.40
1:CG:878:ASN:OD1	1:CG:879:SER:N	2.54	0.40
1:CG:880:ASP:CG	1:CG:881:GLU:HG2	2.47	0.40
5:IN:45:MET:HB3	5:IN:62:ASN:OD1	2.21	0.40
8:JD:107:ARG:HH22	8:Jd:73:ILE:HD11	1.86	0.40
2:JH:340:GLN:NE2	2:JH:341:LYS:HG2	2.36	0.40
4:JL:187:GLU:O	4:JL:190:MET:HG3	2.21	0.40
9:KF:209:ILE:H	9:KF:225:SER:HB3	1.86	0.40
1:DG:965:LEU:HG	1:DG:1008:LEU:HD23	2.03	0.40
9:Kf:214:ALA:O	9:Kf:221:TRP:N	2.53	0.40
2:LH:328:MET:SD	10:GC:116:THR:HA	2.61	0.40
4:LL:105:ILE:O	4:LL:109:LEU:HD22	2.21	0.40
4:LL:134:MET:HE2	4:LL:134:MET:HB2	1.95	0.40
2:MH:283:VAL:O	2:MH:314:ARG:HD2	2.20	0.40
3:MK:40:LYS:HE2	3:MK:40:LYS:HB2	1.72	0.40
3:MK:75:LEU:HG	3:MK:76:ILE:N	2.35	0.40
3:MK:117:THR:OG1	3:MK:181:GLU:OE2	2.26	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:MM:173:LEU:HB3	11:MM:191:LEU:HD12	2.03	0.40
7:MX:70:UNK:H2	2:ZH:146:GLY:H	1.69	0.40
2:XH:190:PRO:HB2	2:XH:231:ARG:NH1	2.36	0.40
10:DC:149:TYR:O	10:DC:197:ASN:ND2	2.54	0.40
9:ZF:253:ARG:NH2	9:ZF:255:LEU:HD21	2.36	0.40
11:FM:212:LEU:HD13	11:FM:212:LEU:HA	1.90	0.40
8:Ad:60:LYS:NZ	8:AD:137:TYR:HA	2.36	0.40
4:BL:114:ILE:HG23	4:BL:127:ILE:HD11	2.03	0.40
4:BL:193:LEU:HD13	4:BL:193:LEU:HA	1.96	0.40
10:EC:240:ILE:HD11	10:FC:133:TYR:HB2	2.02	0.40
10:GC:68:ALA:HA	10:GC:183:GLY:O	2.21	0.40
10:JC:65:LEU:HD22	10:JC:180:TYR:HB3	2.04	0.40
10:LC:70:GLY:HA2	10:LC:183:TRP:HD1	1.86	0.40
10:MC:180:GLU:O	10:MC:183:TRP:HD1	2.04	0.40
8:Cd:109:LEU:HB2	8:Cd:155:GLU:OE2	2.22	0.40
2:DH:202:PHE:HA	2:DH:217:ALA:HA	2.02	0.40
4:DL:216:ASP:OD2	4:DL:219:ILE:N	2.54	0.40
1:HG:966:GLN:O	1:HG:970:ASN:ND2	2.54	0.40
1:MG:903:PHE:CD1	1:MG:912:MET:HE1	2.56	0.40
1:NG:876:SER:HB2	1:NG:1033:SER:HB3	2.03	0.40
1:NG:1044:ASP:N	1:NG:1044:ASP:OD1	2.53	0.40
1:OG:1006:ILE:HG12	1:PG:967:GLY:O	2.21	0.40
1:PG:891:THR:OG1	1:PG:892:GLY:N	2.54	0.40
10:AC:83:GLN:O	10:AC:86:LYS:HB3	2.21	0.40
1:AG:1033:SER:HB2	1:BG:940:ALA:HB3	2.02	0.40
10:BC:151:TYR:CG	10:BC:203:ILE:HD13	2.56	0.40
8:GD:63:THR:HA	8:GD:64:PRO:HD3	1.93	0.40
1:Gg:824:THR:N	2:WH:208:LYS:HD2	2.36	0.40
2:HH:311:MET:HG3	2:HH:341:LYS:HA	2.02	0.40
3:HK:133:THR:HB	3:HK:158:GLY:HA3	2.03	0.40
4:HL:139:ARG:HD2	11:HM:319:PHE:CD1	2.56	0.40
2:IH:183:ASP:OD1	2:IH:185:THR:OG1	2.28	0.40
1:CG:1006:ILE:HD13	1:DG:968:PHE:CD2	2.55	0.40
1:CG:1010:THR:OG1	1:DG:967:GLY:HA3	2.21	0.40
8:Id:64:PRO:HG2	8:Id:67:LYS:HB2	2.03	0.40
3:JK:54:ILE:HA	3:JK:57:MET:HE2	2.03	0.40
3:JK:125:SER:OG	3:JK:126:VAL:N	2.52	0.40
7:JX:70:UNK:H2	2:KH:146:GLY:H	1.67	0.40
2:AH:124:PRO:HB3	2:ZH:140:ALA:CB	2.51	0.40
2:AH:349:TRP:O	2:AH:350:HIS:ND1	2.54	0.40
11:KM:300:ASP:CG	11:KM:302:ARG:HE	2.29	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:CD:61:VAL:HG11	10:KC:267:VAL:O	2.22	0.40
4:LL:45:PRO:N	4:LL:46:PRO:HD2	2.36	0.40
9:Lf:233:ARG:HD3	9:Lf:233:ARG:HA	1.80	0.40
2:MH:313:VAL:HG13	2:MH:337:TYR:HB2	2.02	0.40
9:CF:246:LEU:HB3	9:CF:255:LEU:HB2	2.03	0.40
2:WH:110:LYS:HA	2:WH:113:LYS:HG2	2.03	0.40
9:XF:216:ILE:HD11	9:XF:219:ARG:HB2	2.03	0.40
2:XH:303:ARG:NE	2:XH:303:ARG:HA	2.36	0.40
1:YG:792:GLN:OE1	1:YG:792:GLN:N	2.44	0.40
2:ZH:320:LEU:HD13	10:GC:225:TYR:CZ	2.56	0.40
11:AM:146:LEU:HB3	11:AM:165:ILE:HG23	2.03	0.40
11:BM:160:ASN:H	11:BM:180:ASP:C	2.29	0.40
11:BM:194:LEU:HA	11:BM:194:LEU:HD23	1.87	0.40
11:FM:138:LEU:HD11	11:FM:142:GLY:HA3	2.02	0.40
2:BH:194:TYR:CE2	2:BH:204:ILE:HD13	2.56	0.40
10:EC:154:ASP:N	10:EC:154:ASP:OD1	2.54	0.40
10:GC:150:TYR:CG	10:GC:202:ILE:HD13	2.56	0.40
1:GG:1007:GLY:O	1:GG:1011:VAL:HG22	2.21	0.40
10:LC:70:GLY:CA	10:LC:183:TRP:HD1	2.34	0.40
4:CL:139:ARG:HD2	11:CM:319:PHE:HD2	1.85	0.40
8:Cd:123:THR:HG21	8:Cd:131:ILE:HD11	2.02	0.40
8:DD:72:THR:OG1	8:DD:146:HIS:ND1	2.45	0.40
8:DD:82:ARG:HD3	3:DK:138:ARG:HD2	2.02	0.40
11:DM:156:GLU:HB3	11:DM:178:LYS:HZ1	1.85	0.40
1:IG:876:SER:HB2	1:IG:1033:SER:N	2.37	0.40
1:IG:962:SER:HB3	1:IG:1015:TRP:HB3	2.02	0.40
1:NG:972:PHE:HB3	1:NG:1005:VAL:CG2	2.51	0.40
10:AC:105:ASN:O	10:AC:142:ILE:HG22	2.22	0.40
8:Dd:87:TRP:O	8:Dd:120:SER:HA	2.21	0.40
1:Ag:804:ALA:O	1:Ag:808:LEU:HG	2.21	0.40
1:Eg:793:GLU:H	1:Eg:793:GLU:CD	2.29	0.40
8:FD:35:ASP:OD2	8:FD:38:THR:N	2.43	0.40
8:FD:150:ASN:OD1	8:FD:151:SER:N	2.54	0.40
3:FK:72:GLN:HB2	3:FK:185:ARG:NE	2.36	0.40
5:FN:51:CYS:HB2	5:FN:58:LEU:HD23	2.03	0.40
5:FN:69:TYR:CD1	5:FN:76:MET:HE1	2.56	0.40
8:Fd:36:ASP:N	8:Fd:36:ASP:OD1	2.55	0.40
10:BC:84:LEU:HD21	10:BC:148:TRP:HZ3	1.86	0.40
10:BC:180:TYR:HD1	10:BC:183:ARG:HD2	1.86	0.40
1:Gg:801:MET:SD	2:XH:115:MET:HB3	2.61	0.40
4:GL:125:LEU:HD13	4:GL:125:LEU:HA	1.96	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:Gd:35:ASP:HB3	8:Gd:38:THR:OG1	2.21	0.40
11:HM:180:ASP:OD1	11:HM:199:LYS:HB2	2.21	0.40
11:IM:273:ALA:HB1	11:IM:277:SER:HB2	2.02	0.40
3:JK:133:THR:HG21	3:JK:160:GLY:HA2	2.03	0.40
1:DG:961:ALA:O	1:DG:965:LEU:HD13	2.22	0.40
4:LL:134:MET:HE3	4:LL:139:ARG:NH1	2.36	0.40
8:Ld:151:SER:O	8:Ld:153:VAL:N	2.55	0.40
2:MH:161:SER:O	2:MH:164:SER:OG	2.35	0.40
3:MK:72:GLN:HE22	4:AL:215:SER:HB3	1.86	0.40
4:ML:116:TYR:OH	4:ML:118:GLU:HB2	2.22	0.40
1:EG:969:GLY:HA3	1:EG:1009:ALA:CB	2.44	0.40
2:WH:339:MET:HE2	2:WH:339:MET:HB3	1.90	0.40
4:AL:134:MET:HG3	4:AL:139:ARG:NH1	2.35	0.40
11:BM:187:GLY:O	11:BM:206:TRP:HB2	2.22	0.40
11:EM:174:GLN:NE2	11:EM:192:ARG:HB3	2.36	0.40
11:FM:228:VAL:O	11:FM:248:ALA:HA	2.21	0.40
11:GM:174:GLN:NE2	11:GM:193:GLN:O	2.41	0.40
8:BD:81:ALA:HB3	8:BD:128:LEU:HD21	2.04	0.40
8:BD:94:LEU:O	8:BD:98:ILE:HG12	2.21	0.40
2:BH:176:VAL:HA	2:BH:215:ILE:O	2.22	0.40
3:BK:133:THR:HG21	3:BK:160:GLY:N	2.36	0.40
10:GC:99:LEU:HD22	10:GC:99:LEU:H	1.87	0.40
10:GC:179:TYR:HA	10:GC:182:ARG:HG2	2.03	0.40
10:JC:259:ASN:O	10:JC:263:TRP:NE1	2.53	0.40
10:KC:97:PHE:O	10:KC:101:VAL:HG23	2.21	0.40
10:MC:152:MET:HE2	10:MC:152:MET:HB2	1.80	0.40
11:CM:308:ASP:OD2	9:Cf:263:LYS:NZ	2.46	0.40
8:Cd:35:ASP:O	8:Cd:39:ILE:HG23	2.22	0.40
8:Cd:79:LEU:HA	8:Cd:128:LEU:HD11	2.04	0.40
2:DH:105:GLU:O	2:DH:109:LYS:HE2	2.22	0.40
2:DH:156:GLN:OE1	2:DH:156:GLN:N	2.55	0.40
2:DH:185:THR:OG1	2:DH:264:LYS:HB3	2.20	0.40
4:DL:45:PRO:N	4:DL:46:PRO:HD2	2.36	0.40
1:HG:919:MET:HE3	1:HG:919:MET:HB3	1.98	0.40
1:HG:949:ASN:HA	1:HG:952:TYR:CD2	2.56	0.40
1:HG:1040:LEU:HD23	1:HG:1040:LEU:H	1.86	0.40
1:IG:965:LEU:HG	1:IG:1008:LEU:HD23	2.04	0.40
1:JG:972:PHE:HB3	1:JG:1005:VAL:CG2	2.48	0.40
1:LG:932:ALA:HB1	1:LG:1039:ILE:HG23	2.02	0.40
1:NG:958:SER:O	1:NG:962:SER:OG	2.39	0.40
1:PG:1007:GLY:O	1:PG:1011:VAL:HG22	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:AC:105:ASN:C	10:AC:142:ILE:HG22	2.46	0.40
1:AG:876:SER:O	1:BG:941:ARG:HA	2.22	0.40
1:AG:965:LEU:O	1:AG:1008:LEU:HB3	2.21	0.40
1:AG:1006:ILE:HG22	1:AG:1007:GLY:N	2.36	0.40
2:EH:304:ALA:HA	2:EH:312:TYR:O	2.21	0.40
4:FL:94:VAL:HA	4:FL:97:ILE:HG12	2.04	0.40
1:BG:899:LEU:HB2	1:BG:919:MET:SD	2.62	0.40
4:GL:212:ASN:OD1	4:GL:212:ASN:N	2.52	0.40
5:GN:47:GLY:O	5:GN:61:ASN:N	2.47	0.40
9:Gf:233:ARG:HD2	9:Gf:233:ARG:HA	1.83	0.40
8:HD:82:ARG:HB2	3:HK:156:THR:HG23	2.03	0.40
3:HK:144:LEU:HD13	3:HK:144:LEU:HA	1.87	0.40
11:HM:255:THR:HB	11:HM:259:SER:OG	2.21	0.40
11:IM:145:ARG:HA	11:IM:145:ARG:HD2	1.88	0.40
9:Jf:216:ILE:HG13	9:Jf:217:PRO:HD2	2.02	0.40
2:AH:206:TRP:NE1	2:AH:210:SER:O	2.54	0.40
10:CC:107:PRO:HG2	10:CC:209:MET:SD	2.61	0.40
9:KF:238:ILE:HD12	9:KF:239:PRO:HD2	2.04	0.40
3:KK:143:TYR:O	3:KK:146:SER:OG	2.28	0.40
4:KL:134:MET:HB3	4:KL:139:ARG:HB2	2.04	0.40
11:KM:119:GLU:HG3	11:KM:139:ALA:HB3	2.03	0.40
1:DG:895:LYS:HD3	1:DG:896:GLY:N	2.35	0.40
1:DG:1006:ILE:HD13	1:EG:968:PHE:CD2	2.56	0.40
2:LH:306:LEU:HD11	2:LH:309:GLU:HA	2.03	0.40
11:LM:165:ILE:HD12	11:LM:185:ILE:HG12	2.03	0.40
11:LM:218:LYS:HB2	11:LM:218:LYS:HE2	1.91	0.40
11:LM:301:MET:HE2	11:LM:301:MET:HB3	1.91	0.40
5:LN:92:TYR:CG	5:LN:93:PRO:HD2	2.57	0.40
1:EG:874:ASP:OD1	1:EG:874:ASP:N	2.55	0.40
8:Md:41:LEU:HD13	8:Md:41:LEU:HA	1.85	0.40
1:VG:822:GLU:O	2:CH:208:LYS:NZ	2.44	0.40
2:VH:134:TYR:O	2:VH:137:SER:OG	2.33	0.40
9:CF:248:ASP:H	9:CF:254:ILE:HD13	1.86	0.40
1:WG:808:LEU:HA	1:WG:808:LEU:HD22	1.90	0.40
2:XH:191:ILE:HD12	2:XH:228:VAL:HG11	2.04	0.40
2:YH:170:ARG:HB2	2:YH:249:ASP:CG	2.46	0.40
1:FG:1011:VAL:HG12	1:GG:963:SER:HB3	2.03	0.40
11:EM:217:LYS:HA	11:EM:236:TRP:HD1	1.87	0.40
11:FM:284:LEU:HD23	11:FM:310:LYS:HE3	2.04	0.40
8:Ad:151:SER:O	8:Ad:153:VAL:N	2.54	0.40
8:BD:82:ARG:HG3	3:BK:138:ARG:HG2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:BD:144:SER:HB2	8:BD:157:ARG:HG3	2.03	0.40
2:BH:324:TRP:HA	2:BH:339:MET:HB3	2.04	0.40
10:IC:92:ILE:HG22	10:IC:93:TYR:CD1	2.56	0.40
10:IC:242:ASP:HB2	10:IC:244:ARG:HH21	1.85	0.40
10:JC:166:LEU:H	10:JC:166:LEU:HD23	1.86	0.40
10:KC:111:LEU:HD12	10:KC:213:TYR:HA	2.03	0.40
10:KC:243:ILE:HG22	8:Cd:118:LEU:HD23	2.04	0.40
3:CK:38:VAL:N	3:CK:39:PRO:HD2	2.36	0.40
11:CM:281:TYR:CZ	11:CM:300:ASP:HB2	2.56	0.40
11:CM:292:MET:HE1	11:CM:298:VAL:HB	2.02	0.40
2:DH:166:PRO:HA	2:DH:167:PRO:HD3	1.98	0.40
1:HG:951:HIS:H	1:HG:1027:THR:HG22	1.86	0.40
1:IG:1014:ALA:O	1:IG:1018:GLN:HG2	2.21	0.40
1:JG:912:MET:HB3	1:JG:944:LEU:HB2	2.04	0.40
1:LG:972:PHE:HB3	1:LG:1005:VAL:HG22	2.02	0.40
1:MG:876:SER:HB3	1:NG:941:ARG:HG2	2.03	0.40
1:OG:867:ASP:OD1	1:OG:867:ASP:N	2.49	0.40
8:ED:124:LYS:HA	8:ED:124:LYS:HD2	1.97	0.40
9:EF:207:ARG:HB2	9:EF:208:ILE:H	1.65	0.40
1:AG:898:LYS:HB2	1:AG:898:LYS:HE2	1.78	0.40
1:AG:1024:ASN:OD1	1:AG:1024:ASN:N	2.41	0.40
2:EH:151:PRO:HB2	2:DH:166:PRO:HG3	2.04	0.40
2:EH:207:ASP:OD2	2:EH:209:THR:OG1	2.34	0.40
3:EK:78:ILE:HB	3:EK:180:VAL:HG23	2.04	0.40
4:EL:204:LYS:HZ3	4:EL:204:LYS:HG3	1.75	0.40
8:FD:37:ALA:O	8:FD:41:LEU:HG	2.21	0.40
2:FH:150:LYS:HE2	2:FH:152:THR:HG23	2.04	0.40
3:FK:81:SER:OG	3:FK:173:ASP:O	2.38	0.40
2:GH:179:LEU:HB3	2:GH:254:LEU:HD21	2.03	0.40
1:BG:917:ASN:HA	1:BG:931:SER:HA	2.02	0.40
4:GL:116:TYR:CZ	4:GL:118:GLU:HB2	2.55	0.40
2:HH:321:SER:OG	2:HH:322:PRO:HD3	2.22	0.40
4:HL:206:GLU:HG2	4:HL:208:TYR:CZ	2.56	0.40
11:HM:144:THR:O	11:HM:145:ARG:NE	2.51	0.40
8:ID:73:ILE:HG21	8:ID:133:ARG:HG2	2.02	0.40
3:JK:123:TYR:CD2	3:JK:124:VAL:HG23	2.57	0.40
3:JK:123:TYR:N	3:JK:129:GLU:OE2	2.26	0.40
4:JL:134:MET:HB2	4:JL:139:ARG:HB2	2.02	0.40
4:JL:217:ASN:O	4:JL:223:SER:OG	2.39	0.40
10:CC:90:LEU:HG	10:CC:147:TRP:CD1	2.57	0.40
3:KK:40:LYS:HE2	3:KK:40:LYS:HB2	1.88	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:KL:115:GLN:NE2	4:KL:116:TYR:O	2.54	0.40
9:Kf:211:TYR:CG	9:Kf:265:SER:HB2	2.57	0.40
9:LF:238:ILE:HD13	9:LF:244:VAL:HG22	2.04	0.40
2:LH:174:GLY:N	2:LH:217:ALA:O	2.36	0.40
2:LH:250:TYR:HB3	2:YH:238:MET:SD	2.62	0.40
3:LK:53:ILE:HD11	3:LK:108:GLN:HG2	2.02	0.40
4:LL:191:THR:HG21	11:LM:289:ALA:CB	2.52	0.40
5:LN:87:TRP:CZ2	10:GC:148:ARG:HD2	2.56	0.40
5:LN:111:GLU:OE1	5:LN:111:GLU:N	2.35	0.40
8:MD:86:ASP:OD1	10:HC:87:ARG:NH1	2.54	0.40
9:MF:264:PHE:HB3	9:MF:268:ASP:O	2.20	0.40
5:MN:116:LYS:HD2	5:MN:116:LYS:HA	1.90	0.40
8:Md:105:ARG:HH22	8:Md:151:SER:C	2.29	0.40
1:VG:804:ALA:HA	1:VG:807:GLN:NE2	2.37	0.40
2:VH:280:LEU:HG	2:VH:328:MET:HG3	2.03	0.40
1:WG:797:ARG:HE	1:WG:797:ARG:C	2.30	0.40
2:WH:190:PRO:HD2	2:WH:261:PRO:HG3	2.03	0.40
4:AL:176:SER:HB2	4:AL:180:LYS:NZ	2.36	0.40
10:DC:235:ASP:OD1	10:DC:238:GLU:N	2.46	0.40
2:ZH:184:SER:HB2	2:ZH:259:TYR:CE2	2.56	0.40
2:ZH:196:LEU:HB2	2:ZH:226:LEU:HD13	2.04	0.40
1:FG:1007:GLY:O	1:FG:1011:VAL:HG22	2.22	0.40
11:GM:278:ASP:HB3	11:GM:280:TYR:CE1	2.56	0.40
8:BD:87:TRP:HD1	8:BD:89:GLY:H	1.63	0.40
2:BH:225:ASN:ND2	2:CH:176:VAL:H	2.17	0.40
5:BN:46:GLY:HA3	5:BN:61:ASN:HB2	2.02	0.40
9:Bf:213:GLN:CD	9:Bf:223:ILE:HB	2.46	0.40
10:EC:144:PRO:HA	10:EC:145:PRO:HD3	1.96	0.40
10:EC:259:SER:HA	10:EC:262:TRP:CD1	2.57	0.40
10:GC:83:LEU:HD11	10:GC:90:LEU:HD22	2.02	0.40
1:GG:919:MET:HG3	1:GG:930:ILE:HG23	2.03	0.40
1:GG:1006:ILE:HG22	1:GG:1007:GLY:N	2.35	0.40
10:IC:257:ASN:HB2	10:IC:260:GLU:OE2	2.22	0.40
10:JC:118:LEU:HD13	8:AD:114:SER:OG	2.22	0.40
10:MC:217:MET:HG2	10:MC:219:MET:HE2	2.02	0.40
8:Cd:36:ASP:OD1	8:Cd:37:ALA:N	2.53	0.40
11:DM:210:ASP:HA	11:DM:229:ASN:H	1.87	0.40
1:JG:885:ILE:O	1:JG:900:ILE:HA	2.21	0.40
1:KG:912:MET:HB2	1:KG:1029:VAL:HG21	2.02	0.40
1:OG:893:LYS:HE3	1:OG:893:LYS:HB3	1.97	0.40
1:OG:969:GLY:O	1:OG:1005:VAL:HG13	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:Df:245:LYS:NZ	9:Df:255:LEU:O	2.55	0.40
8:AD:150:ASN:OD1	8:AD:151:SER:N	2.54	0.40
1:Eg:808:LEU:HD13	1:Eg:808:LEU:HA	1.95	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	AG	161/1048 (15%)	149 (92%)	12 (8%)	0	100	100
1	Ag	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	BG	161/1048 (15%)	154 (96%)	7 (4%)	0	100	100
1	Bg	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	CG	161/1048 (15%)	155 (96%)	6 (4%)	0	100	100
1	Cg	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	DG	161/1048 (15%)	153 (95%)	8 (5%)	0	100	100
1	Dg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	EG	161/1048 (15%)	153 (95%)	8 (5%)	0	100	100
1	Eg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	FG	161/1048 (15%)	151 (94%)	10 (6%)	0	100	100
1	Fg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	GG	161/1048 (15%)	153 (95%)	8 (5%)	0	100	100
1	Gg	32/1048 (3%)	32 (100%)	0	0	100	100
1	HG	161/1048 (15%)	156 (97%)	5 (3%)	0	100	100
1	Hg	32/1048 (3%)	32 (100%)	0	0	100	100
1	IG	161/1048 (15%)	154 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Ig	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	JG	161/1048 (15%)	154 (96%)	7 (4%)	0	100	100
1	Jg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	KG	161/1048 (15%)	150 (93%)	11 (7%)	0	100	100
1	Kg	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	LG	161/1048 (15%)	151 (94%)	10 (6%)	0	100	100
1	Lg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	MG	161/1048 (15%)	150 (93%)	11 (7%)	0	100	100
1	Mg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	NG	161/1048 (15%)	153 (95%)	8 (5%)	0	100	100
1	OG	161/1048 (15%)	154 (96%)	7 (4%)	0	100	100
1	PG	161/1048 (15%)	155 (96%)	6 (4%)	0	100	100
1	VG	32/1048 (3%)	32 (100%)	0	0	100	100
1	WG	32/1048 (3%)	32 (100%)	0	0	100	100
1	XG	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	YG	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	ZG	32/1048 (3%)	32 (100%)	0	0	100	100
2	AH	256/361 (71%)	241 (94%)	15 (6%)	0	100	100
2	BH	256/361 (71%)	242 (94%)	14 (6%)	0	100	100
2	CH	256/361 (71%)	244 (95%)	12 (5%)	0	100	100
2	DH	256/361 (71%)	241 (94%)	15 (6%)	0	100	100
2	EH	256/361 (71%)	239 (93%)	17 (7%)	0	100	100
2	FH	256/361 (71%)	245 (96%)	11 (4%)	0	100	100
2	GH	256/361 (71%)	238 (93%)	18 (7%)	0	100	100
2	HH	256/361 (71%)	246 (96%)	10 (4%)	0	100	100
2	IH	256/361 (71%)	240 (94%)	16 (6%)	0	100	100
2	JH	256/361 (71%)	245 (96%)	11 (4%)	0	100	100
2	KH	256/361 (71%)	242 (94%)	14 (6%)	0	100	100
2	LH	256/361 (71%)	243 (95%)	13 (5%)	0	100	100
2	MH	256/361 (71%)	240 (94%)	16 (6%)	0	100	100
2	VH	239/361 (66%)	227 (95%)	12 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	WH	239/361 (66%)	235 (98%)	4 (2%)	0	100	100
2	XH	239/361 (66%)	234 (98%)	5 (2%)	0	100	100
2	YH	239/361 (66%)	229 (96%)	10 (4%)	0	100	100
2	ZH	239/361 (66%)	230 (96%)	9 (4%)	0	100	100
3	AK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
3	BK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
3	CK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
3	DK	149/189 (79%)	142 (95%)	7 (5%)	0	100	100
3	EK	149/189 (79%)	144 (97%)	5 (3%)	0	100	100
3	FK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
3	GK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
3	HK	149/189 (79%)	140 (94%)	9 (6%)	0	100	100
3	IK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
3	JK	149/189 (79%)	144 (97%)	5 (3%)	0	100	100
3	KK	149/189 (79%)	144 (97%)	5 (3%)	0	100	100
3	LK	149/189 (79%)	141 (95%)	8 (5%)	0	100	100
3	MK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
4	AL	169/249 (68%)	162 (96%)	7 (4%)	0	100	100
4	BL	169/249 (68%)	165 (98%)	4 (2%)	0	100	100
4	CL	169/249 (68%)	162 (96%)	7 (4%)	0	100	100
4	DL	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
4	EL	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
4	FL	169/249 (68%)	163 (96%)	6 (4%)	0	100	100
4	GL	169/249 (68%)	162 (96%)	7 (4%)	0	100	100
4	HL	169/249 (68%)	162 (96%)	7 (4%)	0	100	100
4	IL	169/249 (68%)	162 (96%)	7 (4%)	0	100	100
4	JL	169/249 (68%)	163 (96%)	6 (4%)	0	100	100
4	KL	169/249 (68%)	165 (98%)	4 (2%)	0	100	100
4	LL	169/249 (68%)	162 (96%)	7 (4%)	0	100	100
4	ML	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
5	AN	76/124 (61%)	72 (95%)	4 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	BN	76/124 (61%)	70 (92%)	6 (8%)	0	100	100
5	CN	76/124 (61%)	69 (91%)	7 (9%)	0	100	100
5	DN	76/124 (61%)	69 (91%)	7 (9%)	0	100	100
5	EN	76/124 (61%)	67 (88%)	9 (12%)	0	100	100
5	FN	76/124 (61%)	70 (92%)	6 (8%)	0	100	100
5	GN	76/124 (61%)	72 (95%)	4 (5%)	0	100	100
5	HN	76/124 (61%)	73 (96%)	3 (4%)	0	100	100
5	IN	76/124 (61%)	72 (95%)	4 (5%)	0	100	100
5	JN	76/124 (61%)	70 (92%)	6 (8%)	0	100	100
5	KN	76/124 (61%)	70 (92%)	6 (8%)	0	100	100
5	LN	76/124 (61%)	72 (95%)	4 (5%)	0	100	100
5	MN	76/124 (61%)	71 (93%)	5 (7%)	0	100	100
8	AD	138/163 (85%)	132 (96%)	6 (4%)	0	100	100
8	Ad	135/163 (83%)	128 (95%)	7 (5%)	0	100	100
8	BD	138/163 (85%)	132 (96%)	6 (4%)	0	100	100
8	Bd	135/163 (83%)	128 (95%)	7 (5%)	0	100	100
8	CD	138/163 (85%)	130 (94%)	8 (6%)	0	100	100
8	Cd	135/163 (83%)	129 (96%)	6 (4%)	0	100	100
8	DD	138/163 (85%)	132 (96%)	6 (4%)	0	100	100
8	Dd	135/163 (83%)	131 (97%)	4 (3%)	0	100	100
8	ED	138/163 (85%)	132 (96%)	6 (4%)	0	100	100
8	Ed	135/163 (83%)	130 (96%)	5 (4%)	0	100	100
8	FD	138/163 (85%)	133 (96%)	5 (4%)	0	100	100
8	Fd	135/163 (83%)	129 (96%)	6 (4%)	0	100	100
8	GD	138/163 (85%)	132 (96%)	6 (4%)	0	100	100
8	Gd	135/163 (83%)	125 (93%)	10 (7%)	0	100	100
8	HD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
8	Hd	135/163 (83%)	127 (94%)	8 (6%)	0	100	100
8	ID	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
8	Id	135/163 (83%)	131 (97%)	4 (3%)	0	100	100
8	JD	138/163 (85%)	128 (93%)	10 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	Jd	135/163 (83%)	128 (95%)	7 (5%)	0	100	100
8	KD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
8	Kd	135/163 (83%)	125 (93%)	10 (7%)	0	100	100
8	LD	138/163 (85%)	127 (92%)	11 (8%)	0	100	100
8	Ld	135/163 (83%)	129 (96%)	6 (4%)	0	100	100
8	MD	138/163 (85%)	132 (96%)	6 (4%)	0	100	100
8	Md	135/163 (83%)	129 (96%)	6 (4%)	0	100	100
9	AF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
9	Af	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
9	BF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
9	Bf	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
9	CF	61/269 (23%)	60 (98%)	1 (2%)	0	100	100
9	Cf	57/269 (21%)	55 (96%)	2 (4%)	0	100	100
9	DF	61/269 (23%)	61 (100%)	0	0	100	100
9	Df	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
9	EF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
9	Ef	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
9	FF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
9	Ff	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
9	GF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
9	Gf	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
9	HF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
9	Hf	57/269 (21%)	55 (96%)	2 (4%)	0	100	100
9	IF	61/269 (23%)	53 (87%)	8 (13%)	0	100	100
9	If	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
9	JF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
9	Jf	57/269 (21%)	55 (96%)	2 (4%)	0	100	100
9	KF	61/269 (23%)	55 (90%)	6 (10%)	0	100	100
9	Kf	57/269 (21%)	51 (90%)	6 (10%)	0	100	100
9	LF	61/269 (23%)	56 (92%)	5 (8%)	0	100	100
9	Lf	57/269 (21%)	53 (93%)	4 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	MF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
9	Mf	57/269 (21%)	56 (98%)	1 (2%)	0	100	100
9	VF	61/269 (23%)	56 (92%)	5 (8%)	0	100	100
9	WF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
9	XF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
9	YF	61/269 (23%)	60 (98%)	1 (2%)	0	100	100
9	ZF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
10	AC	241/303 (80%)	225 (93%)	16 (7%)	0	100	100
10	BC	241/303 (80%)	229 (95%)	12 (5%)	0	100	100
10	CC	207/303 (68%)	191 (92%)	16 (8%)	0	100	100
10	DC	207/303 (68%)	188 (91%)	19 (9%)	0	100	100
10	EC	207/303 (68%)	192 (93%)	15 (7%)	0	100	100
10	FC	241/303 (80%)	231 (96%)	10 (4%)	0	100	100
10	GC	207/303 (68%)	194 (94%)	13 (6%)	0	100	100
10	HC	207/303 (68%)	198 (96%)	9 (4%)	0	100	100
10	IC	207/303 (68%)	188 (91%)	19 (9%)	0	100	100
10	JC	241/303 (80%)	227 (94%)	14 (6%)	0	100	100
10	KC	241/303 (80%)	226 (94%)	15 (6%)	0	100	100
10	LC	207/303 (68%)	193 (93%)	14 (7%)	0	100	100
10	MC	207/303 (68%)	193 (93%)	14 (7%)	0	100	100
11	AM	206/320 (64%)	188 (91%)	18 (9%)	0	100	100
11	BM	206/320 (64%)	190 (92%)	16 (8%)	0	100	100
11	CM	206/320 (64%)	194 (94%)	12 (6%)	0	100	100
11	DM	206/320 (64%)	192 (93%)	14 (7%)	0	100	100
11	EM	206/320 (64%)	187 (91%)	19 (9%)	0	100	100
11	FM	206/320 (64%)	192 (93%)	14 (7%)	0	100	100
11	GM	206/320 (64%)	187 (91%)	19 (9%)	0	100	100
11	HM	206/320 (64%)	185 (90%)	21 (10%)	0	100	100
11	IM	206/320 (64%)	188 (91%)	18 (9%)	0	100	100
11	JM	206/320 (64%)	192 (93%)	14 (7%)	0	100	100
11	KM	206/320 (64%)	193 (94%)	13 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	LM	206/320 (64%)	193 (94%)	13 (6%)	0	100	100
11	MM	206/320 (64%)	194 (94%)	12 (6%)	0	100	100
All	All	23724/70112 (34%)	22448 (95%)	1276 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AG	135/765 (18%)	125 (93%)	10 (7%)	13	33
1	Ag	31/765 (4%)	26 (84%)	5 (16%)	2	12
1	BG	135/765 (18%)	125 (93%)	10 (7%)	13	33
1	Bg	31/765 (4%)	27 (87%)	4 (13%)	4	17
1	CG	135/765 (18%)	124 (92%)	11 (8%)	11	31
1	Cg	31/765 (4%)	30 (97%)	1 (3%)	34	55
1	DG	135/765 (18%)	120 (89%)	15 (11%)	6	20
1	Dg	31/765 (4%)	27 (87%)	4 (13%)	4	17
1	EG	135/765 (18%)	123 (91%)	12 (9%)	9	28
1	Eg	31/765 (4%)	29 (94%)	2 (6%)	15	37
1	FG	135/765 (18%)	119 (88%)	16 (12%)	5	19
1	Fg	31/765 (4%)	30 (97%)	1 (3%)	34	55
1	GG	135/765 (18%)	123 (91%)	12 (9%)	9	28
1	Gg	31/765 (4%)	25 (81%)	6 (19%)	1	8
1	HG	135/765 (18%)	122 (90%)	13 (10%)	8	25
1	Hg	31/765 (4%)	26 (84%)	5 (16%)	2	12
1	IG	135/765 (18%)	122 (90%)	13 (10%)	8	25
1	Ig	31/765 (4%)	27 (87%)	4 (13%)	4	17
1	JG	135/765 (18%)	121 (90%)	14 (10%)	7	22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Jg	31/765 (4%)	28 (90%)	3 (10%)	8	25
1	KG	135/765 (18%)	123 (91%)	12 (9%)	9	28
1	Kg	31/765 (4%)	27 (87%)	4 (13%)	4	17
1	LG	135/765 (18%)	124 (92%)	11 (8%)	11	31
1	Lg	31/765 (4%)	26 (84%)	5 (16%)	2	12
1	MG	135/765 (18%)	125 (93%)	10 (7%)	13	33
1	Mg	31/765 (4%)	27 (87%)	4 (13%)	4	17
1	NG	135/765 (18%)	125 (93%)	10 (7%)	13	33
1	OG	135/765 (18%)	122 (90%)	13 (10%)	8	25
1	PG	135/765 (18%)	124 (92%)	11 (8%)	11	31
1	VG	31/765 (4%)	29 (94%)	2 (6%)	15	37
1	WG	31/765 (4%)	26 (84%)	5 (16%)	2	12
1	XG	31/765 (4%)	28 (90%)	3 (10%)	8	25
1	YG	31/765 (4%)	25 (81%)	6 (19%)	1	8
1	ZG	31/765 (4%)	25 (81%)	6 (19%)	1	8
2	AH	220/300 (73%)	196 (89%)	24 (11%)	6	21
2	BH	220/300 (73%)	203 (92%)	17 (8%)	12	32
2	CH	220/300 (73%)	204 (93%)	16 (7%)	13	34
2	DH	220/300 (73%)	205 (93%)	15 (7%)	14	36
2	EH	220/300 (73%)	200 (91%)	20 (9%)	9	28
2	FH	220/300 (73%)	206 (94%)	14 (6%)	16	37
2	GH	220/300 (73%)	206 (94%)	14 (6%)	16	37
2	HH	220/300 (73%)	209 (95%)	11 (5%)	22	43
2	IH	220/300 (73%)	212 (96%)	8 (4%)	31	52
2	JH	220/300 (73%)	202 (92%)	18 (8%)	10	31
2	KH	220/300 (73%)	201 (91%)	19 (9%)	10	29
2	LH	220/300 (73%)	203 (92%)	17 (8%)	12	32
2	MH	220/300 (73%)	200 (91%)	20 (9%)	9	28
2	VH	207/300 (69%)	190 (92%)	17 (8%)	10	31
2	WH	207/300 (69%)	184 (89%)	23 (11%)	6	20
2	XH	207/300 (69%)	186 (90%)	21 (10%)	7	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	YH	207/300 (69%)	184 (89%)	23 (11%)	6	20
2	ZH	207/300 (69%)	190 (92%)	17 (8%)	10	31
3	AK	129/163 (79%)	119 (92%)	10 (8%)	11	32
3	BK	129/163 (79%)	120 (93%)	9 (7%)	14	36
3	CK	129/163 (79%)	121 (94%)	8 (6%)	16	38
3	DK	129/163 (79%)	118 (92%)	11 (8%)	10	29
3	EK	129/163 (79%)	122 (95%)	7 (5%)	20	42
3	FK	129/163 (79%)	122 (95%)	7 (5%)	20	42
3	GK	129/163 (79%)	115 (89%)	14 (11%)	6	21
3	HK	129/163 (79%)	122 (95%)	7 (5%)	20	42
3	IK	129/163 (79%)	116 (90%)	13 (10%)	7	23
3	JK	129/163 (79%)	116 (90%)	13 (10%)	7	23
3	KK	129/163 (79%)	120 (93%)	9 (7%)	14	36
3	LK	129/163 (79%)	116 (90%)	13 (10%)	7	23
3	MK	129/163 (79%)	111 (86%)	18 (14%)	3	15
4	AL	148/203 (73%)	140 (95%)	8 (5%)	20	42
4	BL	148/203 (73%)	136 (92%)	12 (8%)	11	31
4	CL	148/203 (73%)	139 (94%)	9 (6%)	17	39
4	DL	148/203 (73%)	138 (93%)	10 (7%)	14	36
4	EL	148/203 (73%)	139 (94%)	9 (6%)	17	39
4	FL	148/203 (73%)	134 (90%)	14 (10%)	8	25
4	GL	148/203 (73%)	141 (95%)	7 (5%)	23	45
4	HL	148/203 (73%)	139 (94%)	9 (6%)	17	39
4	IL	148/203 (73%)	137 (93%)	11 (7%)	13	33
4	JL	148/203 (73%)	139 (94%)	9 (6%)	17	39
4	KL	148/203 (73%)	132 (89%)	16 (11%)	6	22
4	LL	148/203 (73%)	141 (95%)	7 (5%)	23	45
4	ML	148/203 (73%)	135 (91%)	13 (9%)	9	29
5	AN	66/107 (62%)	61 (92%)	5 (8%)	12	33
5	BN	66/107 (62%)	60 (91%)	6 (9%)	9	28
5	CN	66/107 (62%)	59 (89%)	7 (11%)	6	22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	DN	66/107 (62%)	61 (92%)	5 (8%)	12	33
5	EN	66/107 (62%)	62 (94%)	4 (6%)	17	39
5	FN	66/107 (62%)	62 (94%)	4 (6%)	17	39
5	GN	66/107 (62%)	60 (91%)	6 (9%)	9	28
5	HN	66/107 (62%)	63 (96%)	3 (4%)	24	46
5	IN	66/107 (62%)	61 (92%)	5 (8%)	12	33
5	JN	66/107 (62%)	61 (92%)	5 (8%)	12	33
5	KN	66/107 (62%)	63 (96%)	3 (4%)	24	46
5	LN	66/107 (62%)	63 (96%)	3 (4%)	24	46
5	MN	66/107 (62%)	56 (85%)	10 (15%)	3	13
8	AD	121/139 (87%)	114 (94%)	7 (6%)	18	40
8	Ad	118/139 (85%)	108 (92%)	10 (8%)	10	29
8	BD	121/139 (87%)	114 (94%)	7 (6%)	18	40
8	Bd	118/139 (85%)	109 (92%)	9 (8%)	12	33
8	CD	121/139 (87%)	118 (98%)	3 (2%)	42	62
8	Cd	118/139 (85%)	111 (94%)	7 (6%)	18	40
8	DD	121/139 (87%)	114 (94%)	7 (6%)	18	40
8	Dd	118/139 (85%)	110 (93%)	8 (7%)	14	36
8	ED	121/139 (87%)	114 (94%)	7 (6%)	18	40
8	Ed	118/139 (85%)	104 (88%)	14 (12%)	5	19
8	FD	121/139 (87%)	112 (93%)	9 (7%)	13	33
8	Fd	118/139 (85%)	109 (92%)	9 (8%)	12	33
8	GD	121/139 (87%)	110 (91%)	11 (9%)	9	28
8	Gd	118/139 (85%)	111 (94%)	7 (6%)	18	40
8	HD	121/139 (87%)	112 (93%)	9 (7%)	13	33
8	Hd	118/139 (85%)	108 (92%)	10 (8%)	10	29
8	ID	121/139 (87%)	113 (93%)	8 (7%)	15	37
8	Id	118/139 (85%)	114 (97%)	4 (3%)	32	54
8	JD	121/139 (87%)	112 (93%)	9 (7%)	13	33
8	Jd	118/139 (85%)	109 (92%)	9 (8%)	12	33
8	KD	121/139 (87%)	112 (93%)	9 (7%)	13	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	Kd	118/139 (85%)	112 (95%)	6 (5%)	21	43
8	LD	121/139 (87%)	106 (88%)	15 (12%)	4	18
8	Ld	118/139 (85%)	110 (93%)	8 (7%)	14	36
8	MD	121/139 (87%)	113 (93%)	8 (7%)	15	37
8	Md	118/139 (85%)	107 (91%)	11 (9%)	8	26
9	AF	53/237 (22%)	49 (92%)	4 (8%)	12	33
9	Af	49/237 (21%)	44 (90%)	5 (10%)	7	23
9	BF	53/237 (22%)	50 (94%)	3 (6%)	18	40
9	Bf	49/237 (21%)	45 (92%)	4 (8%)	10	31
9	CF	53/237 (22%)	48 (91%)	5 (9%)	8	26
9	Cf	49/237 (21%)	44 (90%)	5 (10%)	7	23
9	DF	53/237 (22%)	50 (94%)	3 (6%)	18	40
9	Df	49/237 (21%)	44 (90%)	5 (10%)	7	23
9	EF	53/237 (22%)	49 (92%)	4 (8%)	12	33
9	Ef	49/237 (21%)	45 (92%)	4 (8%)	10	31
9	FF	53/237 (22%)	49 (92%)	4 (8%)	12	33
9	Ff	49/237 (21%)	45 (92%)	4 (8%)	10	31
9	GF	53/237 (22%)	49 (92%)	4 (8%)	12	33
9	Gf	49/237 (21%)	47 (96%)	2 (4%)	27	49
9	HF	53/237 (22%)	48 (91%)	5 (9%)	8	26
9	Hf	49/237 (21%)	46 (94%)	3 (6%)	17	39
9	IF	53/237 (22%)	50 (94%)	3 (6%)	18	40
9	If	49/237 (21%)	44 (90%)	5 (10%)	7	23
9	JF	53/237 (22%)	46 (87%)	7 (13%)	4	16
9	Jf	49/237 (21%)	46 (94%)	3 (6%)	17	39
9	KF	53/237 (22%)	45 (85%)	8 (15%)	3	13
9	Kf	49/237 (21%)	46 (94%)	3 (6%)	17	39
9	LF	53/237 (22%)	49 (92%)	4 (8%)	12	33
9	Lf	49/237 (21%)	44 (90%)	5 (10%)	7	23
9	MF	53/237 (22%)	49 (92%)	4 (8%)	12	33
9	Mf	49/237 (21%)	46 (94%)	3 (6%)	17	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	VF	53/237 (22%)	52 (98%)	1 (2%)	50	66
9	WF	53/237 (22%)	50 (94%)	3 (6%)	18	40
9	XF	53/237 (22%)	51 (96%)	2 (4%)	29	51
9	YF	53/237 (22%)	49 (92%)	4 (8%)	12	33
9	ZF	53/237 (22%)	48 (91%)	5 (9%)	8	26
10	AC	203/257 (79%)	188 (93%)	15 (7%)	13	33
10	BC	203/257 (79%)	176 (87%)	27 (13%)	4	16
10	CC	178/257 (69%)	159 (89%)	19 (11%)	6	22
10	DC	178/257 (69%)	161 (90%)	17 (10%)	8	25
10	EC	178/257 (69%)	155 (87%)	23 (13%)	4	17
10	FC	203/257 (79%)	189 (93%)	14 (7%)	14	36
10	GC	178/257 (69%)	161 (90%)	17 (10%)	8	25
10	HC	178/257 (69%)	158 (89%)	20 (11%)	6	20
10	IC	178/257 (69%)	161 (90%)	17 (10%)	8	25
10	JC	203/257 (79%)	189 (93%)	14 (7%)	14	36
10	KC	203/257 (79%)	185 (91%)	18 (9%)	9	28
10	LC	178/257 (69%)	157 (88%)	21 (12%)	5	19
10	MC	178/257 (69%)	156 (88%)	22 (12%)	4	18
11	AM	175/276 (63%)	163 (93%)	12 (7%)	14	36
11	BM	175/276 (63%)	162 (93%)	13 (7%)	13	33
11	CM	175/276 (63%)	162 (93%)	13 (7%)	13	33
11	DM	175/276 (63%)	162 (93%)	13 (7%)	13	33
11	EM	175/276 (63%)	160 (91%)	15 (9%)	10	29
11	FM	175/276 (63%)	157 (90%)	18 (10%)	7	23
11	GM	175/276 (63%)	161 (92%)	14 (8%)	11	31
11	HM	175/276 (63%)	168 (96%)	7 (4%)	28	49
11	IM	175/276 (63%)	156 (89%)	19 (11%)	6	21
11	JM	175/276 (63%)	155 (89%)	20 (11%)	5	20
11	KM	175/276 (63%)	161 (92%)	14 (8%)	11	31
11	LM	175/276 (63%)	158 (90%)	17 (10%)	8	25
11	MM	175/276 (63%)	162 (93%)	13 (7%)	13	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	20484/55449 (37%)	18791 (92%)	1693 (8%)	12 30

All (1693) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AG	885	ILE
1	AG	886	LEU
1	AG	898	LYS
1	AG	911	LYS
1	AG	930	ILE
1	AG	944	LEU
1	AG	972	PHE
1	AG	1010	THR
1	AG	1011	VAL
1	AG	1028	THR
2	EH	105	GLU
2	EH	108	ASP
2	EH	147	THR
2	EH	168	VAL
2	EH	219	LYS
2	EH	225	ASN
2	EH	238	MET
2	EH	239	LEU
2	EH	241	LEU
2	EH	249	ASP
2	EH	253	ASP
2	EH	257	GLN
2	EH	266	MET
2	EH	278	ASP
2	EH	287	VAL
2	EH	296	VAL
2	EH	309	GLU
2	EH	321	SER
2	EH	334	THR
2	EH	346	LEU
3	EK	40	LYS
3	EK	50	ASP
3	EK	107	LYS
3	EK	111	LYS
3	EK	156	THR
3	EK	162	ASP
3	EK	183	THR

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Mol	Chain	Res	Type
4	EL	47	TYR
4	EL	49	ASN
4	EL	53	ASP
4	EL	116	TYR
4	EL	121	ASP
4	EL	130	ASP
4	EL	204	LYS
4	EL	210	ASP
4	EL	211	LYS
5	EN	75	VAL
5	EN	81	LEU
5	EN	84	CYS
5	EN	111	GLU
8	Ed	41	LEU
8	Ed	53	LEU
8	Ed	61	VAL
8	Ed	70	THR
8	Ed	78	ASN
8	Ed	107	ARG
8	Ed	111	LYS
8	Ed	115	VAL
8	Ed	126	GLU
8	Ed	131	ILE
8	Ed	142	LYS
8	Ed	145	ILE
8	Ed	147	VAL
8	Ed	152	GLN
9	Ef	216	ILE
9	Ef	223	ILE
9	Ef	245	LYS
9	Ef	250	LEU
8	FD	30	ILE
8	FD	35	ASP
8	FD	71	LEU
8	FD	73	ILE
8	FD	92	GLU
8	FD	109	LEU
8	FD	121	ILE
8	FD	127	SER
8	FD	160	LYS
9	FF	215	VAL
9	FF	223	ILE

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Mol	Chain	Res	Type
9	FF	261	VAL
9	FF	263	LYS
1	Fg	793	GLU
2	FH	105	GLU
2	FH	108	ASP
2	FH	109	LYS
2	FH	129	LYS
2	FH	152	THR
2	FH	221	TYR
2	FH	239	LEU
2	FH	241	LEU
2	FH	249	ASP
2	FH	296	VAL
2	FH	313	VAL
2	FH	317	LEU
2	FH	334	THR
2	FH	352	LYS
3	FK	70	VAL
3	FK	75	LEU
3	FK	83	LEU
3	FK	100	ASN
3	FK	111	LYS
3	FK	180	VAL
3	FK	183	THR
4	FL	44	HIS
4	FL	47	TYR
4	FL	109	LEU
4	FL	129	THR
4	FL	130	ASP
4	FL	140	LEU
4	FL	155	LEU
4	FL	170	ASP
4	FL	172	VAL
4	FL	174	SER
4	FL	177	HIS
4	FL	190	MET
4	FL	228	ARG
4	FL	229	ILE
5	FN	62	ASN
5	FN	78	LEU
5	FN	94	GLN
5	FN	100	LEU

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Mol	Chain	Res	Type
8	Fd	41	LEU
8	Fd	54	GLU
8	Fd	59	GLU
8	Fd	62	ILE
8	Fd	93	GLU
8	Fd	111	LYS
8	Fd	115	VAL
8	Fd	119	ILE
8	Fd	142	LYS
9	Ff	216	ILE
9	Ff	232	VAL
9	Ff	243	MET
9	Ff	244	VAL
10	BC	29	THR
10	BC	42	LYS
10	BC	55	ILE
10	BC	83	GLN
10	BC	84	LEU
10	BC	86	LYS
10	BC	90	ASN
10	BC	91	LEU
10	BC	92	ASP
10	BC	100	LEU
10	BC	106	ILE
10	BC	126	ILE
10	BC	147	THR
10	BC	152	LEU
10	BC	171	LYS
10	BC	175	GLU
10	BC	194	THR
10	BC	196	LEU
10	BC	205	GLU
10	BC	219	MET
10	BC	222	VAL
10	BC	227	VAL
10	BC	229	HIS
10	BC	241	ILE
10	BC	245	ASP
10	BC	250	ILE
10	BC	267	VAL
9	AF	208	ILE
9	AF	215	VAL

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Mol	Chain	Res	Type
9	AF	223	ILE
9	AF	250	LEU
8	GD	30	ILE
8	GD	35	ASP
8	GD	51	SER
8	GD	53	LEU
8	GD	67	LYS
8	GD	73	ILE
8	GD	108	VAL
8	GD	124	LYS
8	GD	126	GLU
8	GD	127	SER
8	GD	154	VAL
9	GF	238	ILE
9	GF	253	ARG
9	GF	256	THR
9	GF	267	GLU
1	Gg	793	GLU
1	Gg	801	MET
1	Gg	802	LEU
1	Gg	808	LEU
1	Gg	809	VAL
1	Gg	814	GLN
2	GH	108	ASP
2	GH	180	VAL
2	GH	215	ILE
2	GH	233	LEU
2	GH	241	LEU
2	GH	248	VAL
2	GH	250	TYR
2	GH	253	ASP
2	GH	264	LYS
2	GH	285	GLU
2	GH	301	ASP
2	GH	313	VAL
2	GH	321	SER
2	GH	353	VAL
3	GK	45	VAL
3	GK	50	ASP
3	GK	60	LEU
3	GK	67	VAL
3	GK	72	GLN

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Mol	Chain	Res	Type
3	GK	83	LEU
3	GK	93	TRP
3	GK	99	LEU
3	GK	100	ASN
3	GK	111	LYS
3	GK	118	SER
3	GK	134	LEU
3	GK	153	ILE
3	GK	156	THR
1	BG	869	MET
1	BG	893	LYS
1	BG	898	LYS
1	BG	913	VAL
1	BG	930	ILE
1	BG	944	LEU
1	BG	972	PHE
1	BG	1010	THR
1	BG	1028	THR
1	BG	1044	ASP
4	GL	57	VAL
4	GL	112	GLN
4	GL	115	GLN
4	GL	130	ASP
4	GL	155	LEU
4	GL	172	VAL
4	GL	221	HIS
5	GN	44	LYS
5	GN	75	VAL
5	GN	81	LEU
5	GN	91	VAL
5	GN	111	GLU
5	GN	114	LEU
8	Gd	61	VAL
8	Gd	62	ILE
8	Gd	91	ILE
8	Gd	108	VAL
8	Gd	118	LEU
8	Gd	119	ILE
8	Gd	147	VAL
9	Gf	216	ILE
9	Gf	264	PHE
8	HD	30	ILE

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Mol	Chain	Res	Type
8	HD	35	ASP
8	HD	52	MET
8	HD	78	ASN
8	HD	91	ILE
8	HD	115	VAL
8	HD	126	GLU
8	HD	130	GLU
8	HD	136	ASP
9	HF	216	ILE
9	HF	223	ILE
9	HF	226	ASN
9	HF	231	THR
9	HF	238	ILE
1	Hg	793	GLU
1	Hg	808	LEU
1	Hg	809	VAL
1	Hg	814	GLN
1	Hg	819	VAL
2	HH	107	ILE
2	HH	138	GLU
2	HH	180	VAL
2	HH	207	ASP
2	HH	238	MET
2	HH	240	THR
2	HH	242	ILE
2	HH	253	ASP
2	HH	284	LEU
2	HH	306	LEU
2	HH	321	SER
3	HK	58	THR
3	HK	66	LYS
3	HK	67	VAL
3	HK	70	VAL
3	HK	75	LEU
3	HK	149	VAL
3	HK	156	THR
4	HL	93	LEU
4	HL	105	ILE
4	HL	125	LEU
4	HL	130	ASP
4	HL	133	PHE
4	HL	217	ASN

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Mol	Chain	Res	Type
4	HL	219	ILE
4	HL	225	GLN
4	HL	226	ASN
11	HM	131	THR
11	HM	134	LEU
11	HM	180	ASP
11	HM	212	LEU
11	HM	222	ILE
11	HM	259	SER
11	HM	300	ASP
5	HN	62	ASN
5	HN	91	VAL
5	HN	115	GLN
8	Hd	31	ASN
8	Hd	35	ASP
8	Hd	36	ASP
8	Hd	55	MET
8	Hd	78	ASN
8	Hd	115	VAL
8	Hd	121	ILE
8	Hd	145	ILE
8	Hd	147	VAL
8	Hd	150	ASN
9	Hf	209	ILE
9	Hf	216	ILE
9	Hf	244	VAL
1	Bg	792	GLN
1	Bg	802	LEU
1	Bg	815	VAL
1	Bg	819	VAL
8	ID	31	ASN
8	ID	35	ASP
8	ID	69	ASN
8	ID	82	ARG
8	ID	115	VAL
8	ID	124	LYS
8	ID	134	ASP
8	ID	147	VAL
9	IF	215	VAL
9	IF	231	THR
9	IF	256	THR
1	Ig	793	GLU

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Mol	Chain	Res	Type
1	Ig	795	GLN
1	Ig	808	LEU
1	Ig	814	GLN
2	IH	108	ASP
2	IH	122	LEU
2	IH	171	LEU
2	IH	180	VAL
2	IH	245	GLN
2	IH	248	VAL
2	IH	250	TYR
2	IH	253	ASP
3	IK	45	VAL
3	IK	57	MET
3	IK	72	GLN
3	IK	78	ILE
3	IK	98	LEU
3	IK	109	PHE
3	IK	111	LYS
3	IK	112	ILE
3	IK	117	THR
3	IK	142	GLU
3	IK	144	LEU
3	IK	156	THR
3	IK	159	LEU
4	IL	47	TYR
4	IL	49	ASN
4	IL	105	ILE
4	IL	109	LEU
4	IL	130	ASP
4	IL	131	LYS
4	IL	142	GLU
4	IL	162	THR
4	IL	172	VAL
4	IL	177	HIS
4	IL	210	ASP
11	IM	134	LEU
11	IM	146	LEU
11	IM	149	ASN
11	IM	150	ILE
11	IM	173	LEU
11	IM	176	VAL
11	IM	178	LYS

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Mol	Chain	Res	Type
11	IM	205	TYR
11	IM	207	ILE
11	IM	208	LYS
11	IM	212	LEU
11	IM	221	LYS
11	IM	229	ASN
11	IM	231	LEU
11	IM	292	MET
11	IM	301	MET
11	IM	312	PHE
11	IM	315	TYR
11	IM	316	ASN
1	CG	869	MET
1	CG	873	LEU
1	CG	898	LYS
1	CG	900	ILE
1	CG	930	ILE
1	CG	944	LEU
1	CG	962	SER
1	CG	965	LEU
1	CG	972	PHE
1	CG	1010	THR
1	CG	1032	TYR
5	IN	65	TYR
5	IN	81	LEU
5	IN	82	MET
5	IN	84	CYS
5	IN	91	VAL
8	Id	26	LYS
8	Id	73	ILE
8	Id	108	VAL
8	Id	115	VAL
9	If	215	VAL
9	If	216	ILE
9	If	238	ILE
9	If	244	VAL
9	If	260	GLN
8	JD	24	LYS
8	JD	35	ASP
8	JD	50	ASP
8	JD	71	LEU
8	JD	91	ILE

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Mol	Chain	Res	Type
8	JD	92	GLU
8	JD	107	ARG
8	JD	115	VAL
8	JD	160	LYS
9	JF	215	VAL
9	JF	216	ILE
9	JF	222	LEU
9	JF	223	ILE
9	JF	238	ILE
9	JF	264	PHE
9	JF	267	GLU
1	Jg	802	LEU
1	Jg	814	GLN
1	Jg	815	VAL
2	JH	107	ILE
2	JH	108	ASP
2	JH	135	GLU
2	JH	159	ASN
2	JH	203	ASN
2	JH	204	ILE
2	JH	233	LEU
2	JH	240	THR
2	JH	241	LEU
2	JH	242	ILE
2	JH	249	ASP
2	JH	253	ASP
2	JH	270	GLU
2	JH	284	LEU
2	JH	321	SER
2	JH	339	MET
2	JH	353	VAL
2	JH	361	LEU
3	JK	50	ASP
3	JK	62	LYS
3	JK	67	VAL
3	JK	70	VAL
3	JK	75	LEU
3	JK	83	LEU
3	JK	86	ASP
3	JK	100	ASN
3	JK	111	LYS
3	JK	125	SER

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Mol	Chain	Res	Type
3	JK	126	VAL
3	JK	156	THR
3	JK	162	ASP
4	JL	47	TYR
4	JL	113	ASP
4	JL	130	ASP
4	JL	133	PHE
4	JL	172	VAL
4	JL	177	HIS
4	JL	181	LEU
4	JL	212	ASN
4	JL	217	ASN
5	JN	52	ASP
5	JN	69	TYR
5	JN	71	THR
5	JN	102	VAL
5	JN	111	GLU
8	Jd	41	LEU
8	Jd	61	VAL
8	Jd	63	THR
8	Jd	92	GLU
8	Jd	93	GLU
8	Jd	108	VAL
8	Jd	115	VAL
8	Jd	141	LYS
8	Jd	142	LYS
9	Jf	208	ILE
9	Jf	232	VAL
9	Jf	263	LYS
2	AH	108	ASP
2	AH	114	ASP
2	AH	134	TYR
2	AH	168	VAL
2	AH	180	VAL
2	AH	196	LEU
2	AH	204	ILE
2	AH	205	GLN
2	AH	211	ASN
2	AH	216	GLN
2	AH	233	LEU
2	AH	240	THR
2	AH	248	VAL

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Mol	Chain	Res	Type
2	AH	253	ASP
2	AH	280	LEU
2	AH	287	VAL
2	AH	296	VAL
2	AH	297	VAL
2	AH	316	ASN
2	AH	321	SER
2	AH	332	ASP
2	AH	344	VAL
2	AH	346	LEU
2	AH	358	VAL
8	KD	32	ASN
8	KD	35	ASP
8	KD	50	ASP
8	KD	85	VAL
8	KD	86	ASP
8	KD	91	ILE
8	KD	108	VAL
8	KD	111	LYS
8	KD	162	TYR
10	CC	61	GLU
10	CC	93	ILE
10	CC	97	ASN
10	CC	101	LEU
10	CC	102	GLU
10	CC	105	ILE
10	CC	116	THR
10	CC	127	ILE
10	CC	143	THR
10	CC	146	THR
10	CC	156	VAL
10	CC	165	LEU
10	CC	173	LYS
10	CC	184	TRP
10	CC	226	VAL
10	CC	247	LEU
10	CC	256	ASN
10	CC	258	ASN
10	CC	266	VAL
9	KF	208	ILE
9	KF	211	TYR
9	KF	215	VAL

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Mol	Chain	Res	Type
9	KF	223	ILE
9	KF	230	LEU
9	KF	238	ILE
9	KF	250	LEU
9	KF	261	VAL
1	Kg	802	LEU
1	Kg	814	GLN
1	Kg	817	THR
1	Kg	819	VAL
2	KH	108	ASP
2	KH	134	TYR
2	KH	168	VAL
2	KH	171	LEU
2	KH	180	VAL
2	KH	183	ASP
2	KH	203	ASN
2	KH	211	ASN
2	KH	218	THR
2	KH	239	LEU
2	KH	240	THR
2	KH	242	ILE
2	KH	248	VAL
2	KH	250	TYR
2	KH	257	GLN
2	KH	287	VAL
2	KH	309	GLU
2	KH	339	MET
2	KH	354	MET
3	KK	46	ASP
3	KK	67	VAL
3	KK	83	LEU
3	KK	99	LEU
3	KK	106	LEU
3	KK	111	LYS
3	KK	117	THR
3	KK	162	ASP
3	KK	183	THR
4	KL	47	TYR
4	KL	93	LEU
4	KL	113	ASP
4	KL	129	THR
4	KL	130	ASP

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Mol	Chain	Res	Type
4	KL	131	LYS
4	KL	133	PHE
4	KL	155	LEU
4	KL	172	VAL
4	KL	183	GLN
4	KL	210	ASP
4	KL	216	ASP
4	KL	217	ASN
4	KL	219	ILE
4	KL	227	ARG
4	KL	229	ILE
11	KM	146	LEU
11	KM	176	VAL
11	KM	192	ARG
11	KM	207	ILE
11	KM	221	LYS
11	KM	222	ILE
11	KM	242	LYS
11	KM	259	SER
11	KM	271	SER
11	KM	279	ILE
11	KM	292	MET
11	KM	299	LEU
11	KM	300	ASP
11	KM	313	ASP
5	KN	65	TYR
5	KN	81	LEU
5	KN	101	VAL
1	DG	869	MET
1	DG	873	LEU
1	DG	893	LYS
1	DG	911	LYS
1	DG	916	PHE
1	DG	930	ILE
1	DG	944	LEU
1	DG	962	SER
1	DG	963	SER
1	DG	965	LEU
1	DG	1010	THR
1	DG	1021	GLN
1	DG	1024	ASN
1	DG	1028	THR

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Mol	Chain	Res	Type
1	DG	1044	ASP
8	Kd	63	THR
8	Kd	67	LYS
8	Kd	93	GLU
8	Kd	111	LYS
8	Kd	142	LYS
8	Kd	147	VAL
9	Kf	216	ILE
9	Kf	222	LEU
9	Kf	244	VAL
8	LD	43	GLU
8	LD	54	GLU
8	LD	67	LYS
8	LD	73	ILE
8	LD	79	LEU
8	LD	85	VAL
8	LD	91	ILE
8	LD	93	GLU
8	LD	95	THR
8	LD	115	VAL
8	LD	123	THR
8	LD	126	GLU
8	LD	127	SER
8	LD	154	VAL
8	LD	156	LEU
9	LF	211	TYR
9	LF	215	VAL
9	LF	234	GLU
9	LF	238	ILE
1	Lg	808	LEU
1	Lg	814	GLN
1	Lg	815	VAL
1	Lg	816	GLU
1	Lg	819	VAL
8	CD	50	ASP
8	CD	82	ARG
8	CD	86	ASP
2	LH	108	ASP
2	LH	138	GLU
2	LH	141	LYS
2	LH	147	THR
2	LH	218	THR

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Mol	Chain	Res	Type
2	LH	226	LEU
2	LH	233	LEU
2	LH	248	VAL
2	LH	249	ASP
2	LH	253	ASP
2	LH	278	ASP
2	LH	280	LEU
2	LH	281	LEU
2	LH	301	ASP
2	LH	313	VAL
2	LH	321	SER
2	LH	354	MET
3	LK	40	LYS
3	LK	50	ASP
3	LK	70	VAL
3	LK	72	GLN
3	LK	75	LEU
3	LK	76	ILE
3	LK	92	ASN
3	LK	111	LYS
3	LK	127	LYS
3	LK	156	THR
3	LK	162	ASP
3	LK	182	ILE
3	LK	183	THR
4	LL	47	TYR
4	LL	49	ASN
4	LL	98	TYR
4	LL	109	LEU
4	LL	133	PHE
4	LL	172	VAL
4	LL	210	ASP
11	LM	134	LEU
11	LM	158	VAL
11	LM	173	LEU
11	LM	180	ASP
11	LM	184	LEU
11	LM	188	PHE
11	LM	191	LEU
11	LM	192	ARG
11	LM	205	TYR
11	LM	207	ILE

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Mol	Chain	Res	Type
11	LM	210	ASP
11	LM	221	LYS
11	LM	285	SER
11	LM	292	MET
11	LM	299	LEU
11	LM	301	MET
11	LM	308	ASP
5	LN	48	ILE
5	LN	62	ASN
5	LN	75	VAL
8	Ld	41	LEU
8	Ld	70	THR
8	Ld	91	ILE
8	Ld	108	VAL
8	Ld	115	VAL
8	Ld	119	ILE
8	Ld	142	LYS
8	Ld	147	VAL
9	Lf	216	ILE
9	Lf	244	VAL
9	Lf	245	LYS
9	Lf	255	LEU
9	Lf	262	ILE
3	AK	67	VAL
3	AK	75	LEU
3	AK	98	LEU
3	AK	102	ILE
3	AK	112	ILE
3	AK	126	VAL
3	AK	156	THR
3	AK	162	ASP
3	AK	163	LYS
3	AK	182	ILE
8	MD	35	ASP
8	MD	50	ASP
8	MD	91	ILE
8	MD	115	VAL
8	MD	121	ILE
8	MD	126	GLU
8	MD	145	ILE
8	MD	156	LEU
9	MF	208	ILE

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Mol	Chain	Res	Type
9	MF	222	LEU
9	MF	231	THR
9	MF	233	ARG
1	Mg	802	LEU
1	Mg	814	GLN
1	Mg	815	VAL
1	Mg	816	GLU
2	MH	108	ASP
2	MH	130	LEU
2	MH	147	THR
2	MH	152	THR
2	MH	158	VAL
2	MH	168	VAL
2	MH	171	LEU
2	MH	180	VAL
2	MH	238	MET
2	MH	248	VAL
2	MH	249	ASP
2	MH	254	LEU
2	MH	255	ARG
2	MH	264	LYS
2	MH	268	THR
2	MH	278	ASP
2	MH	287	VAL
2	MH	308	ASN
2	MH	313	VAL
2	MH	316	ASN
3	MK	40	LYS
3	MK	45	VAL
3	MK	50	ASP
3	MK	67	VAL
3	MK	70	VAL
3	MK	75	LEU
3	MK	92	ASN
3	MK	99	LEU
3	MK	106	LEU
3	MK	111	LYS
3	MK	112	ILE
3	MK	116	VAL
3	MK	127	LYS
3	MK	144	LEU
3	MK	156	THR

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Mol	Chain	Res	Type
3	MK	179	ARG
3	MK	181	GLU
3	MK	182	ILE
4	ML	47	TYR
4	ML	91	VAL
4	ML	112	GLN
4	ML	113	ASP
4	ML	123	ARG
4	ML	130	ASP
4	ML	131	LYS
4	ML	139	ARG
4	ML	140	LEU
4	ML	172	VAL
4	ML	189	MET
4	ML	193	LEU
4	ML	219	ILE
11	MM	134	LEU
11	MM	149	ASN
11	MM	152	LEU
11	MM	180	ASP
11	MM	184	LEU
11	MM	205	TYR
11	MM	221	LYS
11	MM	232	ASP
11	MM	257	ASP
11	MM	262	GLU
11	MM	277	SER
11	MM	292	MET
11	MM	318	GLN
5	MN	69	TYR
5	MN	70	CYS
5	MN	72	ARG
5	MN	91	VAL
5	MN	95	LEU
5	MN	100	LEU
5	MN	110	GLU
5	MN	112	CYS
5	MN	114	LEU
5	MN	115	GLN
1	EG	869	MET
1	EG	885	ILE
1	EG	886	LEU

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Mol	Chain	Res	Type
1	EG	895	LYS
1	EG	911	LYS
1	EG	930	ILE
1	EG	944	LEU
1	EG	962	SER
1	EG	965	LEU
1	EG	972	PHE
1	EG	1010	THR
1	EG	1021	GLN
8	Md	32	ASN
8	Md	41	LEU
8	Md	55	MET
8	Md	73	ILE
8	Md	78	ASN
8	Md	85	VAL
8	Md	108	VAL
8	Md	115	VAL
8	Md	142	LYS
8	Md	145	ILE
8	Md	147	VAL
9	Mf	236	SER
9	Mf	245	LYS
9	Mf	255	LEU
9	VF	223	ILE
1	VG	793	GLU
1	VG	814	GLN
2	VH	105	GLU
2	VH	134	TYR
2	VH	135	GLU
2	VH	138	GLU
2	VH	160	LEU
2	VH	171	LEU
2	VH	203	ASN
2	VH	219	LYS
2	VH	233	LEU
2	VH	238	MET
2	VH	240	THR
2	VH	241	LEU
2	VH	248	VAL
2	VH	249	ASP
2	VH	253	ASP
2	VH	306	LEU

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Mol	Chain	Res	Type
2	VH	321	SER
9	CF	211	TYR
9	CF	215	VAL
9	CF	223	ILE
9	CF	245	LYS
9	CF	256	THR
9	WF	208	ILE
9	WF	231	THR
9	WF	250	LEU
1	WG	795	GLN
1	WG	797	ARG
1	WG	801	MET
1	WG	808	LEU
1	WG	817	THR
2	WH	108	ASP
2	WH	115	MET
2	WH	134	TYR
2	WH	136	THR
2	WH	144	THR
2	WH	171	LEU
2	WH	215	ILE
2	WH	225	ASN
2	WH	231	ARG
2	WH	239	LEU
2	WH	241	LEU
2	WH	242	ILE
2	WH	248	VAL
2	WH	249	ASP
2	WH	253	ASP
2	WH	262	ASN
2	WH	313	VAL
2	WH	315	THR
2	WH	332	ASP
2	WH	337	TYR
2	WH	345	LEU
2	WH	354	MET
2	WH	355	GLN
9	XF	215	VAL
9	XF	256	THR
1	XG	795	GLN
1	XG	810	GLN
1	XG	818	GLN

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Mol	Chain	Res	Type
2	XH	105	GLU
2	XH	108	ASP
2	XH	154	THR
2	XH	180	VAL
2	XH	203	ASN
2	XH	211	ASN
2	XH	220	LEU
2	XH	233	LEU
2	XH	239	LEU
2	XH	241	LEU
2	XH	248	VAL
2	XH	249	ASP
2	XH	253	ASP
2	XH	262	ASN
2	XH	297	VAL
2	XH	303	ARG
2	XH	308	ASN
2	XH	329	THR
2	XH	338	GLU
2	XH	341	LYS
2	XH	358	VAL
9	YF	231	THR
9	YF	238	ILE
9	YF	256	THR
9	YF	263	LYS
4	AL	47	TYR
4	AL	51	GLN
4	AL	57	VAL
4	AL	91	VAL
4	AL	133	PHE
4	AL	174	SER
4	AL	191	THR
4	AL	210	ASP
1	YG	795	GLN
1	YG	815	VAL
1	YG	816	GLU
1	YG	817	THR
1	YG	819	VAL
1	YG	822	GLU
2	YH	105	GLU
2	YH	115	MET
2	YH	118	ASN

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Mol	Chain	Res	Type
2	YH	147	THR
2	YH	171	LEU
2	YH	176	VAL
2	YH	180	VAL
2	YH	204	ILE
2	YH	205	GLN
2	YH	214	MET
2	YH	220	LEU
2	YH	233	LEU
2	YH	239	LEU
2	YH	241	LEU
2	YH	248	VAL
2	YH	253	ASP
2	YH	294	ARG
2	YH	306	LEU
2	YH	316	ASN
2	YH	345	LEU
2	YH	353	VAL
2	YH	356	LEU
2	YH	358	VAL
10	DC	68	GLN
10	DC	85	GLN
10	DC	89	LEU
10	DC	90	ASP
10	DC	104	ILE
10	DC	115	THR
10	DC	122	GLN
10	DC	126	ILE
10	DC	145	THR
10	DC	153	ASP
10	DC	155	VAL
10	DC	173	GLU
10	DC	183	TRP
10	DC	203	GLU
10	DC	225	VAL
10	DC	227	HIS
10	DC	243	ASP
9	ZF	212	ILE
9	ZF	223	ILE
9	ZF	231	THR
9	ZF	238	ILE
9	ZF	264	PHE

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Mol	Chain	Res	Type
1	ZG	793	GLU
1	ZG	794	ILE
1	ZG	796	GLN
1	ZG	802	LEU
1	ZG	810	GLN
1	ZG	814	GLN
2	ZH	105	GLU
2	ZH	130	LEU
2	ZH	207	ASP
2	ZH	213	LEU
2	ZH	233	LEU
2	ZH	239	LEU
2	ZH	241	LEU
2	ZH	242	ILE
2	ZH	248	VAL
2	ZH	253	ASP
2	ZH	285	GLU
2	ZH	287	VAL
2	ZH	320	LEU
2	ZH	321	SER
2	ZH	329	THR
2	ZH	334	THR
2	ZH	338	GLU
1	FG	864	LYS
1	FG	885	ILE
1	FG	898	LYS
1	FG	900	ILE
1	FG	911	LYS
1	FG	919	MET
1	FG	930	ILE
1	FG	944	LEU
1	FG	962	SER
1	FG	965	LEU
1	FG	972	PHE
1	FG	1010	THR
1	FG	1021	GLN
1	FG	1024	ASN
1	FG	1028	THR
1	FG	1044	ASP
11	AM	136	LEU
11	AM	146	LEU
11	AM	152	LEU

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Mol	Chain	Res	Type
11	AM	175	ILE
11	AM	184	LEU
11	AM	203	SER
11	AM	204	LEU
11	AM	212	LEU
11	AM	222	ILE
11	AM	246	LEU
11	AM	263	ILE
11	AM	292	MET
11	BM	134	LEU
11	BM	146	LEU
11	BM	152	LEU
11	BM	175	ILE
11	BM	184	LEU
11	BM	204	LEU
11	BM	215	ARG
11	BM	221	LYS
11	BM	229	ASN
11	BM	287	THR
11	BM	292	MET
11	BM	303	GLU
11	BM	304	TRP
11	EM	136	LEU
11	EM	144	THR
11	EM	175	ILE
11	EM	184	LEU
11	EM	193	GLN
11	EM	204	LEU
11	EM	205	TYR
11	EM	210	ASP
11	EM	212	LEU
11	EM	222	ILE
11	EM	240	GLN
11	EM	262	GLU
11	EM	292	MET
11	EM	301	MET
11	EM	303	GLU
11	FM	114	ASN
11	FM	129	LEU
11	FM	136	LEU
11	FM	146	LEU
11	FM	152	LEU

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Mol	Chain	Res	Type
11	FM	160	ASN
11	FM	171	ARG
11	FM	173	LEU
11	FM	175	ILE
11	FM	192	ARG
11	FM	194	LEU
11	FM	204	LEU
11	FM	210	ASP
11	FM	222	ILE
11	FM	263	ILE
11	FM	279	ILE
11	FM	292	MET
11	FM	304	TRP
11	GM	127	ASN
11	GM	146	LEU
11	GM	152	LEU
11	GM	175	ILE
11	GM	191	LEU
11	GM	201	THR
11	GM	204	LEU
11	GM	210	ASP
11	GM	221	LYS
11	GM	222	ILE
11	GM	275	ASP
11	GM	292	MET
11	GM	304	TRP
11	GM	312	PHE
11	JM	129	LEU
11	JM	144	THR
11	JM	152	LEU
11	JM	175	ILE
11	JM	184	LEU
11	JM	191	LEU
11	JM	204	LEU
11	JM	205	TYR
11	JM	221	LYS
11	JM	229	ASN
11	JM	262	GLU
11	JM	263	ILE
11	JM	269	GLN
11	JM	279	ILE
11	JM	287	THR

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Mol	Chain	Res	Type
11	JM	292	MET
11	JM	299	LEU
11	JM	301	MET
11	JM	303	GLU
11	JM	304	TRP
5	AN	62	ASN
5	AN	71	THR
5	AN	72	ARG
5	AN	91	VAL
5	AN	95	LEU
1	Cg	815	VAL
8	Ad	36	ASP
8	Ad	41	LEU
8	Ad	53	LEU
8	Ad	54	GLU
8	Ad	61	VAL
8	Ad	73	ILE
8	Ad	97	ARG
8	Ad	117	VAL
8	Ad	119	ILE
8	Ad	142	LYS
9	Af	212	ILE
9	Af	215	VAL
9	Af	216	ILE
9	Af	238	ILE
9	Af	260	GLN
8	BD	38	THR
8	BD	50	ASP
8	BD	68	ASP
8	BD	85	VAL
8	BD	86	ASP
8	BD	123	THR
8	BD	128	LEU
9	BF	208	ILE
9	BF	238	ILE
9	BF	250	LEU
2	BH	105	GLU
2	BH	108	ASP
2	BH	160	LEU
2	BH	179	LEU
2	BH	203	ASN
2	BH	233	LEU

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Mol	Chain	Res	Type
2	BH	238	MET
2	BH	241	LEU
2	BH	242	ILE
2	BH	248	VAL
2	BH	253	ASP
2	BH	285	GLU
2	BH	287	VAL
2	BH	296	VAL
2	BH	345	LEU
2	BH	352	LYS
2	BH	356	LEU
3	BK	45	VAL
3	BK	70	VAL
3	BK	92	ASN
3	BK	100	ASN
3	BK	101	GLU
3	BK	111	LYS
3	BK	117	THR
3	BK	137	SER
3	BK	169	THR
4	BL	47	TYR
4	BL	91	VAL
4	BL	109	LEU
4	BL	112	GLN
4	BL	113	ASP
4	BL	129	THR
4	BL	133	PHE
4	BL	134	MET
4	BL	163	ILE
4	BL	203	LEU
4	BL	212	ASN
4	BL	225	GLN
5	BN	57	ARG
5	BN	78	LEU
5	BN	81	LEU
5	BN	95	LEU
5	BN	104	ASN
5	BN	108	VAL
8	Bd	27	LYS
8	Bd	36	ASP
8	Bd	55	MET
8	Bd	61	VAL

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Mol	Chain	Res	Type
8	Bd	63	THR
8	Bd	111	LYS
8	Bd	115	VAL
8	Bd	121	ILE
8	Bd	131	ILE
9	Bf	216	ILE
9	Bf	221	TRP
9	Bf	247	ILE
9	Bf	260	GLN
10	EC	80	ASP
10	EC	84	ASN
10	EC	95	ASP
10	EC	97	ASN
10	EC	103	HIS
10	EC	105	ILE
10	EC	112	GLU
10	EC	119	LEU
10	EC	127	ILE
10	EC	143	THR
10	EC	146	THR
10	EC	149	GLN
10	EC	156	VAL
10	EC	165	LEU
10	EC	174	GLU
10	EC	180	THR
10	EC	184	TRP
10	EC	193	THR
10	EC	215	LEU
10	EC	221	VAL
10	EC	249	ILE
10	EC	255	LEU
10	EC	266	VAL
10	FC	29	THR
10	FC	57	GLU
10	FC	80	ILE
10	FC	90	ASN
10	FC	92	ASP
10	FC	100	LEU
10	FC	124	GLN
10	FC	128	ILE
10	FC	155	ASP
10	FC	164	VAL

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Mol	Chain	Res	Type
10	FC	166	LEU
10	FC	175	GLU
10	FC	227	VAL
10	FC	231	ASP
10	GC	91	ASP
10	GC	105	ILE
10	GC	116	THR
10	GC	127	ILE
10	GC	141	ILE
10	GC	143	THR
10	GC	146	THR
10	GC	153	MET
10	GC	154	ASP
10	GC	156	VAL
10	GC	165	LEU
10	GC	180	THR
10	GC	184	TRP
10	GC	195	LEU
10	GC	259	SER
10	GC	266	VAL
10	GC	268	LYS
1	GG	886	LEU
1	GG	895	LYS
1	GG	900	ILE
1	GG	930	ILE
1	GG	944	LEU
1	GG	947	ARG
1	GG	962	SER
1	GG	963	SER
1	GG	972	PHE
1	GG	1010	THR
1	GG	1024	ASN
1	GG	1044	ASP
10	HC	84	LYS
10	HC	90	ASP
10	HC	96	ASN
10	HC	104	ILE
10	HC	108	VAL
10	HC	110	LEU
10	HC	117	ASN
10	HC	118	LEU
10	HC	122	GLN

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Mol	Chain	Res	Type
10	HC	126	ILE
10	HC	132	LYS
10	HC	138	HIS
10	HC	142	THR
10	HC	145	THR
10	HC	147	ARG
10	HC	168	THR
10	HC	183	TRP
10	HC	209	ILE
10	HC	243	ASP
10	HC	265	VAL
10	IC	79	ASP
10	IC	80	GLU
10	IC	89	LEU
10	IC	104	ILE
10	IC	110	LEU
10	IC	124	ILE
10	IC	126	ILE
10	IC	128	ASP
10	IC	140	ILE
10	IC	142	THR
10	IC	167	LYS
10	IC	168	THR
10	IC	172	LYS
10	IC	210	LEU
10	IC	225	VAL
10	IC	254	LEU
10	IC	265	VAL
10	JC	29	THR
10	JC	45	ARG
10	JC	61	LYS
10	JC	80	ILE
10	JC	98	ASN
10	JC	118	LEU
10	JC	124	GLN
10	JC	147	THR
10	JC	174	LYS
10	JC	194	THR
10	JC	205	GLU
10	JC	222	VAL
10	JC	227	VAL
10	JC	259	ASN

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Mol	Chain	Res	Type
10	KC	29	THR
10	KC	56	ARG
10	KC	57	GLU
10	KC	91	LEU
10	KC	98	ASN
10	KC	106	ILE
10	KC	142	ILE
10	KC	155	ASP
10	KC	171	LYS
10	KC	182	GLU
10	KC	183	ARG
10	KC	204	LYS
10	KC	205	GLU
10	KC	215	LYS
10	KC	229	HIS
10	KC	250	ILE
10	KC	256	LEU
10	KC	262	GLU
10	LC	60	GLU
10	LC	88	ASN
10	LC	94	ASP
10	LC	96	ASN
10	LC	101	GLU
10	LC	102	HIS
10	LC	103	ASN
10	LC	104	ILE
10	LC	108	VAL
10	LC	109	LEU
10	LC	115	THR
10	LC	118	LEU
10	LC	126	ILE
10	LC	145	THR
10	LC	169	LYS
10	LC	183	TRP
10	LC	225	VAL
10	LC	227	HIS
10	LC	242	ASP
10	LC	262	ARG
10	LC	265	VAL
10	MC	98	LEU
10	MC	102	HIS
10	MC	104	ILE

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Mol	Chain	Res	Type
10	MC	108	VAL
10	MC	111	GLU
10	MC	132	LYS
10	MC	141	THR
10	MC	142	THR
10	MC	145	THR
10	MC	147	ARG
10	MC	155	VAL
10	MC	162	VAL
10	MC	173	GLU
10	MC	180	GLU
10	MC	183	TRP
10	MC	203	GLU
10	MC	213	LYS
10	MC	233	THR
10	MC	240	HIS
10	MC	254	LEU
10	MC	265	VAL
10	MC	267	LYS
2	CH	105	GLU
2	CH	108	ASP
2	CH	130	LEU
2	CH	182	LEU
2	CH	204	ILE
2	CH	211	ASN
2	CH	233	LEU
2	CH	242	ILE
2	CH	248	VAL
2	CH	264	LYS
2	CH	278	ASP
2	CH	287	VAL
2	CH	313	VAL
2	CH	321	SER
2	CH	332	ASP
2	CH	361	LEU
3	CK	45	VAL
3	CK	50	ASP
3	CK	73	ASN
3	CK	92	ASN
3	CK	99	LEU
3	CK	111	LYS
3	CK	156	THR

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Mol	Chain	Res	Type
3	CK	163	LYS
4	CL	47	TYR
4	CL	49	ASN
4	CL	104	LYS
4	CL	112	GLN
4	CL	129	THR
4	CL	140	LEU
4	CL	155	LEU
4	CL	175	ARG
4	CL	225	GLN
11	CM	129	LEU
11	CM	133	TYR
11	CM	134	LEU
11	CM	160	ASN
11	CM	164	GLN
11	CM	178	LYS
11	CM	184	LEU
11	CM	207	ILE
11	CM	279	ILE
11	CM	284	LEU
11	CM	287	THR
11	CM	292	MET
11	CM	314	ARG
5	CN	70	CYS
5	CN	71	THR
5	CN	95	LEU
5	CN	101	VAL
5	CN	107	TYR
5	CN	112	CYS
5	CN	114	LEU
8	Cd	67	LYS
8	Cd	91	ILE
8	Cd	93	GLU
8	Cd	111	LYS
8	Cd	115	VAL
8	Cd	128	LEU
8	Cd	147	VAL
9	Cf	216	ILE
9	Cf	233	ARG
9	Cf	236	SER
9	Cf	243	MET
9	Cf	247	ILE

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Mol	Chain	Res	Type
8	DD	50	ASP
8	DD	91	ILE
8	DD	100	LYS
8	DD	108	VAL
8	DD	111	LYS
8	DD	115	VAL
8	DD	123	THR
9	DF	215	VAL
9	DF	230	LEU
9	DF	268	ASP
1	Dg	794	ILE
1	Dg	800	ASP
1	Dg	811	ASP
1	Dg	819	VAL
2	DH	123	ASN
2	DH	138	GLU
2	DH	180	VAL
2	DH	213	LEU
2	DH	231	ARG
2	DH	241	LEU
2	DH	249	ASP
2	DH	254	LEU
2	DH	262	ASN
2	DH	278	ASP
2	DH	287	VAL
2	DH	321	SER
2	DH	342	SER
2	DH	354	MET
2	DH	361	LEU
3	DK	50	ASP
3	DK	56	MET
3	DK	58	THR
3	DK	75	LEU
3	DK	86	ASP
3	DK	111	LYS
3	DK	116	VAL
3	DK	124	VAL
3	DK	149	VAL
3	DK	156	THR
3	DK	165	ILE
4	DL	47	TYR
4	DL	49	ASN

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Mol	Chain	Res	Type
4	DL	109	LEU
4	DL	116	TYR
4	DL	130	ASP
4	DL	172	VAL
4	DL	177	HIS
4	DL	193	LEU
4	DL	210	ASP
4	DL	212	ASN
11	DM	146	LEU
11	DM	150	ILE
11	DM	164	GLN
11	DM	176	VAL
11	DM	184	LEU
11	DM	191	LEU
11	DM	212	LEU
11	DM	222	ILE
11	DM	229	ASN
11	DM	242	LYS
11	DM	292	MET
11	DM	310	LYS
11	DM	315	TYR
5	DN	77	ASP
5	DN	94	GLN
5	DN	108	VAL
5	DN	114	LEU
5	DN	115	GLN
1	HG	872	VAL
1	HG	885	ILE
1	HG	895	LYS
1	HG	900	ILE
1	HG	911	LYS
1	HG	913	VAL
1	HG	930	ILE
1	HG	944	LEU
1	HG	956	TYR
1	HG	962	SER
1	HG	963	SER
1	HG	965	LEU
1	HG	1024	ASN
1	IG	869	MET
1	IG	872	VAL
1	IG	885	ILE

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Mol	Chain	Res	Type
1	IG	911	LYS
1	IG	930	ILE
1	IG	944	LEU
1	IG	956	TYR
1	IG	962	SER
1	IG	963	SER
1	IG	965	LEU
1	IG	972	PHE
1	IG	1010	THR
1	IG	1044	ASP
1	JG	869	MET
1	JG	895	LYS
1	JG	898	LYS
1	JG	900	ILE
1	JG	911	LYS
1	JG	913	VAL
1	JG	916	PHE
1	JG	926	LYS
1	JG	930	ILE
1	JG	950	HIS
1	JG	962	SER
1	JG	965	LEU
1	JG	972	PHE
1	JG	1010	THR
1	KG	874	ASP
1	KG	886	LEU
1	KG	898	LYS
1	KG	916	PHE
1	KG	930	ILE
1	KG	944	LEU
1	KG	962	SER
1	KG	972	PHE
1	KG	1010	THR
1	KG	1011	VAL
1	KG	1024	ASN
1	KG	1028	THR
1	LG	869	MET
1	LG	872	VAL
1	LG	873	LEU
1	LG	886	LEU
1	LG	895	LYS
1	LG	898	LYS

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Mol	Chain	Res	Type
1	LG	930	ILE
1	LG	939	THR
1	LG	944	LEU
1	LG	962	SER
1	LG	1010	THR
1	MG	869	MET
1	MG	885	ILE
1	MG	898	LYS
1	MG	930	ILE
1	MG	944	LEU
1	MG	956	TYR
1	MG	965	LEU
1	MG	1010	THR
1	MG	1017	GLN
1	MG	1028	THR
1	NG	885	ILE
1	NG	898	LYS
1	NG	910	ASP
1	NG	930	ILE
1	NG	944	LEU
1	NG	962	SER
1	NG	972	PHE
1	NG	1010	THR
1	NG	1028	THR
1	NG	1044	ASP
1	OG	865	THR
1	OG	885	ILE
1	OG	910	ASP
1	OG	930	ILE
1	OG	944	LEU
1	OG	947	ARG
1	OG	962	SER
1	OG	965	LEU
1	OG	966	GLN
1	OG	972	PHE
1	OG	1010	THR
1	OG	1020	GLN
1	OG	1028	THR
1	PG	863	ILE
1	PG	869	MET
1	PG	886	LEU
1	PG	898	LYS

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Mol	Chain	Res	Type
1	PG	912	MET
1	PG	913	VAL
1	PG	930	ILE
1	PG	944	LEU
1	PG	965	LEU
1	PG	972	PHE
1	PG	1010	THR
10	AC	29	THR
10	AC	90	ASN
10	AC	106	ILE
10	AC	113	GLU
10	AC	126	ILE
10	AC	149	ARG
10	AC	163	ASN
10	AC	170	THR
10	AC	174	LYS
10	AC	175	GLU
10	AC	196	LEU
10	AC	215	LYS
10	AC	221	MET
10	AC	232	LEU
10	AC	234	VAL
8	Dd	41	LEU
8	Dd	85	VAL
8	Dd	93	GLU
8	Dd	115	VAL
8	Dd	123	THR
8	Dd	126	GLU
8	Dd	128	LEU
8	Dd	147	VAL
1	Ag	796	GLN
1	Ag	809	VAL
1	Ag	814	GLN
1	Ag	815	VAL
1	Ag	819	VAL
9	Df	215	VAL
9	Df	216	ILE
9	Df	222	LEU
9	Df	232	VAL
9	Df	245	LYS
8	AD	35	ASP
8	AD	78	ASN

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Mol	Chain	Res	Type
8	AD	85	VAL
8	AD	115	VAL
8	AD	119	ILE
8	AD	145	ILE
8	AD	155	GLU
8	ED	32	ASN
8	ED	50	ASP
8	ED	55	MET
8	ED	115	VAL
8	ED	127	SER
8	ED	131	ILE
8	ED	156	LEU
9	EF	222	LEU
9	EF	223	ILE
9	EF	230	LEU
9	EF	238	ILE
1	Eg	810	GLN
1	Eg	814	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (206) such sidechains are listed below:

Mol	Chain	Res	Type
1	AG	976	ASN
2	EH	118	ASN
2	EH	173	GLN
2	EH	282	HIS
4	EL	196	ASN
4	EL	221	HIS
4	EL	226	ASN
5	EN	61	ASN
8	Ed	32	ASN
8	Ed	152	GLN
8	FD	32	ASN
2	FH	355	GLN
4	FL	156	ASN
4	FL	221	HIS
5	FN	61	ASN
9	Ff	213	GLN
9	Ff	251	GLN
10	BC	124	GLN
10	BC	187	ASN
8	GD	138	GLN

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Mol	Chain	Res	Type
1	Gg	796	GLN
1	Gg	807	GLN
2	GH	355	GLN
1	BG	938	ASN
1	BG	1020	GLN
4	GL	150	ASN
4	GL	177	HIS
5	GN	79	GLN
5	GN	104	ASN
8	Gd	32	ASN
9	Gf	251	GLN
9	HF	226	ASN
1	Hg	818	GLN
2	HH	205	GLN
2	HH	211	ASN
3	HK	92	ASN
4	HL	48	ASN
4	HL	49	ASN
4	HL	217	ASN
11	HM	160	ASN
8	Hd	146	HIS
1	Bg	796	GLN
1	Bg	810	GLN
8	ID	69	ASN
9	IF	260	GLN
1	Ig	818	GLN
2	IH	203	ASN
2	IH	205	GLN
2	IH	211	ASN
2	IH	234	ASN
3	IK	87	GLN
4	IL	141	ASN
11	IM	174	GLN
1	CG	1020	GLN
9	If	251	GLN
9	If	260	GLN
9	JF	213	GLN
2	JH	173	GLN
2	JH	282	HIS
2	JH	308	ASN
2	JH	340	GLN
4	JL	110	GLN

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Mol	Chain	Res	Type
4	JL	217	ASN
8	Jd	32	ASN
8	Jd	152	GLN
8	KD	32	ASN
1	Kg	796	GLN
2	KH	132	GLN
2	KH	205	GLN
2	KH	234	ASN
2	KH	308	ASN
2	KH	355	GLN
4	KL	110	GLN
4	KL	115	GLN
11	KM	269	GLN
1	DG	1017	GLN
1	DG	1020	GLN
8	Kd	32	ASN
9	Kf	213	GLN
9	Kf	260	GLN
8	LD	80	GLN
8	LD	150	ASN
8	LD	152	GLN
9	LF	266	GLN
2	LH	118	ASN
2	LH	257	GLN
4	LL	115	GLN
8	Ld	32	ASN
8	MD	32	ASN
1	Mg	807	GLN
2	MH	205	GLN
2	MH	222	ASN
2	MH	225	ASN
2	MH	282	HIS
11	MM	128	ASN
11	MM	249	GLN
11	MM	267	ASN
11	MM	316	ASN
1	EG	1017	GLN
8	Md	152	GLN
9	Mf	266	GLN
1	VG	818	GLN
2	VH	222	ASN
2	VH	245	GLN

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Mol	Chain	Res	Type
2	WH	132	GLN
2	WH	222	ASN
2	WH	350	HIS
9	XF	266	GLN
2	XH	234	ASN
4	AL	149	ASN
2	YH	156	GLN
2	YH	308	ASN
2	YH	355	GLN
1	ZG	807	GLN
1	ZG	810	GLN
1	ZG	818	GLN
2	ZH	118	ASN
2	ZH	156	GLN
2	ZH	203	ASN
2	ZH	205	GLN
2	ZH	225	ASN
11	AM	128	ASN
11	AM	174	GLN
11	BM	127	ASN
11	BM	128	ASN
11	BM	140	ASN
11	BM	166	ASN
11	EM	128	ASN
11	EM	174	GLN
11	EM	267	ASN
11	FM	174	GLN
11	FM	306	GLN
11	JM	174	GLN
11	JM	306	GLN
1	Cg	810	GLN
8	Ad	32	ASN
8	Ad	146	HIS
2	BH	222	ASN
2	BH	225	ASN
3	BK	87	GLN
4	BL	44	HIS
4	BL	217	ASN
4	BL	221	HIS
4	BL	225	GLN
5	BN	61	ASN
8	Bd	152	GLN

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Mol	Chain	Res	Type
9	Bf	266	GLN
10	EC	149	GLN
10	EC	192	ASN
10	FC	104	HIS
10	FC	119	ASN
10	FC	163	ASN
10	FC	187	ASN
1	GG	976	ASN
1	GG	1017	GLN
1	GG	1020	GLN
1	GG	1043	GLN
10	IC	96	ASN
10	IC	114	ASN
10	JC	36	GLN
10	JC	70	GLN
10	KC	90	ASN
10	KC	105	ASN
10	KC	116	ASN
10	KC	193	ASN
10	LC	85	GLN
10	LC	96	ASN
10	MC	83	ASN
10	MC	85	GLN
2	CH	211	ASN
2	CH	257	GLN
2	CH	262	ASN
3	CK	61	ASN
3	CK	147	GLN
4	CL	196	ASN
11	CM	164	GLN
11	CM	174	GLN
8	Cd	32	ASN
8	DD	80	GLN
8	DD	152	GLN
9	DF	260	GLN
1	Dg	796	GLN
2	DH	225	ASN
3	DK	147	GLN
4	DL	115	GLN
4	DL	185	GLN
4	DL	225	GLN
5	DN	79	GLN

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Mol	Chain	Res	Type
1	HG	938	ASN
1	IG	1017	GLN
1	JG	973	GLN
1	JG	976	ASN
1	JG	1020	GLN
1	LG	1017	GLN
1	LG	1020	GLN
1	MG	1017	GLN
1	NG	1020	GLN
1	OG	1017	GLN
1	PG	976	ASN
1	PG	1017	GLN
10	AC	199	ASN
9	Df	266	GLN
8	AD	80	GLN
8	ED	80	GLN
8	ED	138	GLN
1	Eg	810	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
7	EX	1
7	GX	1
7	YX	1
7	VX	1
7	CX	1
7	AX	1
7	FX	1
7	JX	1
7	KX	1
7	MX	1
7	WX	1
7	XX	1
7	LX	1
7	BX	1
7	HX	1
7	ZX	1
7	IX	1
7	DX	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	EX	38:UNK	C	70:UNK	N	24.84
1	GX	38:UNK	C	70:UNK	N	24.65
1	YX	38:UNK	C	70:UNK	N	24.61
1	VX	38:UNK	C	70:UNK	N	24.52
1	CX	38:UNK	C	70:UNK	N	24.52
1	AX	38:UNK	C	70:UNK	N	23.98
1	FX	38:UNK	C	70:UNK	N	23.93
1	JX	38:UNK	C	70:UNK	N	23.86
1	KX	38:UNK	C	70:UNK	N	23.86
1	MX	38:UNK	C	70:UNK	N	23.79
1	WX	38:UNK	C	70:UNK	N	23.46
1	XX	38:UNK	C	70:UNK	N	23.39
1	LX	38:UNK	C	70:UNK	N	23.18
1	BX	38:UNK	C	70:UNK	N	23.14
1	HX	38:UNK	C	70:UNK	N	22.95
1	ZX	38:UNK	C	70:UNK	N	22.81
1	IX	38:UNK	C	70:UNK	N	22.08
1	DX	38:UNK	C	70:UNK	N	21.48

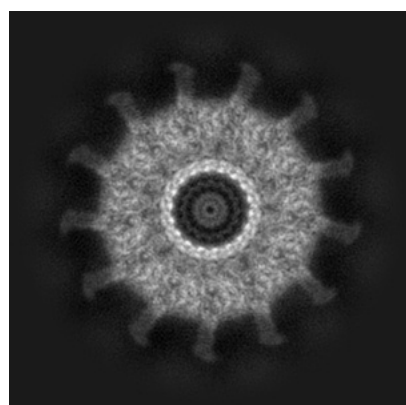
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24023. These allow visual inspection of the internal detail of the map and identification of artifacts.

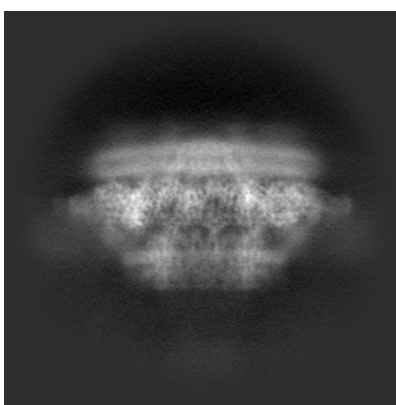
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

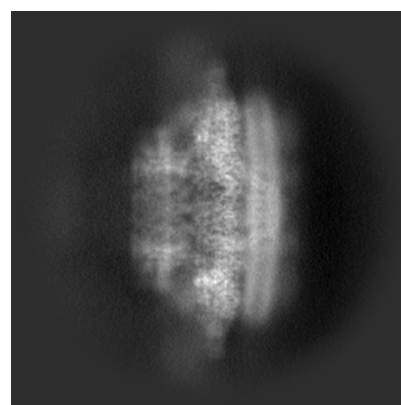
6.1.1 Primary map



X



Y

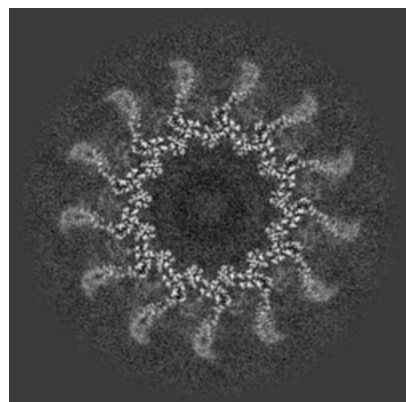


Z

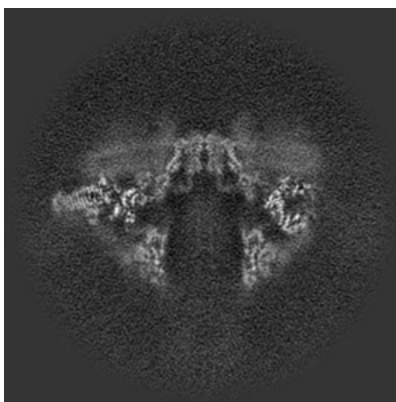
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

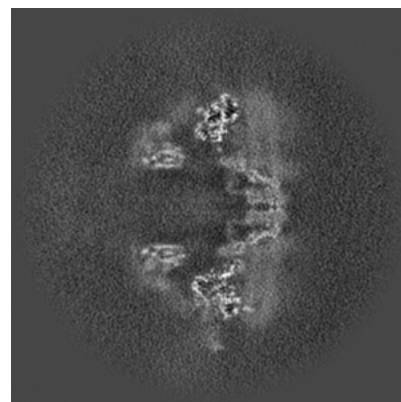
6.2.1 Primary map



X Index: 125



Y Index: 125

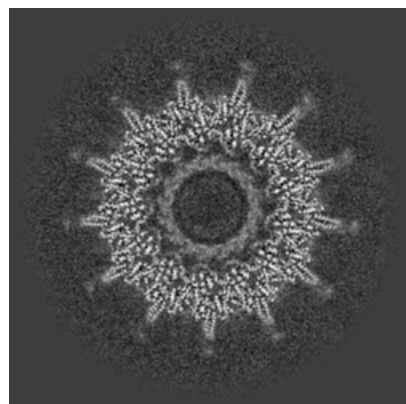


Z Index: 125

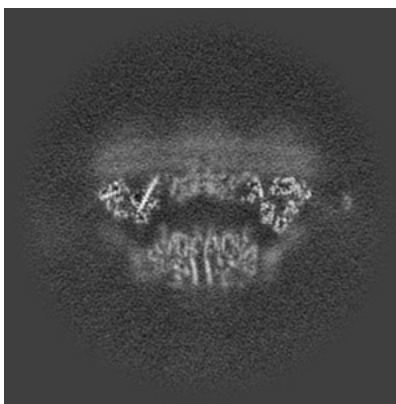
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

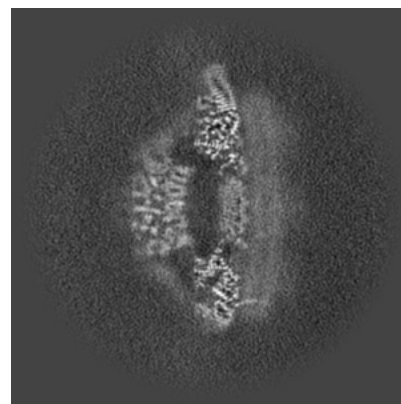
6.3.1 Primary map



X Index: 134



Y Index: 101

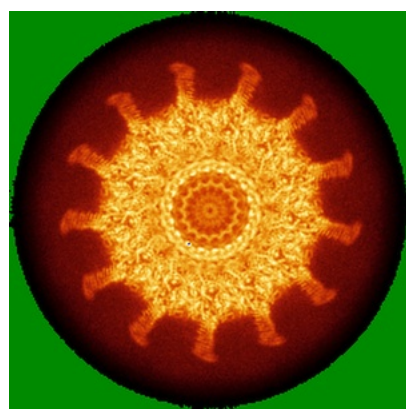


Z Index: 151

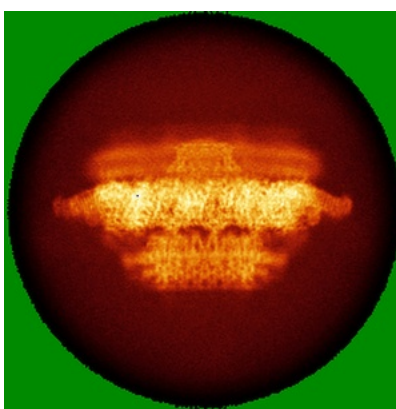
The images above show the largest variance slices of the map in three orthogonal directions.

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

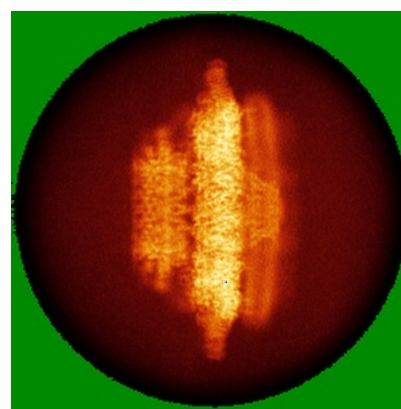
6.4.1 Primary map



X



Y

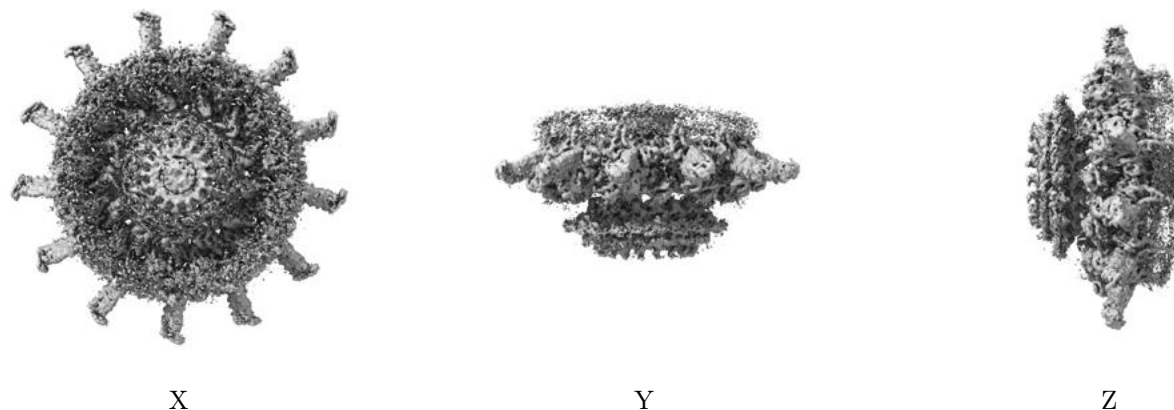


Z

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



The images above show the 3D surface view of the map at the recommended contour level 2.25. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

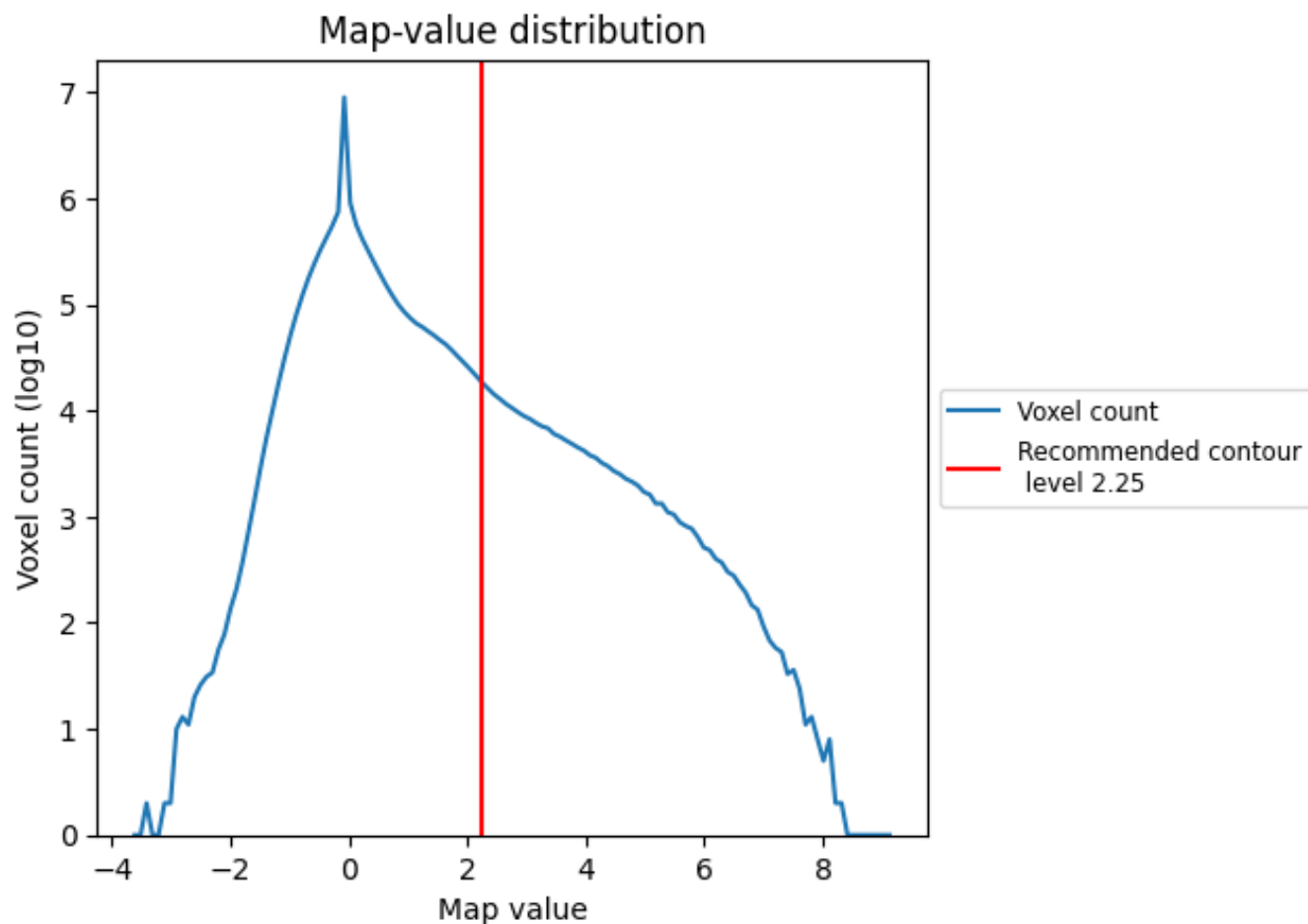
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

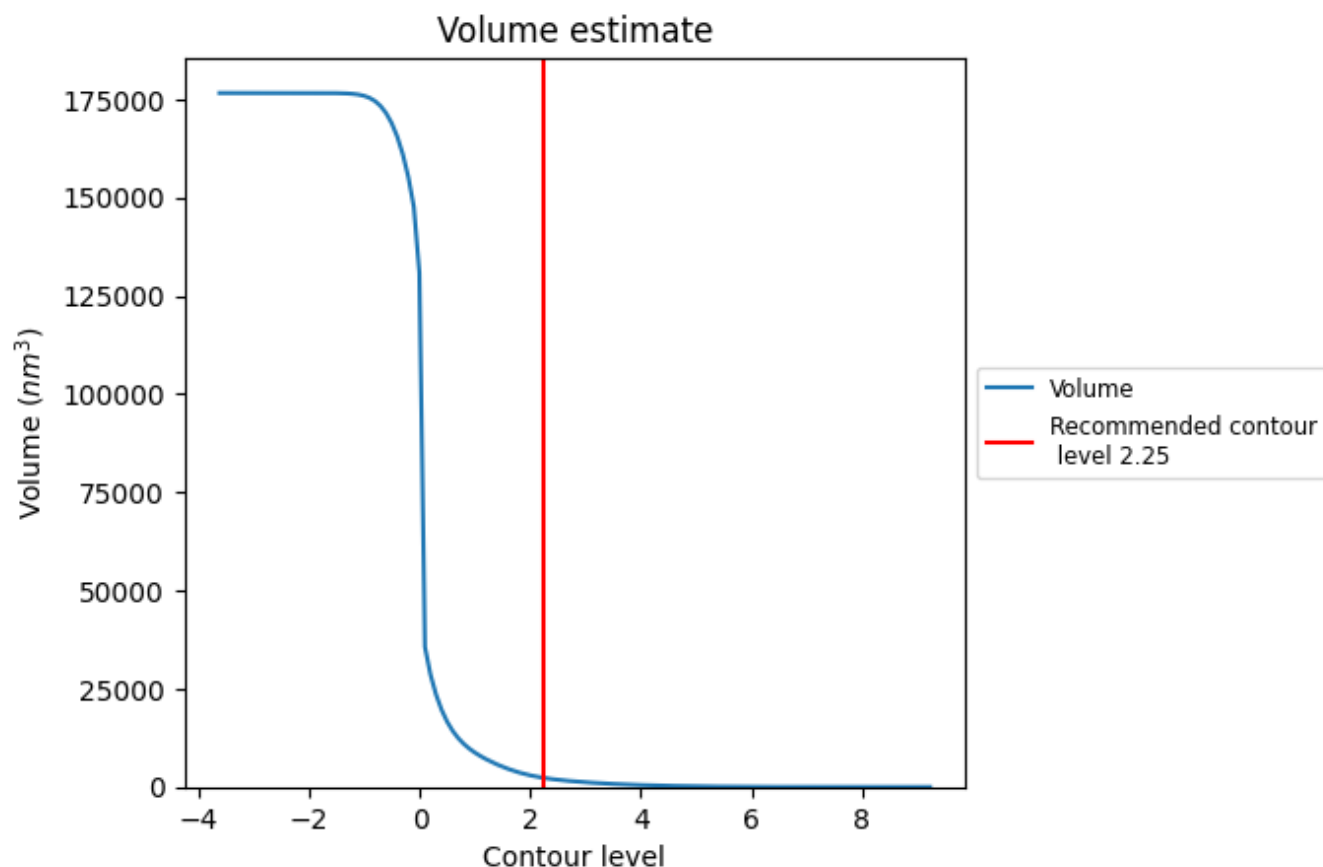
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

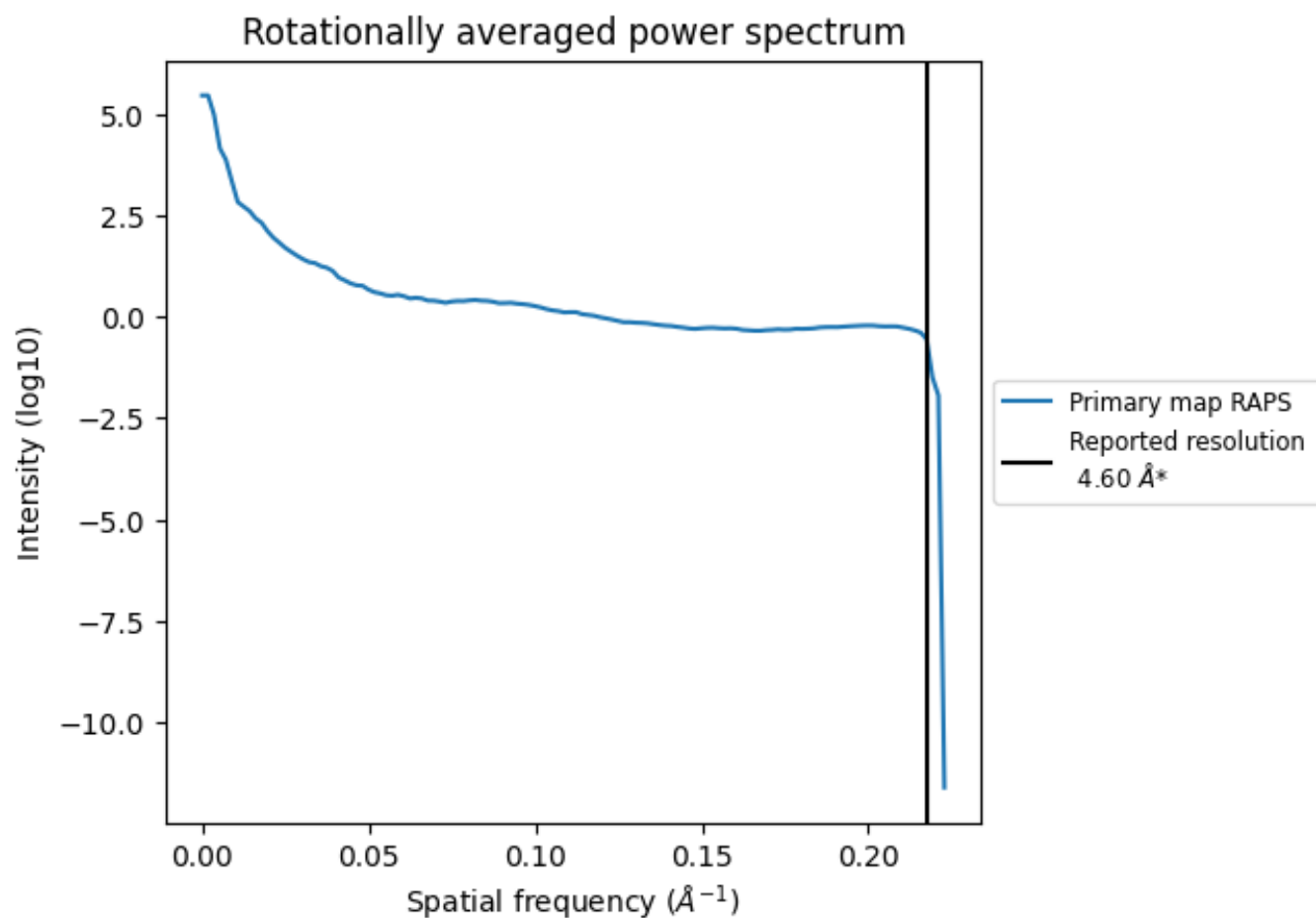
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2290 nm^3 ; this corresponds to an approximate mass of 2069 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.217 $\text{\AA}^{-1}$

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

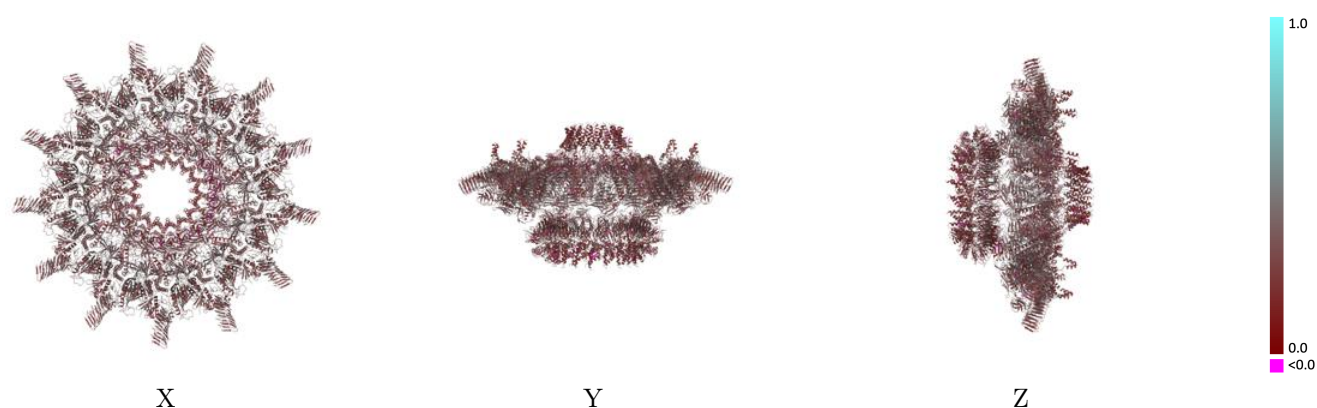
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24023 and PDB model 7MUV. Per-residue inclusion information can be found in section 3 on page 23.

9.1 Map-model overlay [i](#)

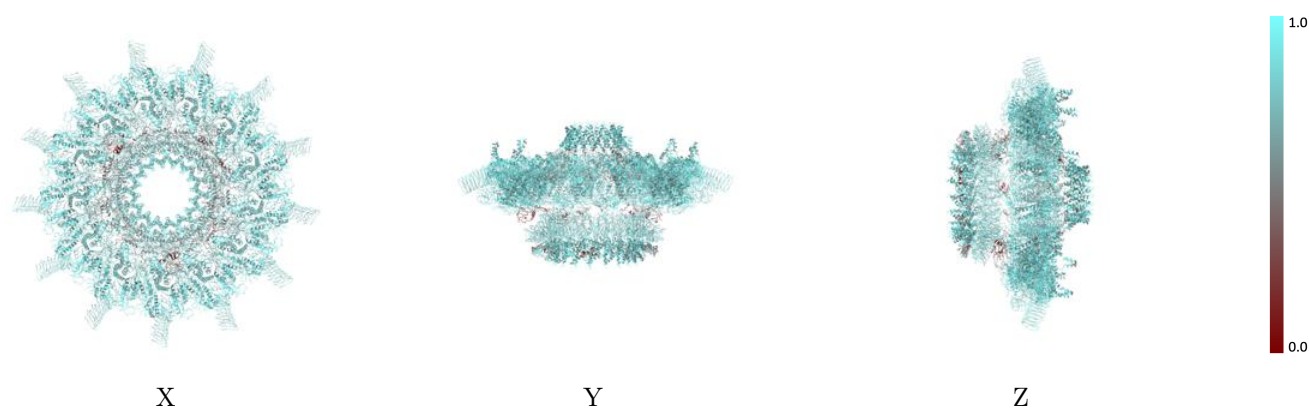
This section was not generated.

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



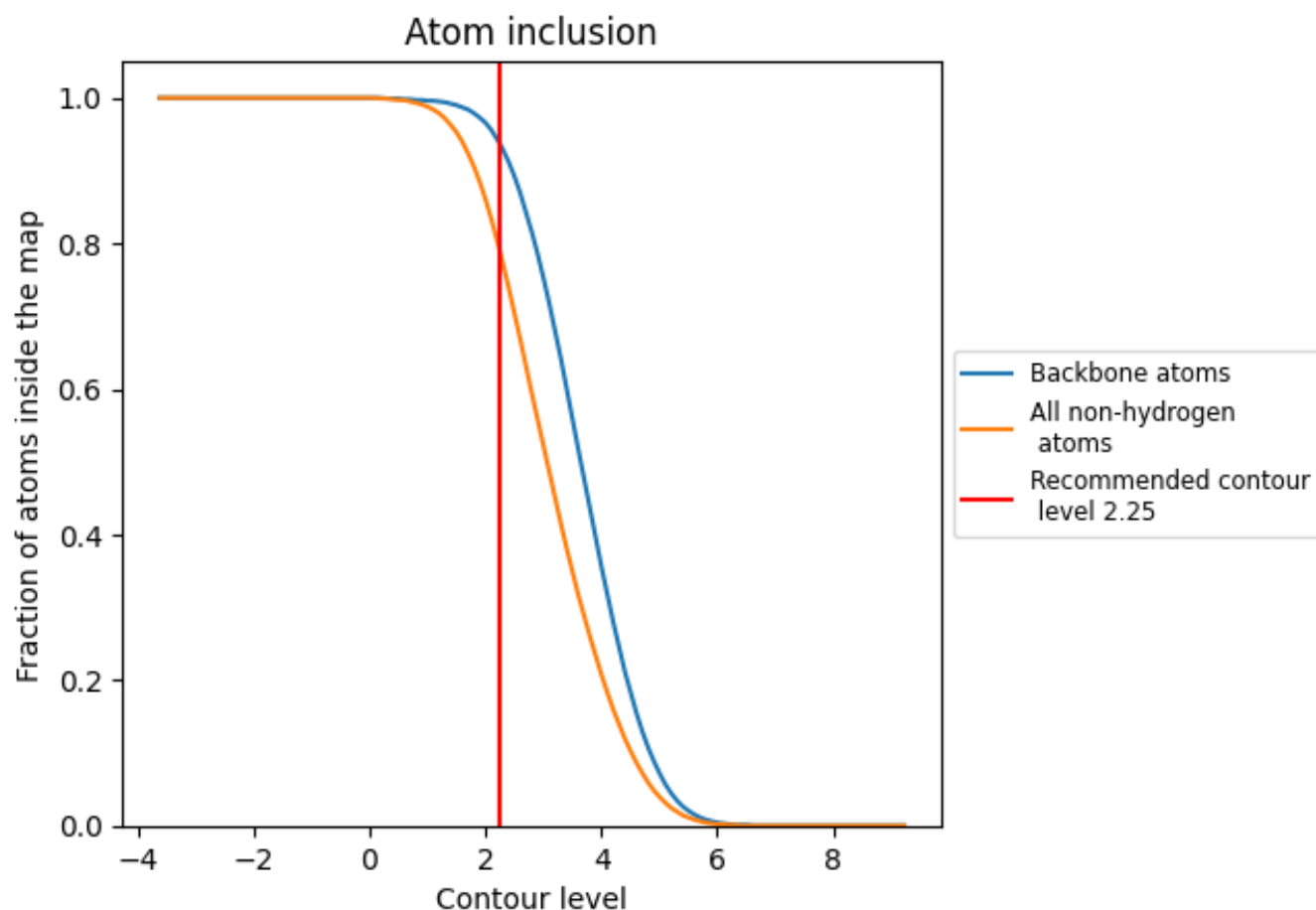
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 79% 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 (2.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7900	 0.3160
AC	 0.7910	 0.3300
AD	 0.8170	 0.3540
AF	 0.7810	 0.2420
AG	 0.6540	 0.2680
AH	 0.8060	 0.3150
AK	 0.8390	 0.3520
AL	 0.8400	 0.3280
AM	 0.8120	 0.3270
AN	 0.7920	 0.3720
AU	 0.9780	 0.4790
AX	 0.6210	 0.2160
Ad	 0.8370	 0.3450
Af	 0.7950	 0.3120
Ag	 0.8310	 0.2930
BC	 0.7890	 0.3280
BD	 0.8170	 0.3640
BF	 0.7880	 0.2480
BG	 0.6470	 0.2540
BH	 0.7950	 0.3180
BK	 0.8320	 0.3460
BL	 0.8350	 0.3320
BM	 0.8190	 0.3220
BN	 0.7670	 0.3530
BU	 1.0000	 0.4510
BX	 0.5710	 0.2670
Bd	 0.8310	 0.3400
Bf	 0.8180	 0.3170
Bg	 0.8310	 0.2720
CC	 0.8250	 0.3270
CD	 0.8240	 0.3540
CF	 0.7220	 0.2560
CG	 0.6560	 0.2470
CH	 0.8150	 0.3260
CK	 0.8350	 0.3520



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Chain	Atom inclusion	Q-score
CL	 0.8490	 0.3310
CM	 0.8060	 0.3270
CN	 0.7710	 0.3610
CU	 1.0000	 0.4840
CX	 0.6330	 0.3280
Cd	 0.8370	 0.3330
Cf	 0.7860	 0.3050
Cg	 0.8050	 0.2830
DC	 0.8530	 0.3310
DD	 0.8330	 0.3500
DF	 0.7900	 0.2560
DG	 0.6650	 0.2520
DH	 0.8020	 0.3090
DK	 0.8520	 0.3550
DL	 0.8430	 0.3320
DM	 0.8000	 0.3230
DN	 0.8090	 0.3700
DU	 0.9560	 0.4600
DX	 0.6000	 0.2440
Dd	 0.8240	 0.3380
Df	 0.7900	 0.3130
Dg	 0.8490	 0.2700
EC	 0.8360	 0.3380
ED	 0.8120	 0.3470
EF	 0.7920	 0.2660
EG	 0.6560	 0.2530
EH	 0.8160	 0.3140
EK	 0.8390	 0.3450
EL	 0.8470	 0.3380
EM	 0.8230	 0.3300
EN	 0.8040	 0.3600
EU	 1.0000	 0.4750
EX	 0.5330	 0.2410
Ed	 0.8380	 0.3450
Ef	 0.7930	 0.3120
Eg	 0.8710	 0.2920
FC	 0.7930	 0.3300
FD	 0.8320	 0.3460
FF	 0.7620	 0.2750
FG	 0.6910	 0.2440
FH	 0.7920	 0.3080
FK	 0.8280	 0.3490

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Chain	Atom inclusion	Q-score
FL	 0.8580	 0.3350
FM	 0.8190	 0.3170
FN	 0.7850	 0.3610
FU	 0.9330	 0.4430
FX	 0.6620	 0.2630
Fd	 0.8400	 0.3330
Ff	 0.7810	 0.3070
Fg	 0.8640	 0.2760
GC	 0.8310	 0.3350
GD	 0.8190	 0.3590
GF	 0.7660	 0.2370
GG	 0.6690	 0.2290
GH	 0.8110	 0.3180
GK	 0.8410	 0.3520
GL	 0.8440	 0.3350
GM	 0.8420	 0.3320
GN	 0.7710	 0.3580
GU	 1.0000	 0.4310
GX	 0.6210	 0.2760
Gd	 0.8340	 0.3420
Gf	 0.7490	 0.3190
Gg	 0.8270	 0.2770
HC	 0.8490	 0.3370
HD	 0.8240	 0.3560
HF	 0.7920	 0.2750
HG	 0.6470	 0.2210
HH	 0.8060	 0.3160
HK	 0.8490	 0.3450
HL	 0.8490	 0.3290
HM	 0.8400	 0.3300
HN	 0.8250	 0.3720
HU	 0.9560	 0.4740
HX	 0.5330	 0.2320
Hd	 0.8470	 0.3440
Hf	 0.8430	 0.3040
Hg	 0.8090	 0.2740
IC	 0.8410	 0.3450
ID	 0.8390	 0.3520
IF	 0.8020	 0.2490
IG	 0.6130	 0.2190
IH	 0.8020	 0.3150
IK	 0.8500	 0.3530

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Chain	Atom inclusion	Q-score
IL	 0.8360	 0.3350
IM	 0.8140	 0.3230
IN	 0.8250	 0.3640
IU	 0.9780	 0.4440
IX	 0.5460	 0.2540
Id	 0.8420	 0.3400
If	 0.8130	 0.2930
Ig	 0.8460	 0.2780
JC	 0.7810	 0.3290
JD	 0.8290	 0.3430
JF	 0.7750	 0.2470
JG	 0.6050	 0.2030
JH	 0.8210	 0.3110
JK	 0.8500	 0.3450
JL	 0.8510	 0.3270
JM	 0.8310	 0.3370
JN	 0.7970	 0.3470
JU	 1.0000	 0.4940
JX	 0.6540	 0.2890
Jd	 0.8310	 0.3310
Jf	 0.7930	 0.3150
Jg	 0.8380	 0.2510
KC	 0.7800	 0.3320
KD	 0.8290	 0.3440
KF	 0.7620	 0.2430
KG	 0.6030	 0.1930
KH	 0.8140	 0.3070
KK	 0.8530	 0.3620
KL	 0.8500	 0.3270
KM	 0.8350	 0.3340
KN	 0.7760	 0.3630
KU	 0.9560	 0.4680
KX	 0.5670	 0.2750
Kd	 0.8520	 0.3390
Kf	 0.8020	 0.3060
Kg	 0.8350	 0.2850
LC	 0.8370	 0.3450
LD	 0.8400	 0.3450
LF	 0.7640	 0.2590
LG	 0.6220	 0.1990
LH	 0.8190	 0.3190
LK	 0.8510	 0.3500

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Chain	Atom inclusion	Q-score
LL	 0.8410	 0.3350
LM	 0.8200	 0.3280
LN	 0.7880	 0.3650
LU	 0.9780	 0.4900
LX	 0.6710	 0.2650
Ld	 0.8210	 0.3420
Lf	 0.8060	 0.3300
Lg	 0.8600	 0.2730
MC	 0.8440	 0.3440
MD	 0.8250	 0.3510
MF	 0.7600	 0.2660
MG	 0.6780	 0.2680
MH	 0.8180	 0.3190
MK	 0.8430	 0.3510
ML	 0.8410	 0.3290
MM	 0.8130	 0.3180
MN	 0.8510	 0.3560
MU	 1.0000	 0.4940
MX	 0.6250	 0.2650
Md	 0.8440	 0.3390
Mf	 0.8130	 0.3070
Mg	 0.8310	 0.2970
NG	 0.6620	 0.2630
OG	 0.7310	 0.2650
PG	 0.6860	 0.2770
VF	 0.8130	 0.2690
VG	 0.8420	 0.2760
VH	 0.6680	 0.2990
VX	 0.5210	 0.2560
WF	 0.7640	 0.2630
WG	 0.8160	 0.2840
WH	 0.5420	 0.2340
WX	 0.5880	 0.2760
XF	 0.7880	 0.2710
XG	 0.7900	 0.2520
XH	 0.6960	 0.2910
XX	 0.6420	 0.2460
YF	 0.7750	 0.2460
YG	 0.8460	 0.2770
YH	 0.5510	 0.2760
YX	 0.6370	 0.2940
ZF	 0.7960	 0.2710

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Chain	Atom inclusion	Q-score
ZG	 0.8120	 0.2820
ZH	 0.6650	 0.3070
ZX	 0.5500	 0.2810