



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 07:01 AM UTC

PDB ID : 7MUY / pdb_00007muy
EMDB ID : EMD-24026
Title : Reconstruction of the Legionella pneumophila Dot/Icm T4SS 3DVA Map 5
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

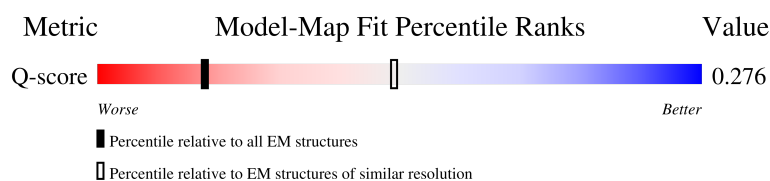
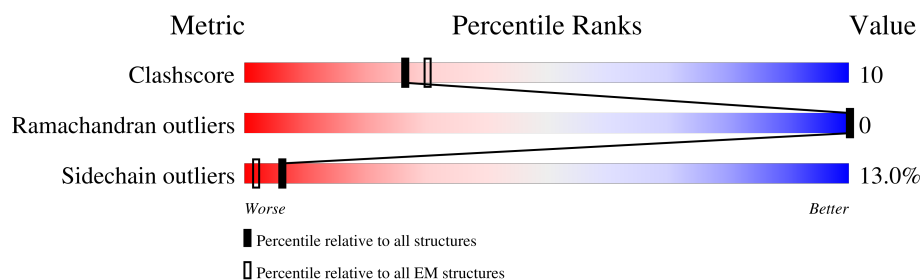
1 Overall quality at a glance i

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	10% 5% 84%
1	Ag	1048	97%
1	BG	1048	9% 6% 84%
1	Bg	1048	97%

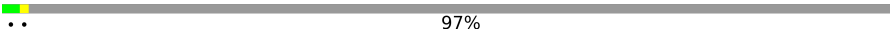
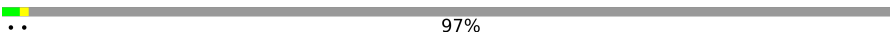
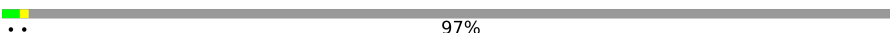
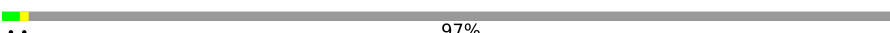
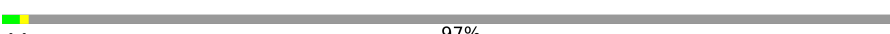
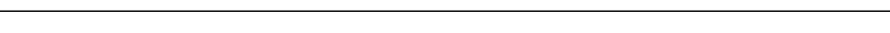
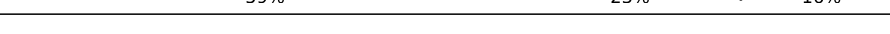
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Mol	Chain	Length	Quality of chain
1	CG	1048	
1	Cg	1048	
1	DG	1048	
1	Dg	1048	
1	EG	1048	
1	Eg	1048	
1	FG	1048	
1	Fg	1048	
1	GG	1048	
1	Gg	1048	
1	HG	1048	
1	Hg	1048	
1	IG	1048	
1	Ig	1048	
1	JG	1048	
1	Jg	1048	
1	KG	1048	
1	Kg	1048	
1	LG	1048	
1	Lg	1048	
1	MG	1048	
1	Mg	1048	
1	NG	1048	
1	OG	1048	
1	PG	1048	

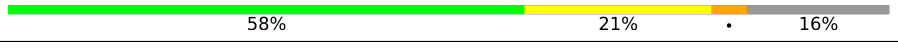
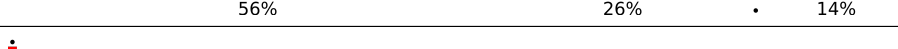
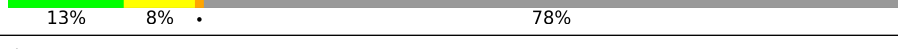
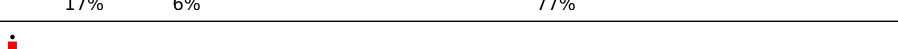
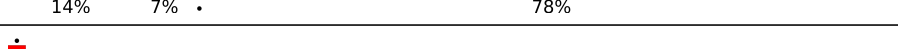
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Mol	Chain	Length	Quality of chain
1	VG	1048	 97%
1	WG	1048	 97%
1	XG	1048	 97%
1	YG	1048	 97%
1	ZG	1048	 97%
2	AD	163	 58% 24% 14%
2	Ad	163	 57% 23% 16%
2	BD	163	 63% 21% 14%
2	Bd	163	 65% 14% 5% 16%
2	CD	163	 54% 27% 5% 14%
2	Cd	163	 63% 20% 16%
2	DD	163	 62% 24% 14%
2	Dd	163	 60% 23% 16%
2	ED	163	 65% 19% 14%
2	Ed	163	 59% 23% 16%
2	FD	163	 62% 21% 14%
2	Fd	163	 60% 22% 16%
2	GD	163	 60% 23% 14%
2	Gd	163	 61% 20% 16%
2	HD	163	 63% 21% 14%
2	Hd	163	 64% 18% 16%
2	ID	163	 58% 26% 14%
2	Id	163	 64% 18% 16%
2	JD	163	 55% 28% 14%
2	Jd	163	 64% 20% 16%

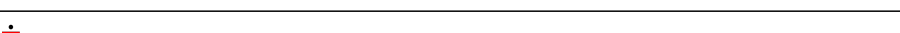
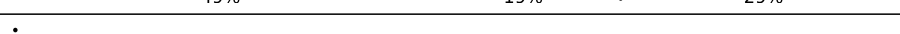
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Mol	Chain	Length	Quality of chain
2	KD	163	
2	Kd	163	
2	LD	163	
2	Ld	163	
2	MD	163	
2	Md	163	
3	AF	269	
3	Af	269	
3	BF	269	
3	Bf	269	
3	CF	269	
3	Cf	269	
3	DF	269	
3	Df	269	
3	EF	269	
3	Ef	269	
3	FF	269	
3	Ff	269	
3	GF	269	
3	Gf	269	
3	HF	269	
3	Hf	269	
3	IF	269	
3	If	269	
3	JF	269	

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Mol	Chain	Length	Quality of chain
3	Jf	269	
3	KF	269	
3	Kf	269	
3	LF	269	
3	Lf	269	
3	MF	269	
3	Mf	269	
3	VF	269	
3	WF	269	
3	XF	269	
3	YF	269	
3	ZF	269	
4	AH	361	
4	BH	361	
4	CH	361	
4	DH	361	
4	EH	361	
4	FH	361	
4	GH	361	
4	HH	361	
4	IH	361	
4	JH	361	
4	KH	361	
4	LH	361	
4	MH	361	

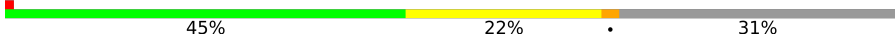
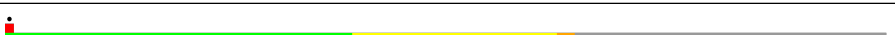
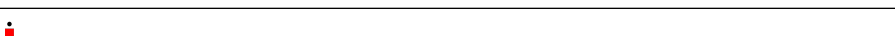
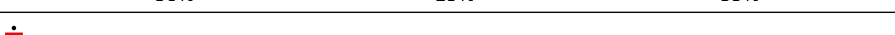
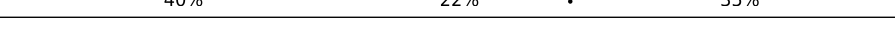
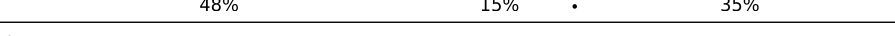
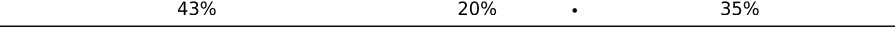
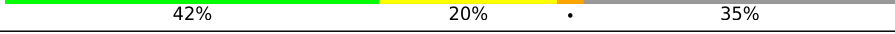
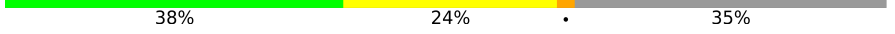
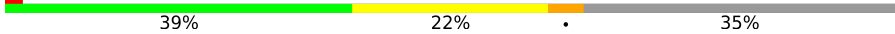
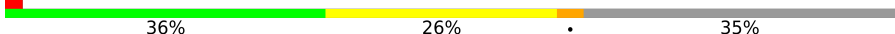
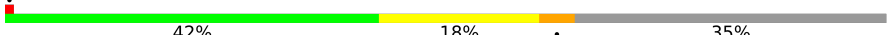
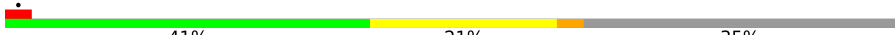
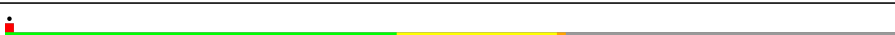
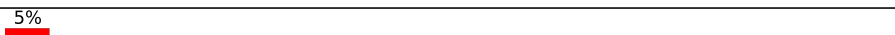
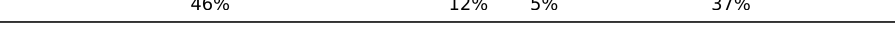
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Mol	Chain	Length	Quality of chain
4	VH	361	
4	WH	361	
4	XH	361	
4	YH	361	
4	ZH	361	
5	AK	189	
5	BK	189	
5	CK	189	
5	DK	189	
5	EK	189	
5	FK	189	
5	GK	189	
5	HK	189	
5	IK	189	
5	JK	189	
5	KK	189	
5	LK	189	
5	MK	189	
6	AL	249	
6	BL	249	
6	CL	249	
6	DL	249	
6	EL	249	
6	FL	249	
6	GL	249	

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Mol	Chain	Length	Quality of chain
6	HL	249	
6	IL	249	
6	JL	249	
6	KL	249	
6	LL	249	
6	ML	249	
7	AM	320	
7	BM	320	
7	CM	320	
7	DM	320	
7	EM	320	
7	FM	320	
7	GM	320	
7	HM	320	
7	IM	320	
7	JM	320	
7	KM	320	
7	LM	320	
7	MM	320	
8	AN	124	
8	BN	124	
8	CN	124	
8	DN	124	
8	EN	124	
8	FN	124	

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Mol	Chain	Length	Quality of chain
8	GN	124	
8	HN	124	
8	IN	124	
8	JN	124	
8	KN	124	
8	LN	124	
8	MN	124	
9	AU	9	
9	BU	9	
9	CU	9	
9	DU	9	
9	EU	9	
9	FU	9	
9	GU	9	
9	HU	9	
9	IU	9	
9	JU	9	
9	KU	9	
9	LU	9	
9	MU	9	
10	AX	48	
10	BX	48	
10	CX	48	
10	DX	48	
10	EX	48	

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Mol	Chain	Length	Quality of chain
10	FX	48	
10	GX	48	
10	HX	48	
10	IX	48	
10	JX	48	
10	KX	48	
10	LX	48	
10	MX	48	
10	VX	48	
10	WX	48	
10	XX	48	
10	YX	48	
10	ZX	48	
11	AC	303	
11	BC	303	
11	CC	303	
11	DC	303	
11	EC	303	
11	FC	303	
11	GC	303	
11	HC	303	
11	IC	303	
11	JC	303	
11	KC	303	
11	LC	303	

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Mol	Chain	Length	Quality of chain
11	MC	303	46% 20% . 31%

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	Eg	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
1	Fg	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	Gg	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
1	Hg	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	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	Jg	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	Kg	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
1	Lg	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	Mg	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
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		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	XG	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	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	GG	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	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		

- Molecule 2 is a protein called DotD.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	ED	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
2	Ed	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	FD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
2	Fd	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
2	GD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
2	Gd	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
2	HD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
2	Hd	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
2	ID	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
2	Id	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
2	JD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
2	Jd	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
2	KD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
2	Kd	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
2	LD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
2	Ld	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
2	MD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
2	Md	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
2	Ad	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
2	BD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
2	Bd	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
2	CD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
2	Cd	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	DD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
2	Dd	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
2	AD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		

- Molecule 3 is a protein called DotF.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	EF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	Ef	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	FF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	Ff	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	AF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	GF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	Gf	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	HF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	Hf	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	IF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	If	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	JF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	Jf	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	KF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	Kf	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	LF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	Lf	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	MF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	Mf	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	VF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	WF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	XF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	YF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	ZF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	Af	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	BF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	Bf	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	CF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	Cf	59	Total	C	N	O	S	0	0
			449	290	77	81	1		
3	DF	63	Total	C	N	O	S	0	0
			483	308	84	90	1		
3	Df	59	Total	C	N	O	S	0	0
			449	290	77	81	1		

- Molecule 4 is a protein called Type IV secretion protein IcmK.

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

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

- Molecule 5 is a protein called Inner membrane lipoprotein YiaD.

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

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

- Molecule 6 is a protein called Outer membrane protein, OmpA family protein.

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

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

- Molecule 7 is a protein called DUF2807 domain-containing protein.

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

- Molecule 8 is a protein called Neurogenic locus notch.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	EN	78	Total	C	N	O	S	0	0
			582	357	99	113	13		
8	FN	78	Total	C	N	O	S	0	0
			582	357	99	113	13		

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

- Molecule 9 is a protein called Unknown protein fragment.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	EU	9	Total	C	N	O	0	0
			45	27	9	9		
9	FU	9	Total	C	N	O	0	0
			45	27	9	9		
9	GU	9	Total	C	N	O	0	0
			45	27	9	9		
9	HU	9	Total	C	N	O	0	0
			45	27	9	9		
9	IU	9	Total	C	N	O	0	0
			45	27	9	9		
9	JU	9	Total	C	N	O	0	0
			45	27	9	9		
9	KU	9	Total	C	N	O	0	0
			45	27	9	9		
9	LU	9	Total	C	N	O	0	0
			45	27	9	9		

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Mol	Chain	Residues	Atoms				AltConf	Trace
9	MU	9	Total	C	N	O	0	0
			45	27	9	9		
9	AU	9	Total	C	N	O	0	0
			45	27	9	9		
9	BU	9	Total	C	N	O	0	0
			45	27	9	9		
9	CU	9	Total	C	N	O	0	0
			45	27	9	9		
9	DU	9	Total	C	N	O	0	0
			45	27	9	9		

- Molecule 10 is a protein called Unknown protein fragment.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	EX	48	Total	C	N	O	0	0
			240	144	48	48		
10	FX	48	Total	C	N	O	0	0
			240	144	48	48		
10	GX	48	Total	C	N	O	0	0
			240	144	48	48		
10	HX	48	Total	C	N	O	0	0
			240	144	48	48		
10	IX	48	Total	C	N	O	0	0
			240	144	48	48		
10	JX	48	Total	C	N	O	0	0
			240	144	48	48		
10	KX	48	Total	C	N	O	0	0
			240	144	48	48		
10	LX	48	Total	C	N	O	0	0
			240	144	48	48		
10	MX	48	Total	C	N	O	0	0
			240	144	48	48		
10	VX	48	Total	C	N	O	0	0
			240	144	48	48		
10	WX	48	Total	C	N	O	0	0
			240	144	48	48		
10	XX	48	Total	C	N	O	0	0
			240	144	48	48		
10	YX	48	Total	C	N	O	0	0
			240	144	48	48		
10	ZX	48	Total	C	N	O	0	0
			240	144	48	48		

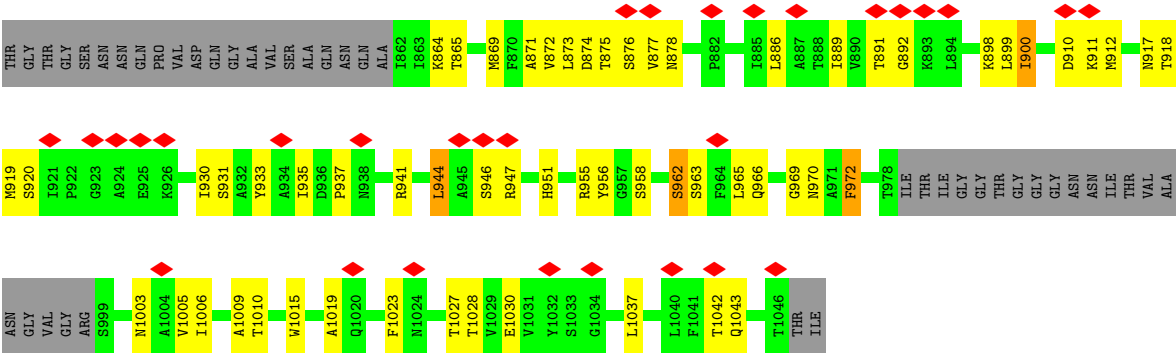
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Mol	Chain	Residues	Atoms				AltConf	Trace
10	AX	48	Total	C	N	O	0	0
			240	144	48	48		
10	BX	48	Total	C	N	O	0	0
			240	144	48	48		
10	CX	48	Total	C	N	O	0	0
			240	144	48	48		
10	DX	48	Total	C	N	O	0	0
			240	144	48	48		

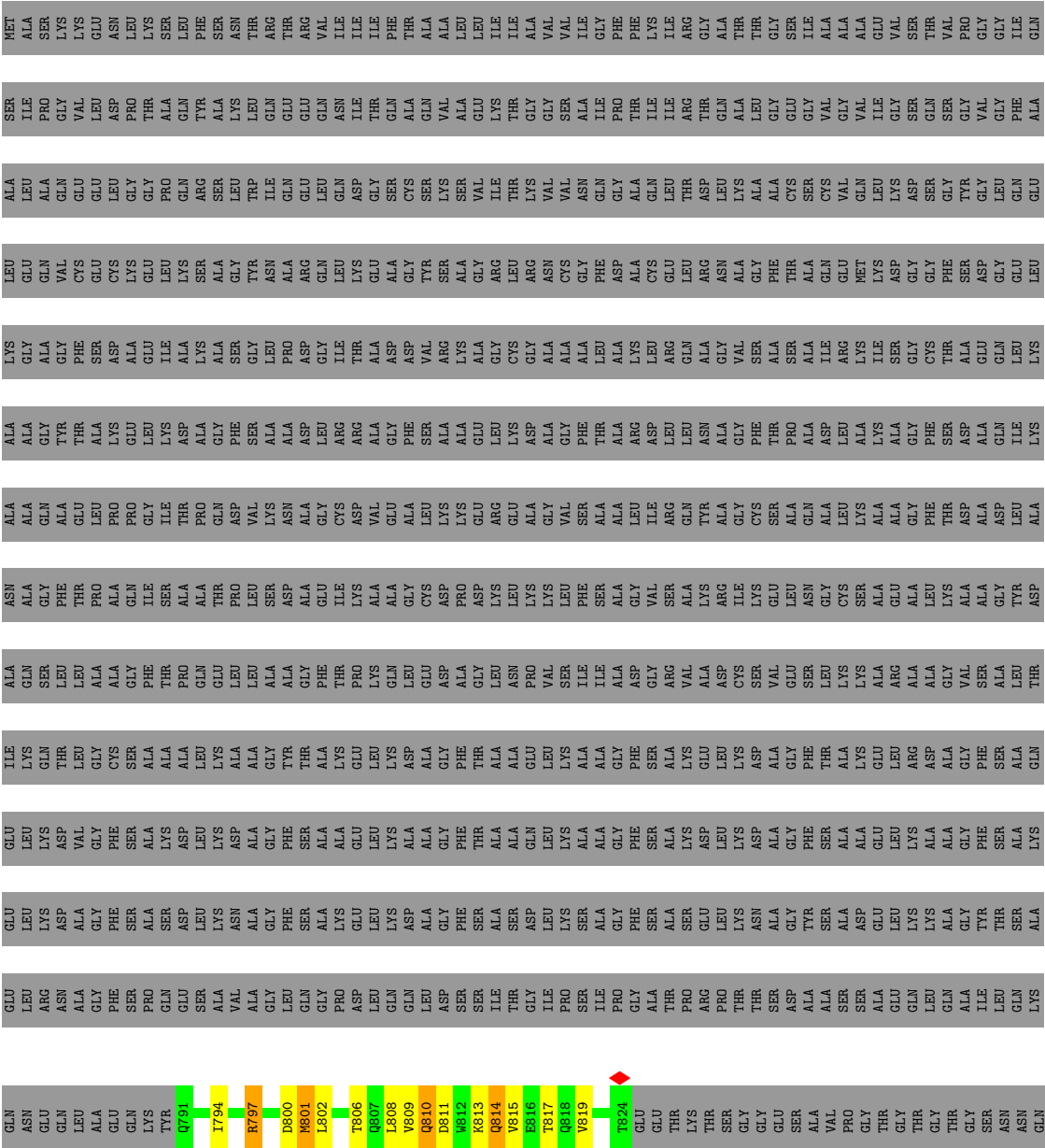
- Molecule 11 is a protein called DotC.

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



● Molecule 1: IcmE protein

Chain Eg: .. 97%



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- Molecule 1: IcmE protein

[illegible]

PHE	GLY	ASN	ALA	GLN	SER	ALA	ASN	THR	THR	ILE	THR	ILE	GLY	THR	GLY	GLY	GLY	ASN	ASN	ILE	THR	VAL	ASN	GLY	VAL	GLY	ARG	SER	THR	THR	LEU	GLU	ASN	ALA	ALA	VAL	VAL	ILE	ILE	LYS	GLY	THR	ALA	ALA	TRP	SER	GLN	GLN	ALA	GLN	GLN	LEU	PHE	ASN	THR	THR	PRO	THR
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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



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

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

lys	gly	ala	gly	phe	ser	asp	ala	ala	glu	ile	ala	lys	ala	ser	gly	leu	pro	asp	gly	ile	thr	ala	ala	asp	asp	val	arg	lys	gly	cys	gly	ala	ala	ala	leu	ala	lys	arg	leu	glu	gln	gly	val	ser	ala	ala	ser	ser	ala	ile	arg	lys	ile	le	ser	gly	cys	thr	ala	glu	gln	leu	lys
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ALA ALA GLY TYR THR ALA LYS LEU ASP ALA GLY PHE SER ALA ALA ASP ARG ARG GLY PHE SER ALA ALA GLY LEU LYS ASP ALA ALA GLY PHE THR THR PRO ASP LEU ASN ALA GLY PHE THR THR PRO ASP LEU ASN ALA ALA GLY PHE THR THR PRO ASP LEU ASN

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

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

LIE	LYS	GLN	THR	LEU	GLY	CYS	SER	ALA	ALA	ALA	ALA	LEU	LYS	ALA	ALA	GLY	TYR	THR	ALA	LYS	GLU	LEU	LYS	ASP	ALA	ASP	GLY	PHE	THR	THR	ALA	ALA	GLU	LEU	LYS	ALA	ALA	GLY	PHE	SER	ALA	LYS	GLU	LEU	ARG	ASP	ALA	GLY	PHE	SER	THR	ALA	GLN
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[illegible]

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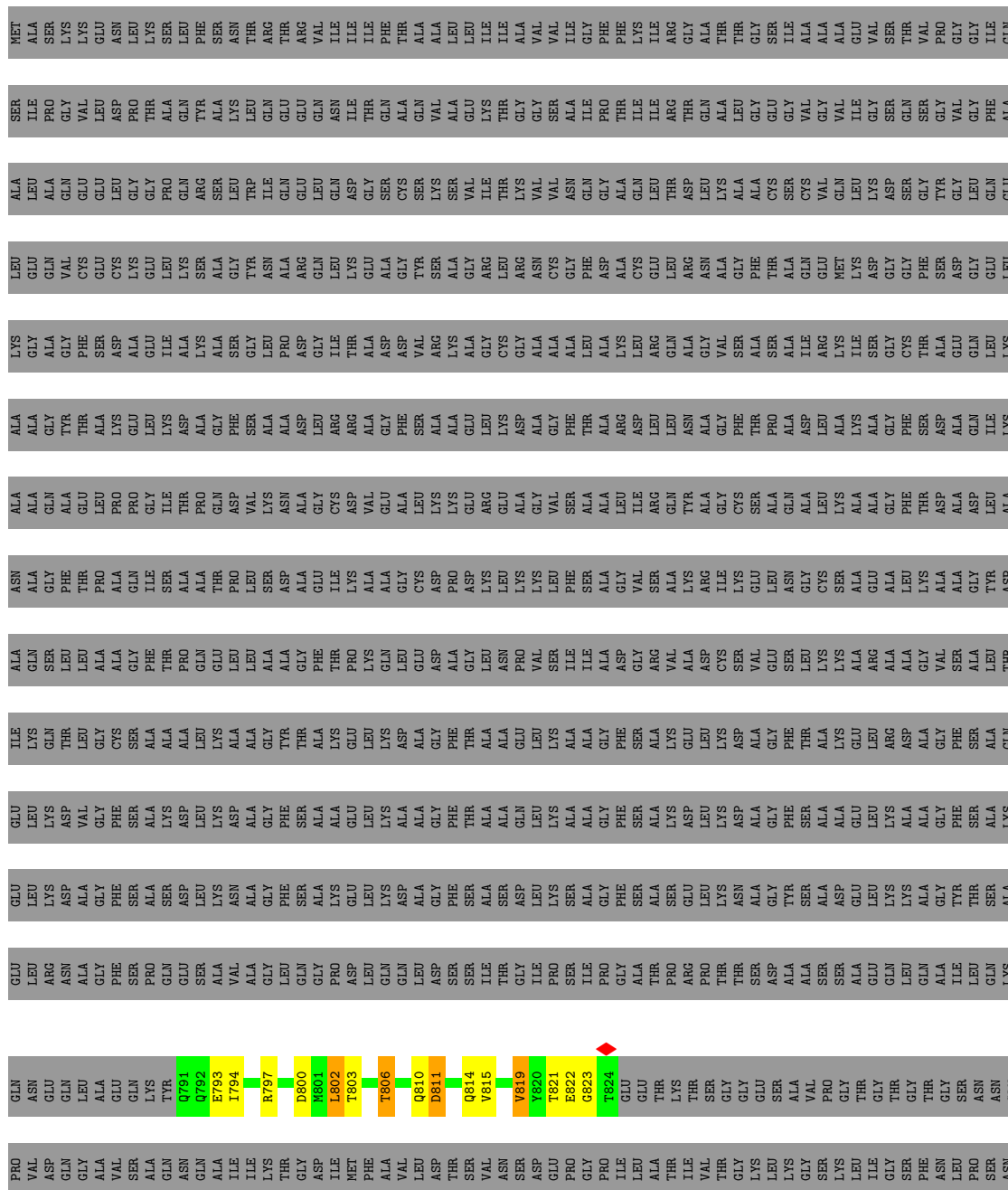
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GLN	ASN	GLU	GLN	LEU	ALA	GLU	GLN	LYS	TYR	GLN	GLN	GLU	ILE	GLN	GLN	ARG	THR	SER	ASP	MET	LEU	THR	ALA	ALA	THR	GLN	LEU	VAL	GLN	ASP	TRP	GLN	VAL	THR	TYR	GLU	GLY	THR	GLU	GLU	THR	LYS	THR	SER	GLY	GLY	GLU	SER	ALA	VAL	PRO	GLY	GLY	THR	TYR
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[illegible]



Chain Gg: 97%



[illegible]

- Molecule 1: IcmE protein



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

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

LYS GLY ALA ALA GLY PHE SER ASP ALA ALA LYS ALA ALA GLY SER LYS LEU PRO LEU ASP GLY ILE ILE THR ALA ALA ASP VAL VAL LYS LYS ALA ALA ALA ALA ALA ALA LYS LEU LEU LYS LEU ARG ARG ALA GLN GLN GLY GLY VAL SER SER SER SER ILE ARG LYS ILE LYS SER GLY CYS THR ALA ALA GLN GLN LEU LEU

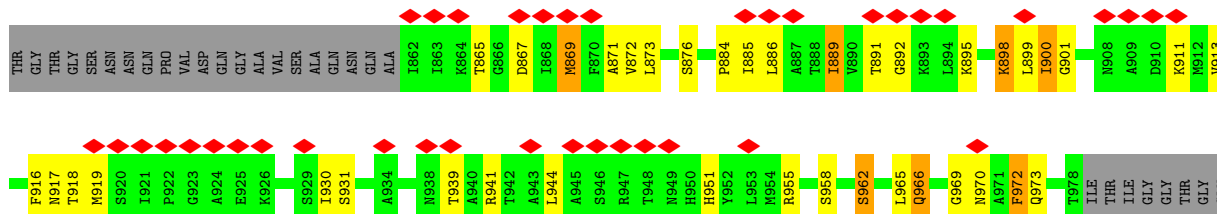
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ALA	ALA	GLN	ALA	GLU	LEU	PRO	PRO	GLY	ILE	THR	PRO	GLN	ASP	VAL	LYS	ASN	ALA	GLY	CYS	ASP	VAL	GLU	ALA	LEU	LYS	GLU	ARG	GLU	ALA	ALA	ALA	LEU	ILE	ARG	GLN	GLN	ALA	ALA	GLY	CYS	SER	SER	ALA	ALA	ALA	GLY	ALA	GLY	PHE	THR	ASP	ALA	ALA	ASP	LEU	ALA
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ASN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

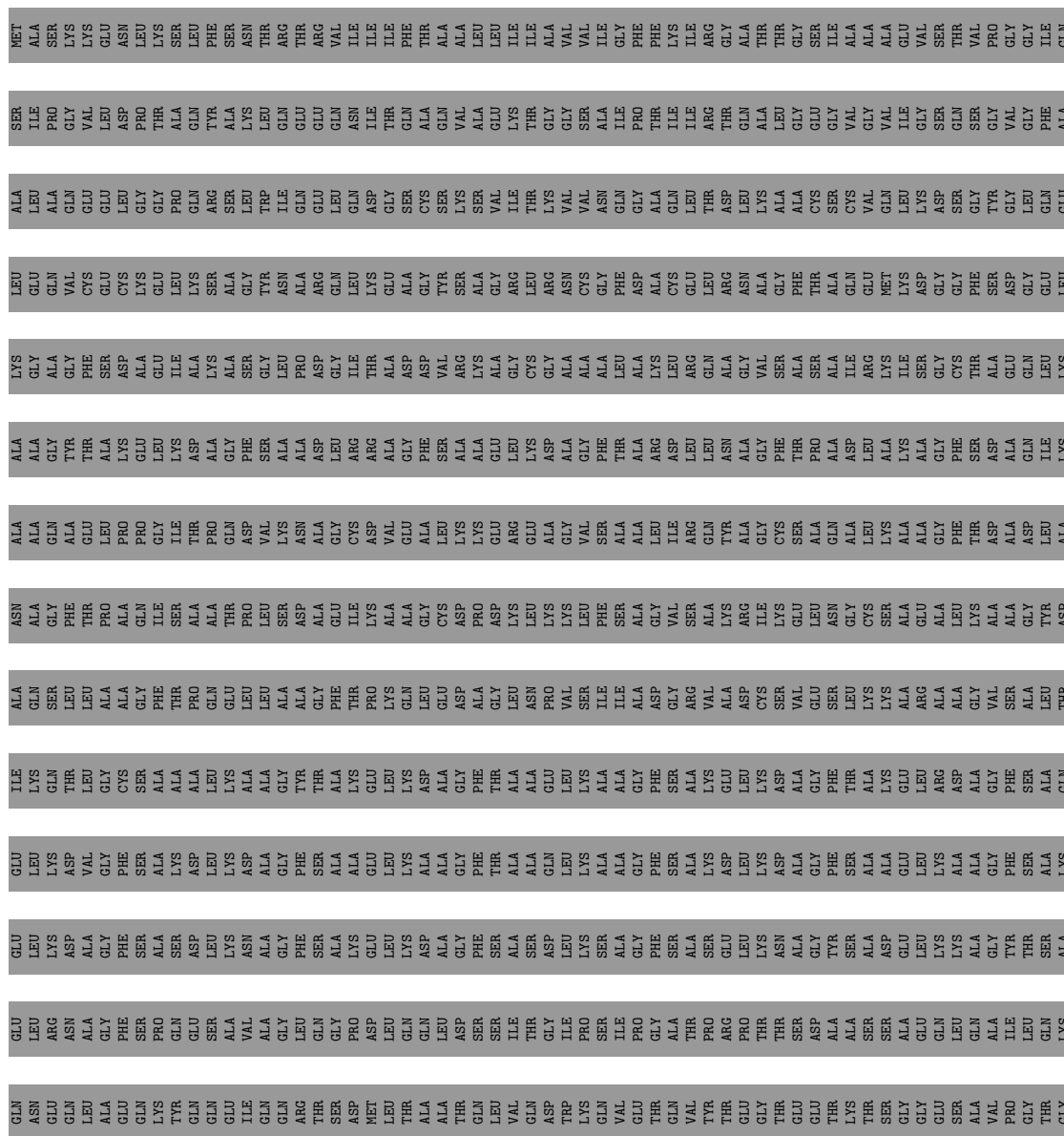
ALA	GLN	SER	LEU	LEU	ALA	ALA	GLY	PHE	THR	PRO	GLN	GLU	LEU	LEU	ALA	ALA	GLY	PHE	THR	PRO	LYS	GLN	LEU	GLU	ASP	VAL	SER	ILE	ILE	ALA	ASP	CYS	SER	VAL	GLU	LEU	SER	LYS	ALA	ALA	ARG	ALA	ALA	ALA	GLY	VAL	SER	SER	ALA	LEU	THR
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TLE	LYS	GLN	THR	LEU	GLY	CYS	SER	ALA	ALA	ALA	ALA	LEU	LEU	LYS	LYS	GLY	THR	THR	ALA	ALA	GLU	LEU	LEU	LYS	LYS	GLY	PHE	SER	ALA	LYS	GLY	PHE	THR	ALA	LYS	GLU	LEU	ARG	ASP	ALA	GLY	PHE	SER	ALA	GLN
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[illegible][illegible][illegible][illegible]

Chain Jg: .. 97%

- Molecule 1: IcmE protein

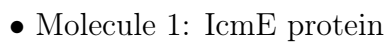




Chain Lg: 97%



Chain EG:



97%

- Molecule 1: IcmE protein

97%

- Molecule 1: IcmE protein



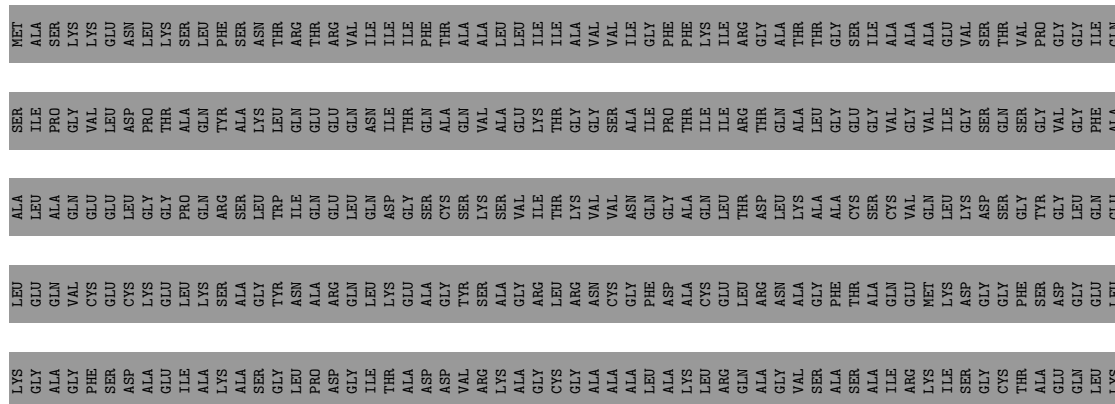
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[illegible]

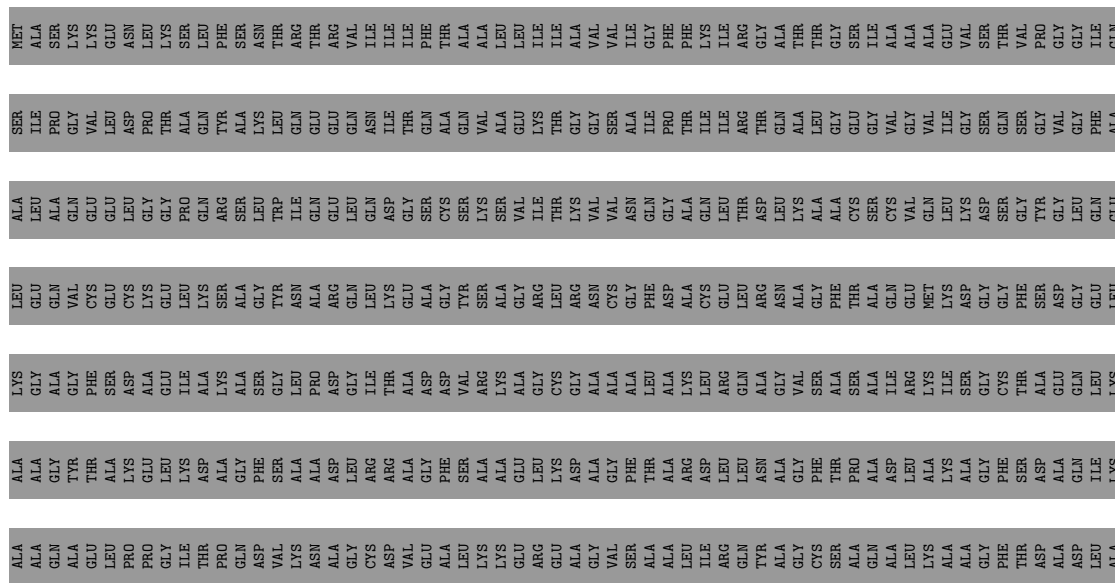
Chain ZG: 97%



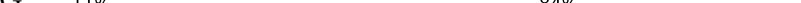
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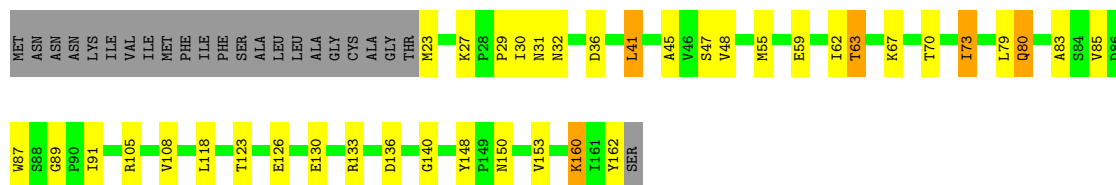
Chain JG:  5% 11% 84%





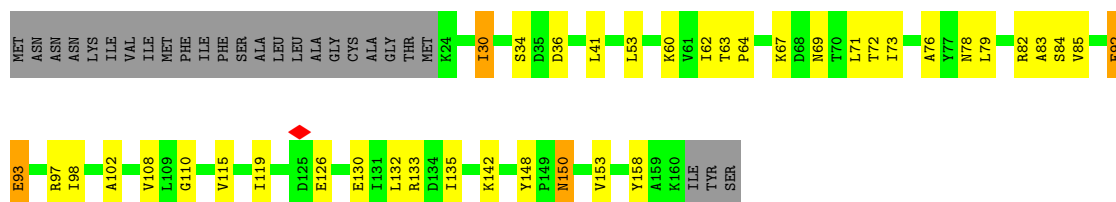


Chain FD:  62% 21% 14%



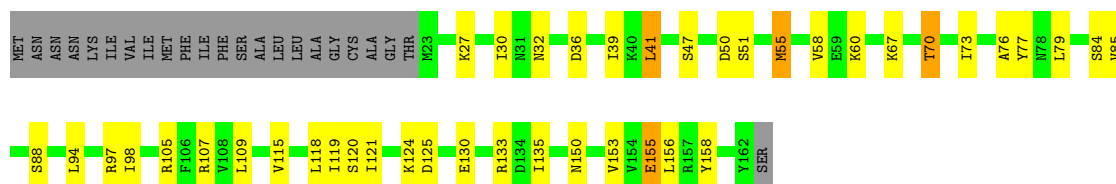
• Molecule 2: DotD

Chain Fd:  60% 22% 16%



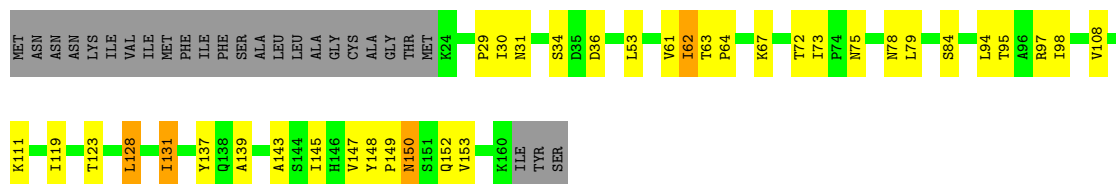
• Molecule 2: DotD

Chain GD:  60% 23% 14%



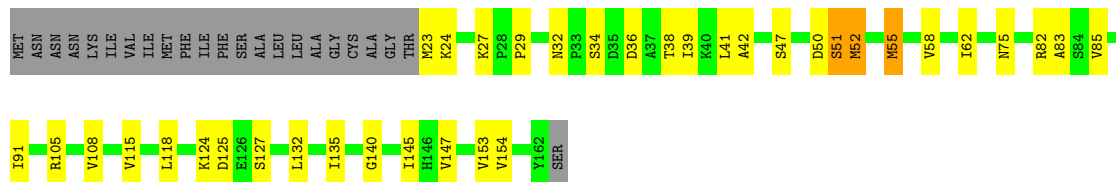
• Molecule 2: DotD

Chain Gd:  61% 20% 16%



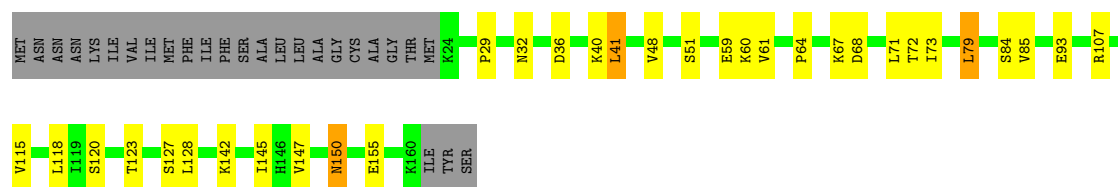
• Molecule 2: DotD

Chain HD:  63% 21% 14%



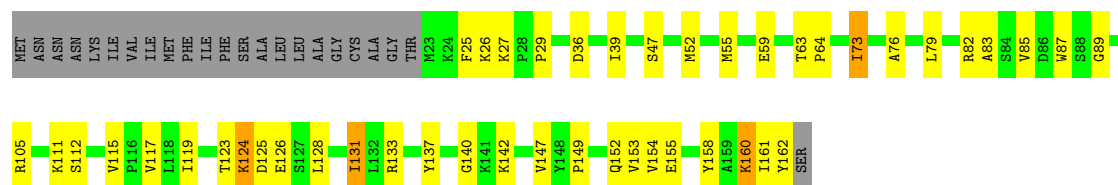
• Molecule 2: DotD

Chain Hd:  64% 18% 16%



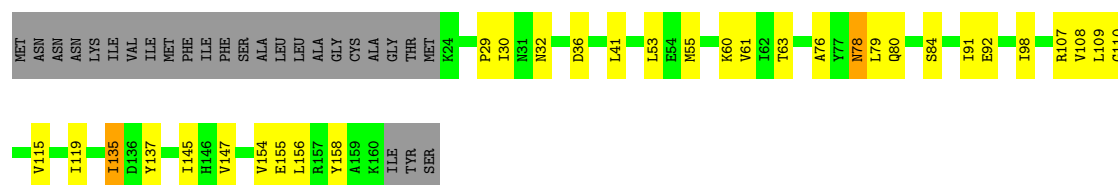
• Molecule 2: DotD

Chain ID:  58% 26% 14%



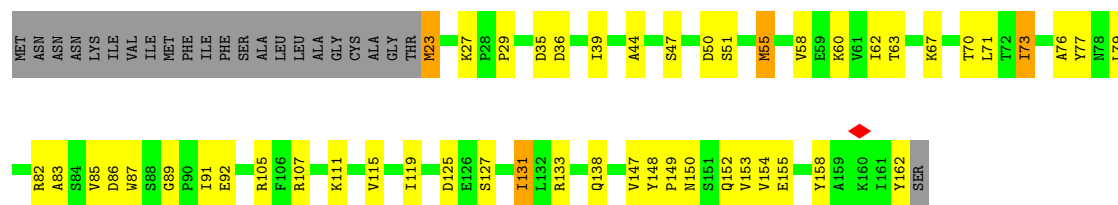
• Molecule 2: DotD

Chain Id:  64% 18% 16%



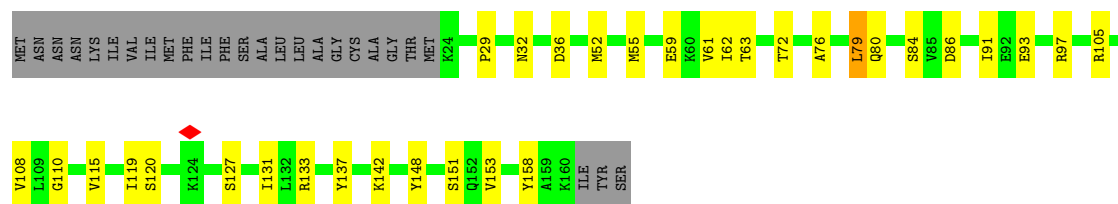
• Molecule 2: DotD

Chain JD:  55% 28% 14%

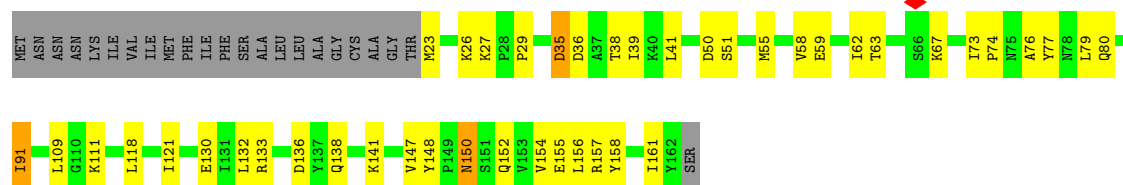


• Molecule 2: DotD

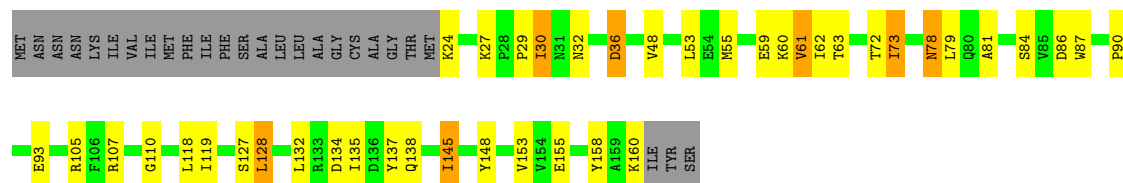
Chain Jd:  64% 20% 16%



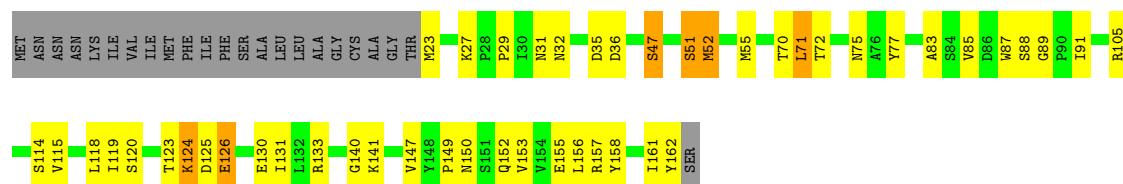
• Molecule 2: DotD



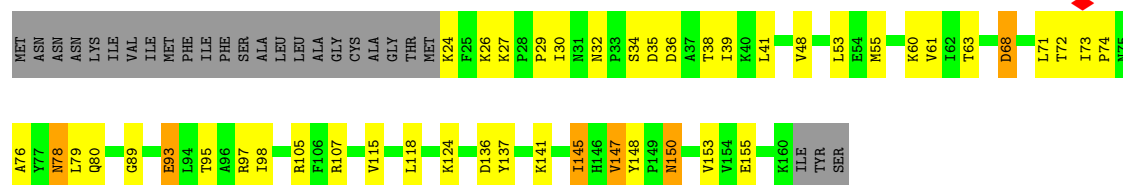
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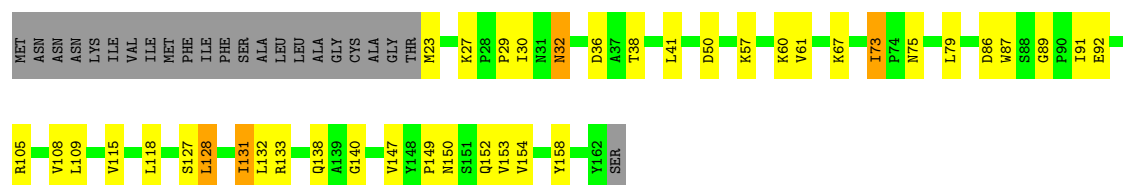
• Molecule 2: DotD



• Molecule 2: DotD

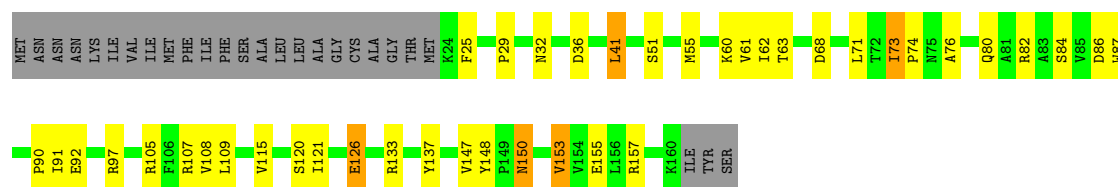


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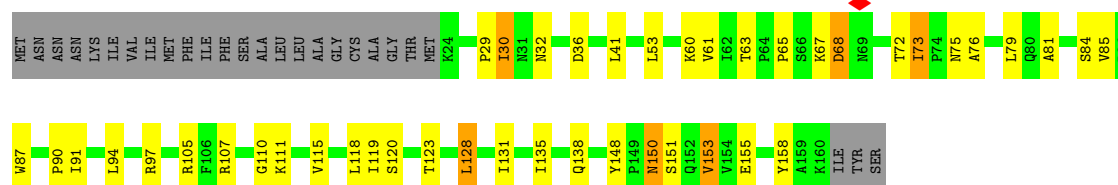
• Molecule 2: DotD

Chain Md:  59% 22% 16%



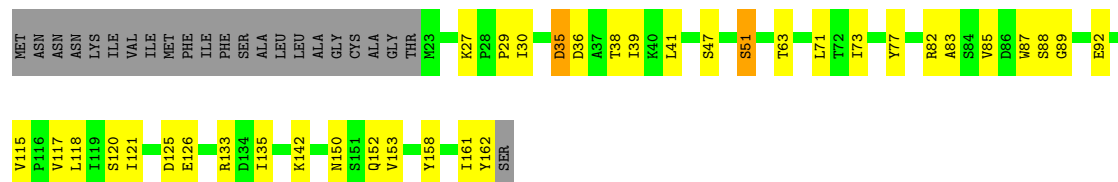
• Molecule 2: DotD

Chain Ad:  57% 23% 16%



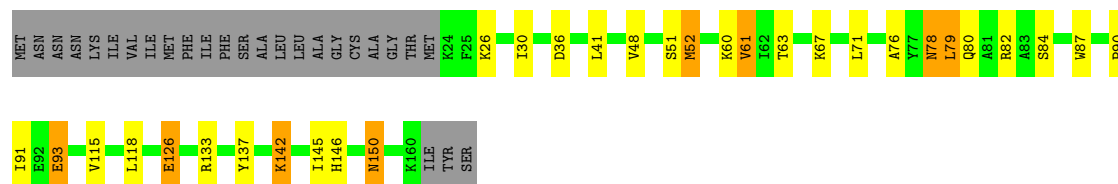
• Molecule 2: DotD

Chain BD:  63% 21% 14%



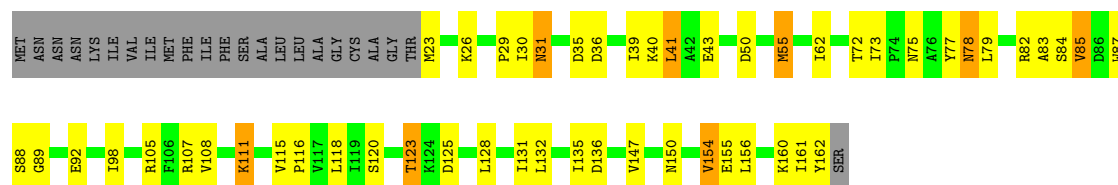
• Molecule 2: DotD

Chain Bd:  65% 14% 5% 16%



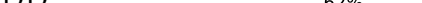
• Molecule 2: DotD

Chain CD:  54% 27% 5% 14%



• Molecule 2: DotD

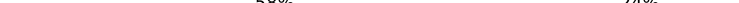
L109	G110	V115	E126	I131	D136	A139	K142	A143	S144	I145	H146	V147	Y148	P149	M150	V153	Y158	A159	K160	I16	TYR	SER																				
MET	ASN	ASN	ASN	I16	VAL	MET	PHE	TLE	PHE	SER	LEU	ALA	ALA	GLY	CYS	GLY	THR	MET	K24	I30	D35	D36	A37	T38	I39	K40	L41	S51	E59	K60	V61	I62	D68	A76	L79	S84	I91	L94	K97	I98	R105	V109

Chain DD:  62% 24% 14%

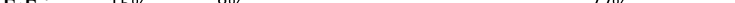
I119	S120	T123	K124	D125	E126	S127	E130	I131	L132	R133	D136	I145	M150	V154	Y158	I161	Y162	SER																								
MET	ASN	ASN	LYS	ILE	VAL	ILE	MET	PHE	PHE	SER	LEU	LEU	ALA	GLY	CYS	ALA	ALA	GLY	THR	K23	K26	K27	I30	D36	L41	S51	M52	M55	T63	S66	I73	R82	A83	S84	D86	W87	S88	G89	I98	V108	V115	...

Chain Dd: 60% 23% • 16%

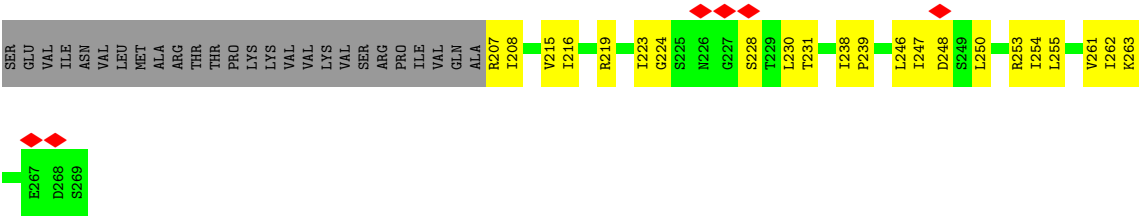
V108	V109	G110	V115	L118	L119	S120	L121	S122	E126	S127	L128	R133	D136	Y137	K142	L145	R146	V147	Y148	P149	N150	V153	V154	E155	L156	R157	Y158	A159	K160	L161	TYR	SER	MET	ASN	ASN	LYS	ILE	VAL	ILE	MET	PHE	ILE	PHE	SER	LEU	ALA	LEU	ALA	GLY	CYS	ALA	GLY	THR	MET	R24	P29	R31	R32	D36	L41	V43	M52	L53	E54	K60	V61	L71	N73	A81	R85	D86	W87	E92	R97	I98	E105
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Chain AD: 

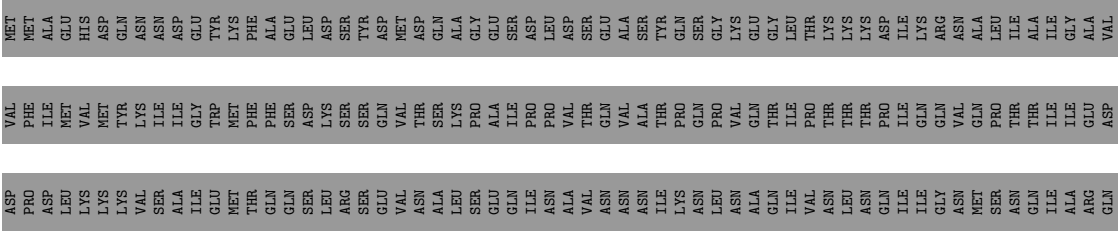
S88	G89	I98	R105	V115	P116	V117	L118	I119	S120	S121	S122	T123	K124	L132	R133	Q138	A139	G140	I145	H146	V147	Y148	P149	M150	S151	Q152	V153	V154	E155	L156	Y162	SER	NET											
ASN	ASN	ASN	LYS	ILE	VAL	ILE	VAL	ILE	PHE	PHE	THR	GLY	ALA	GLY	CYS	GLY	THR	M23	K24	K27	P28	P29	M32	P33	S34	D35	D36	I39	S47	S51	E54	M55	I62	D63	M65	T70	L71	T72	I73	A76	Q80	V85	D86	H87

Chain EF: 

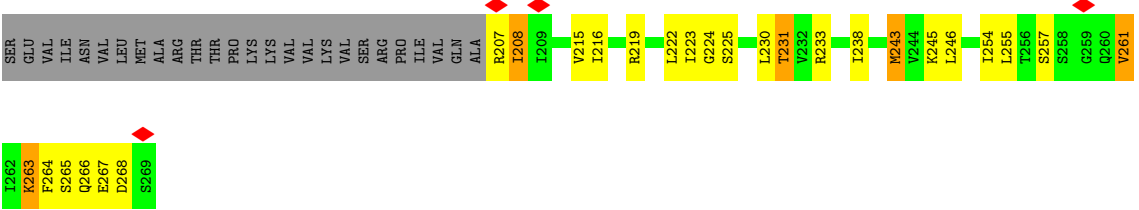
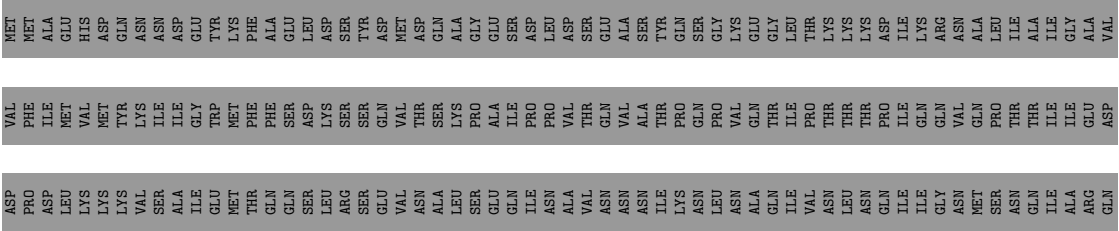
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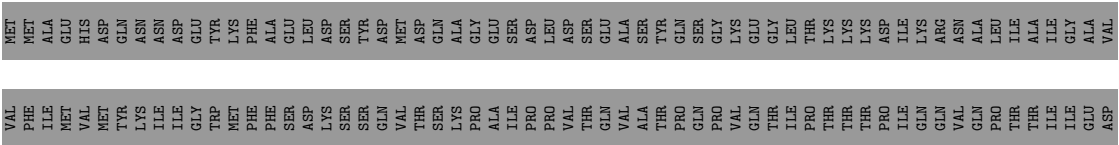
• Molecule 3: DotF

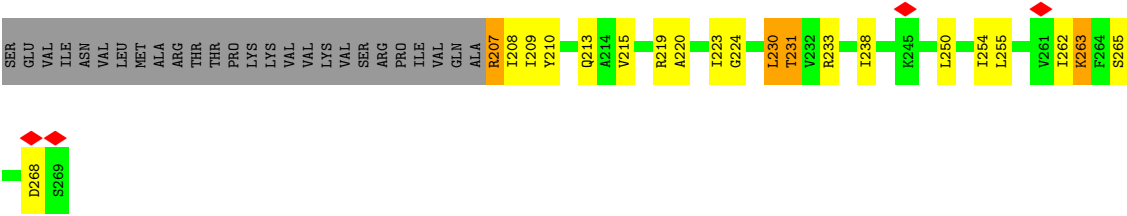


• Molecule 3: DotF

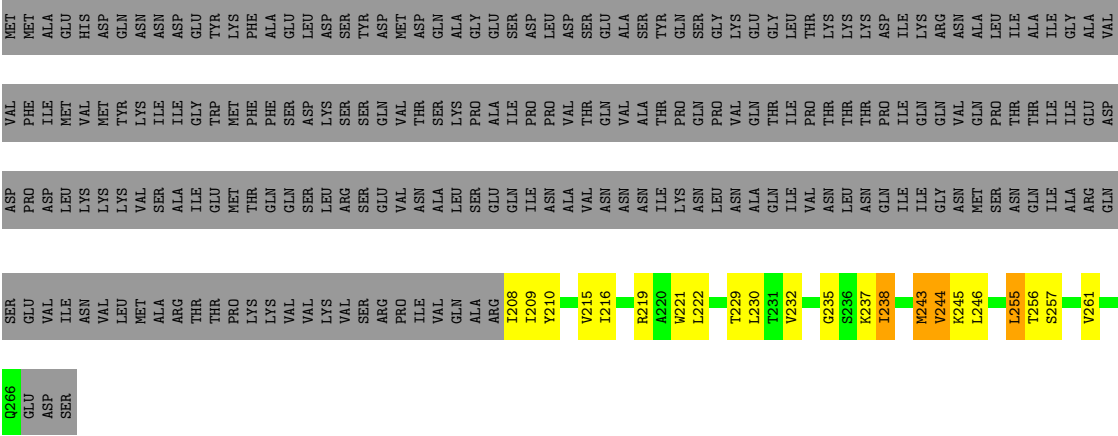


• Molecule 3: DotF

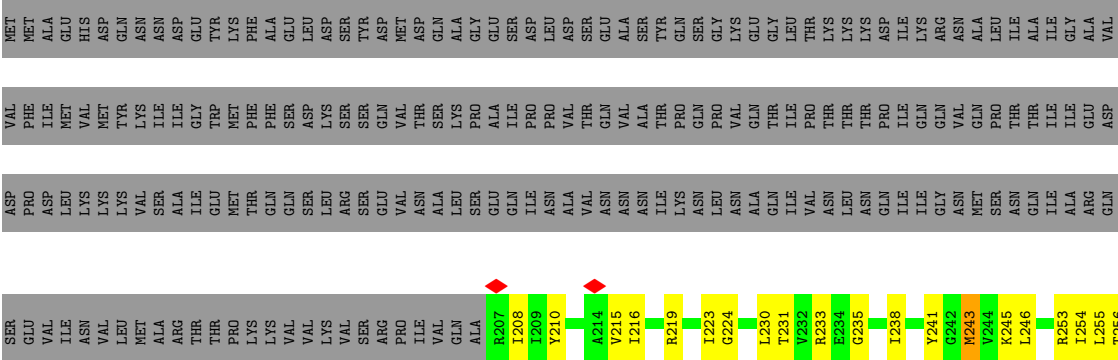




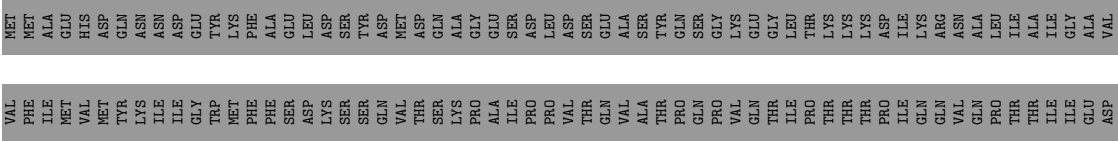
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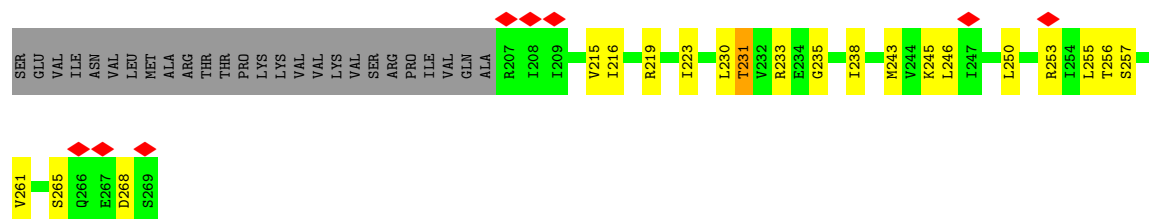
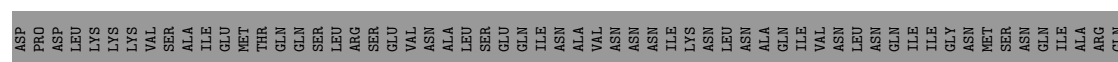
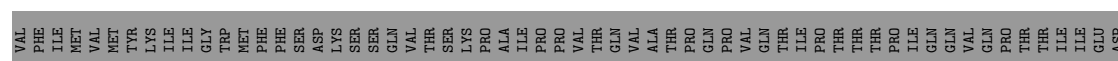
• Molecule 3: DotF



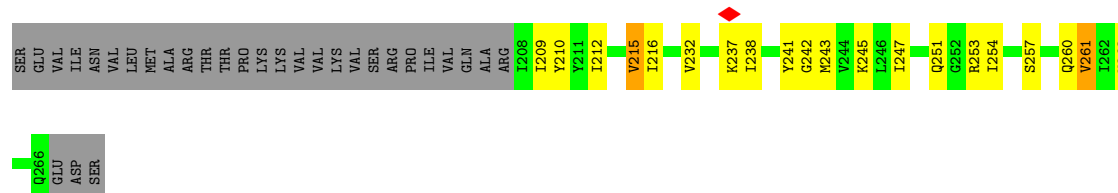
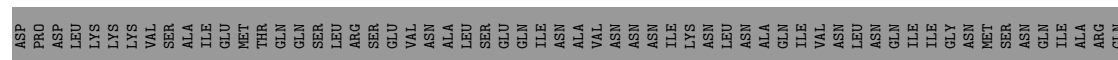
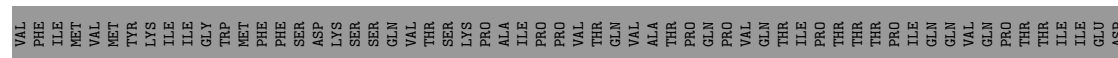
• Molecule 3: DotF



- Molecule 3: DotF



- Molecule 3: DotF



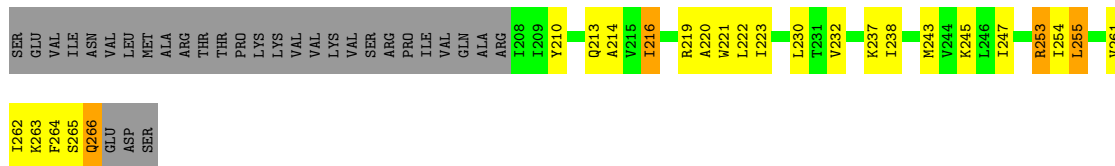
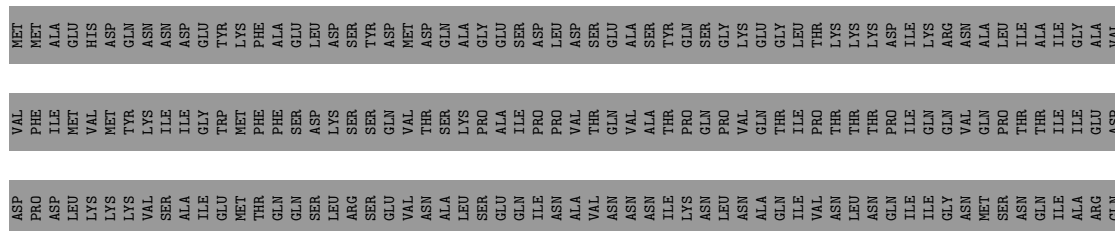
- Molecule 3: DotF



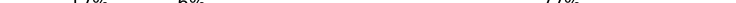


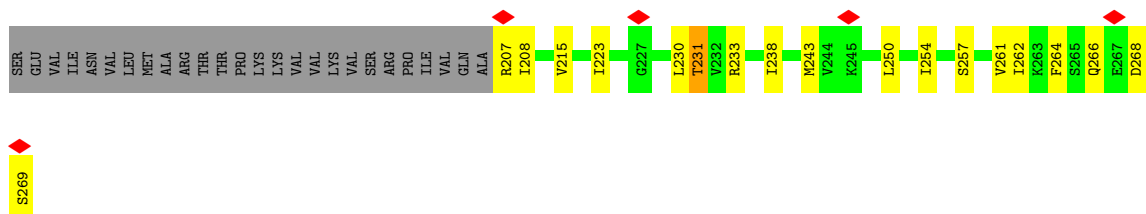
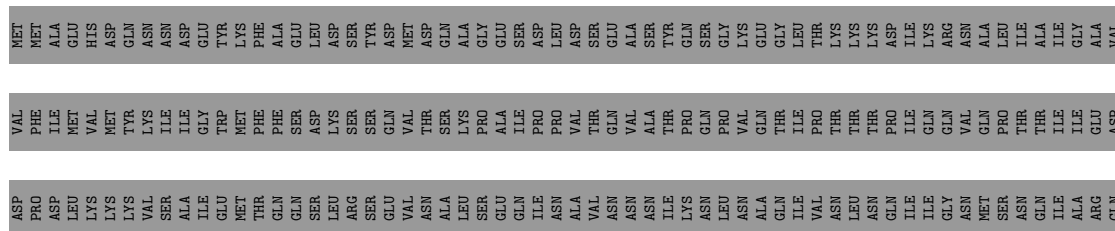
- Molecule 3: DotF

Chain Af: 13% 8% 78%



- Molecule 3: DotF

Chain BF: 

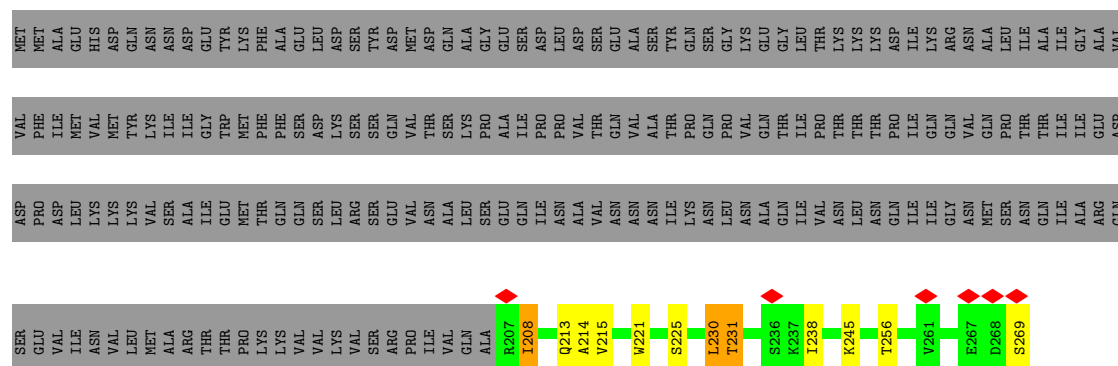


- Molecule 3: DotF

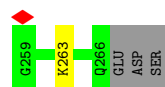
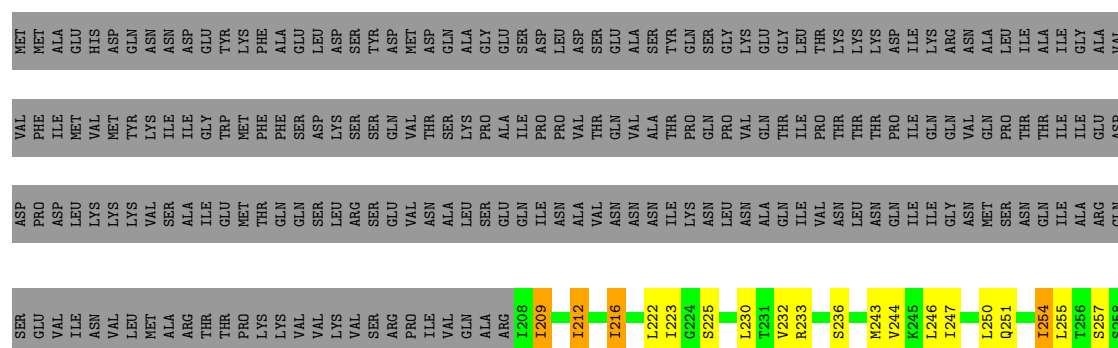
Chain Bf:



- Molecule 3: DotF

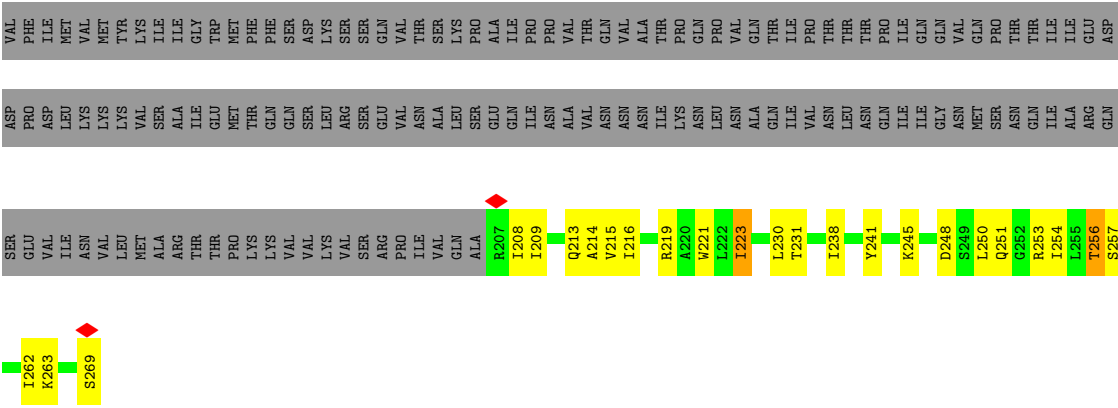


- Molecule 3: DotF

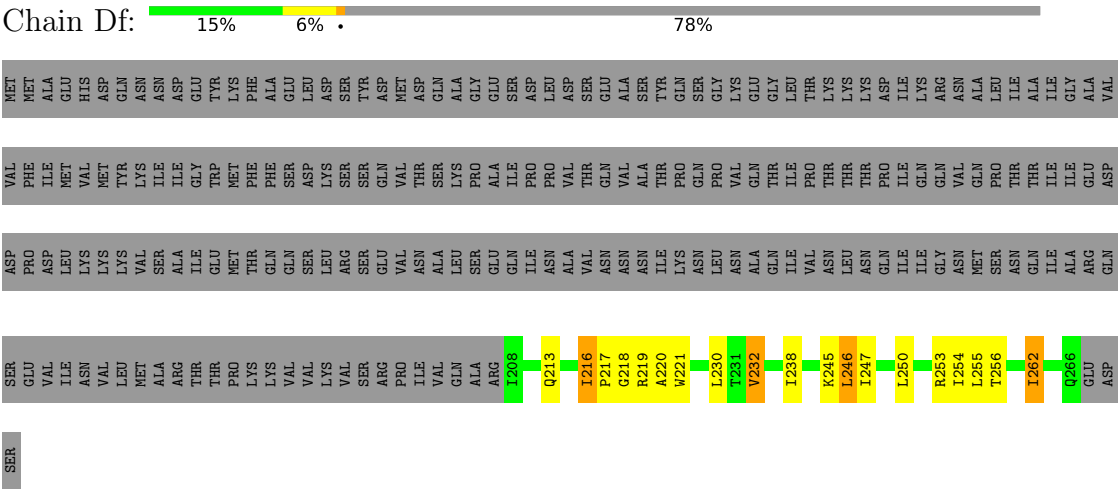


- Molecule 3: DotF

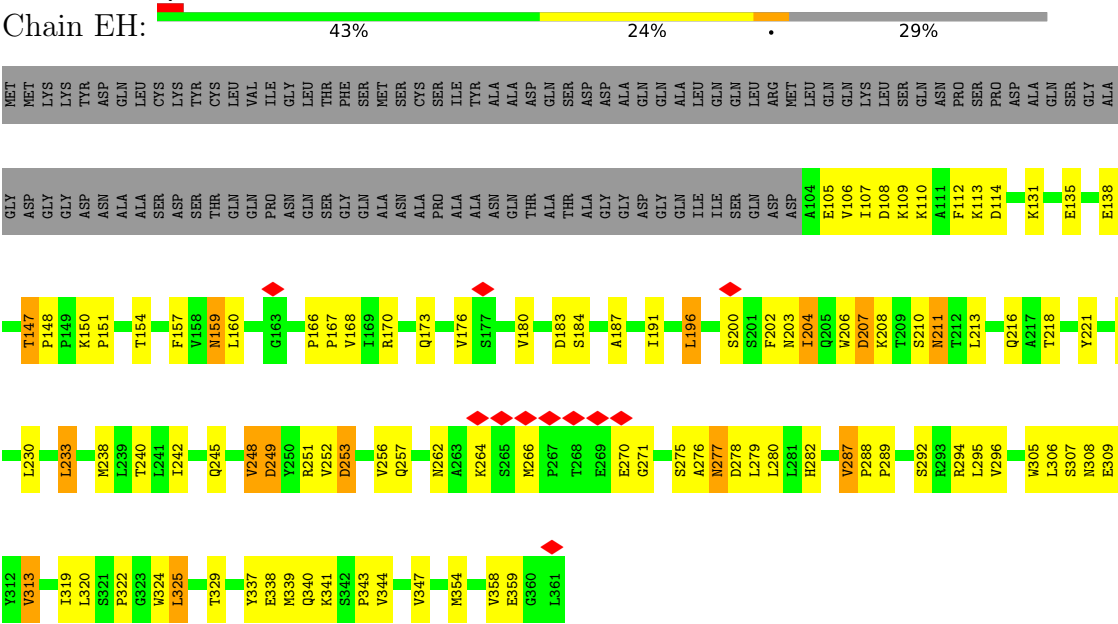




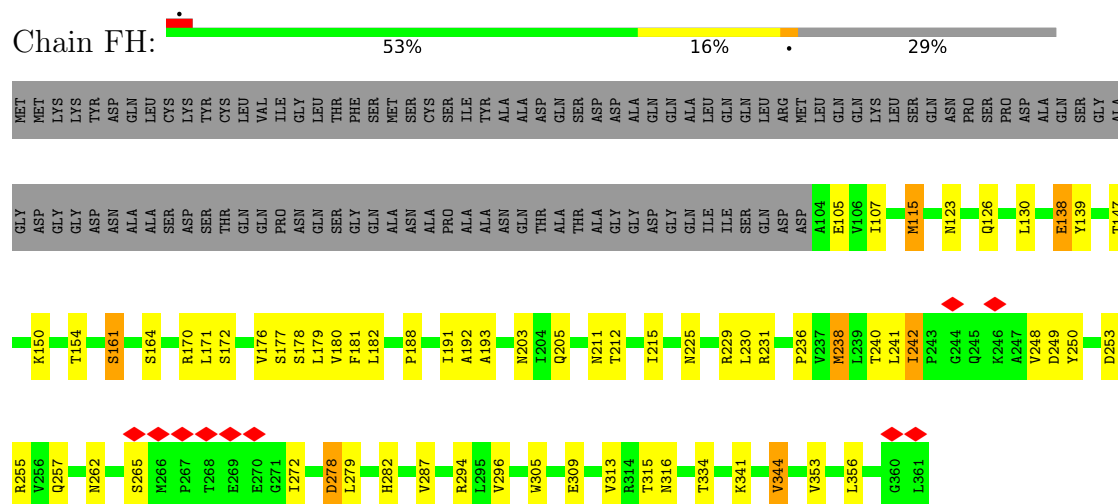
• Molecule 3: DotF



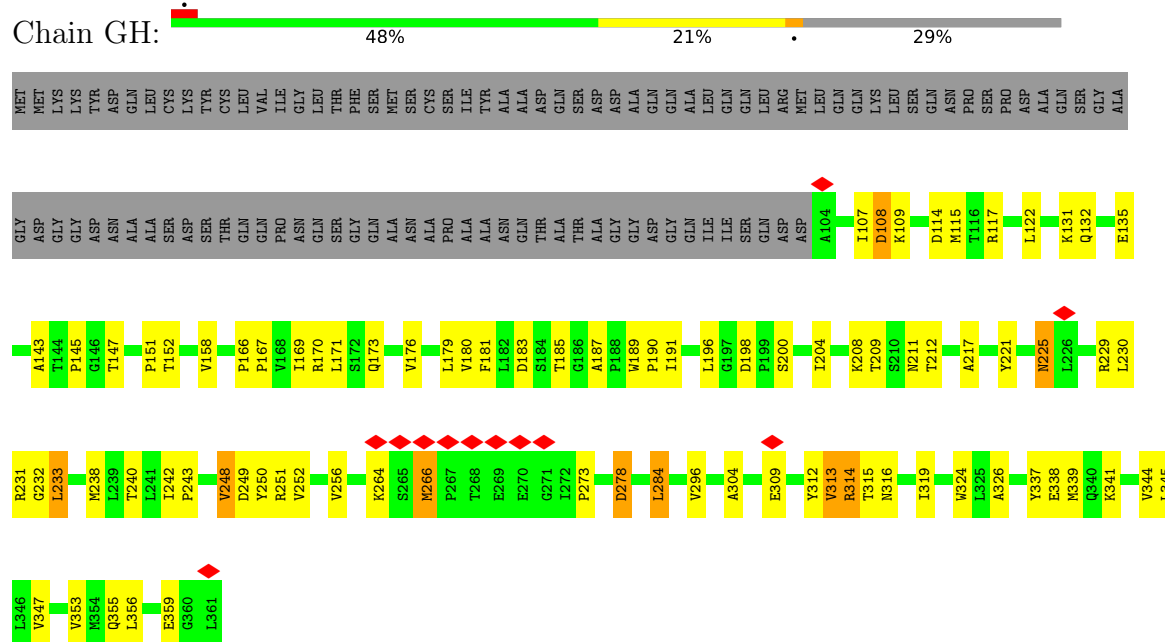
• Molecule 4: Type IV secretion protein IcmK



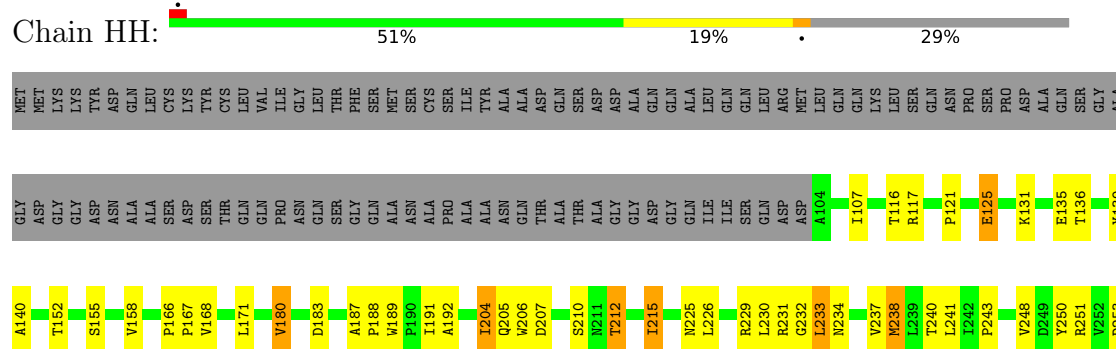
• Molecule 4: Type IV secretion protein IcmK



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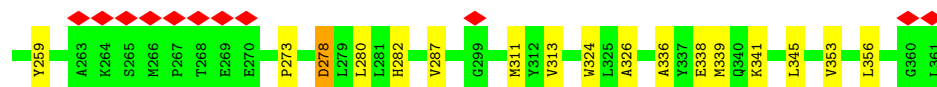
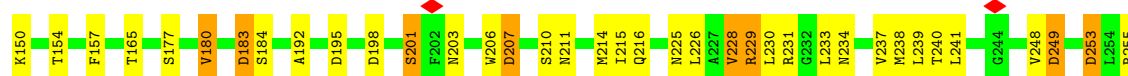
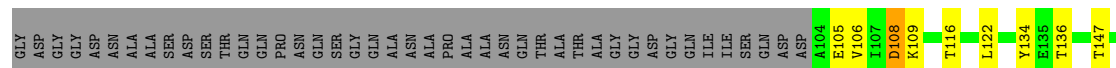
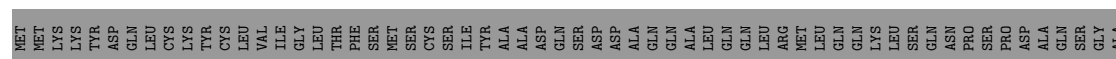


• Molecule 4: Type IV secretion protein IcmK

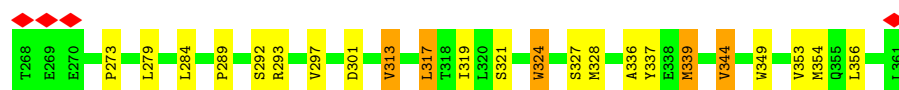
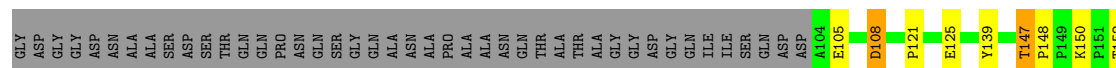
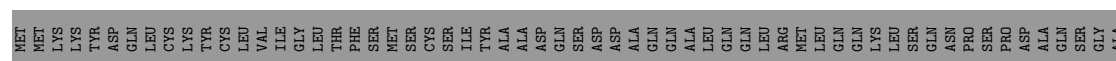




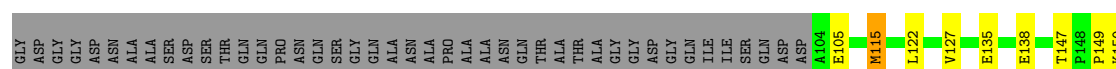
• Molecule 4: Type IV secretion protein IcmK



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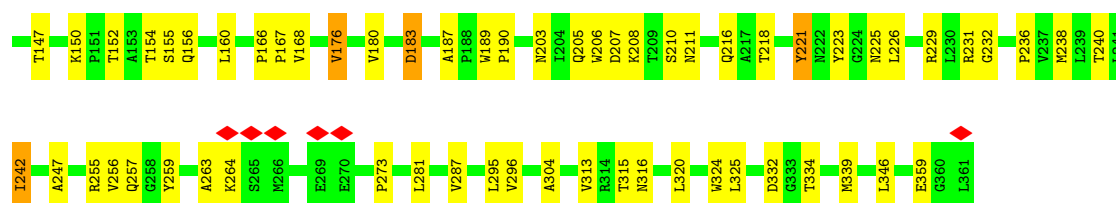
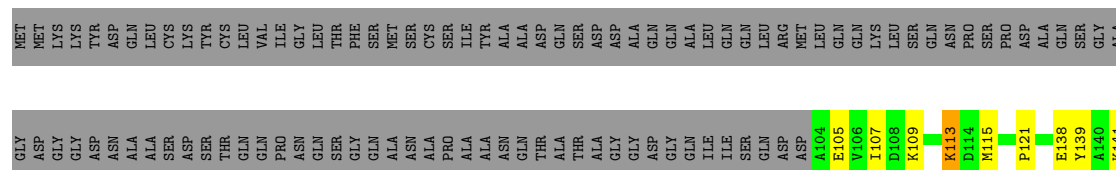


• Molecule 4: Type IV secretion protein IcmK

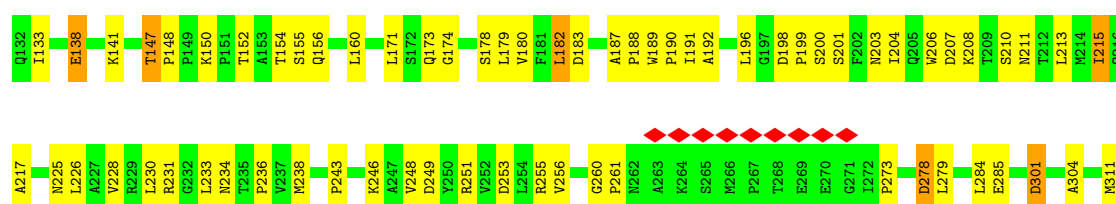
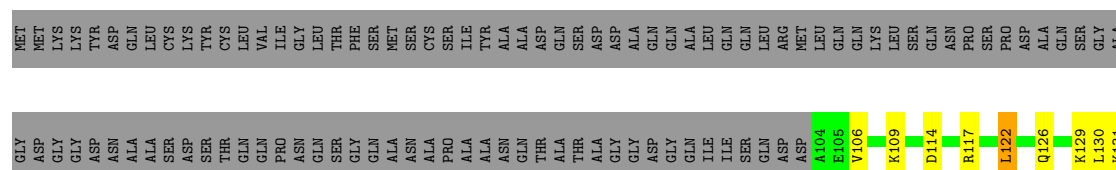




• Molecule 4: Type IV secretion protein IcmK

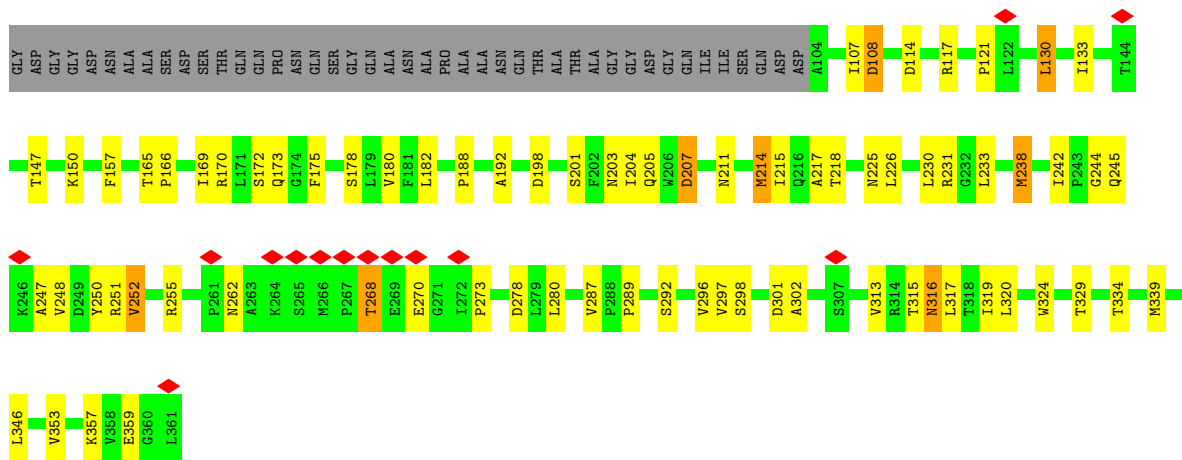


• Molecule 4: Type IV secretion protein IcmK

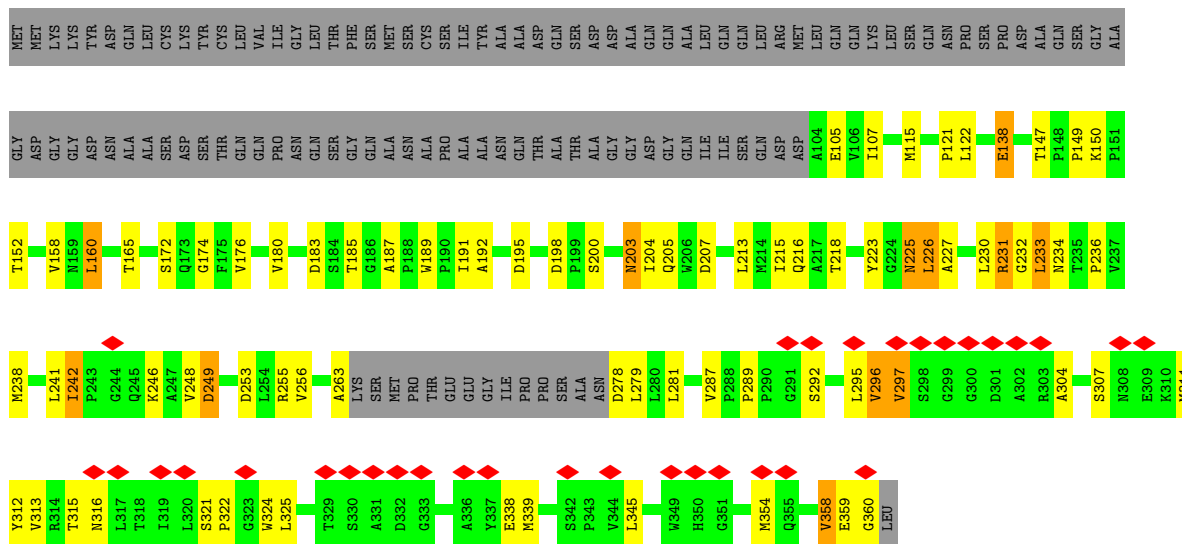


• Molecule 4: Type IV secretion protein IcmK

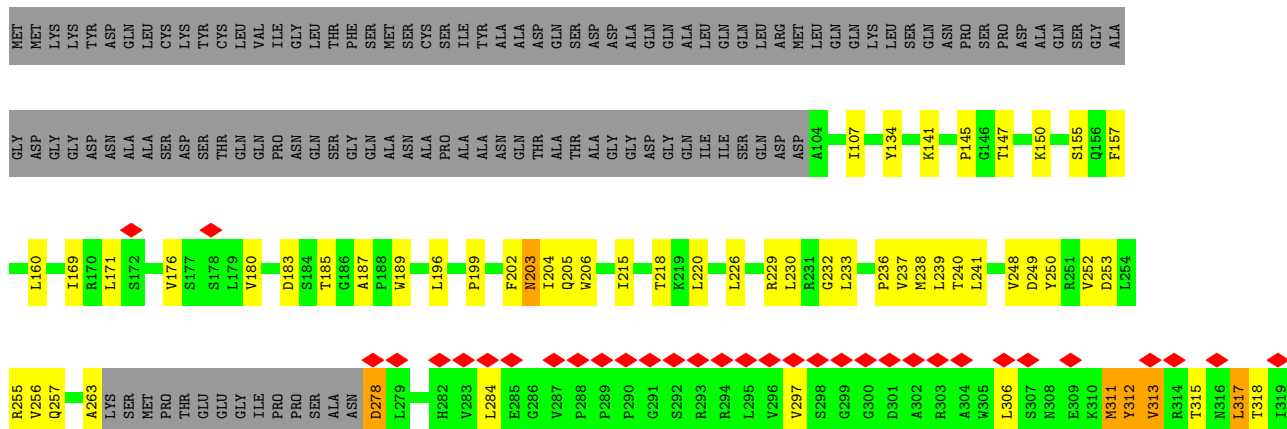




- Molecule 4: Type IV secretion protein IcmK

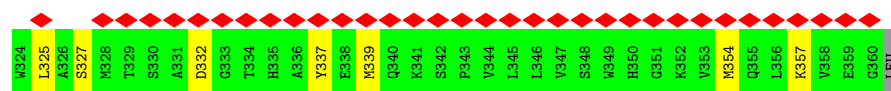
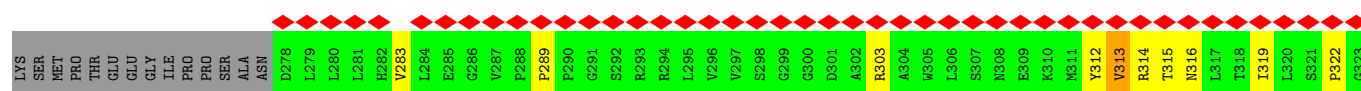
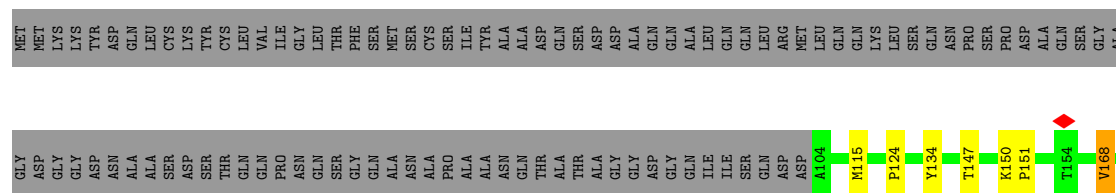


- Molecule 4: Type IV secretion protein IcmK

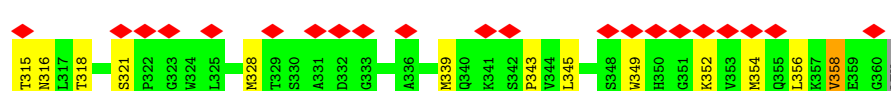
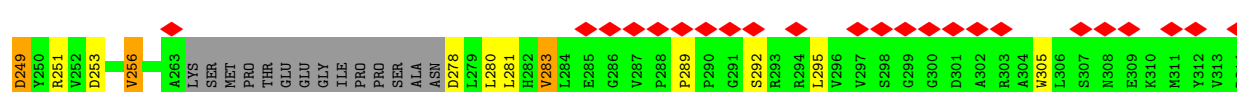
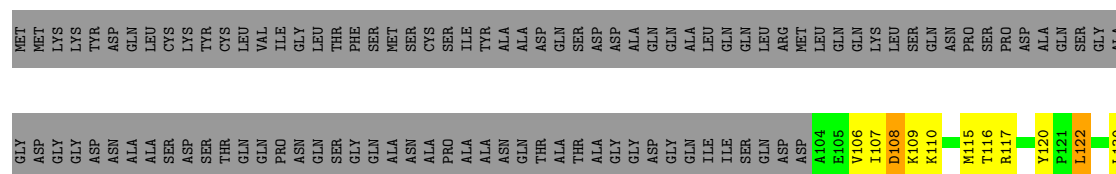




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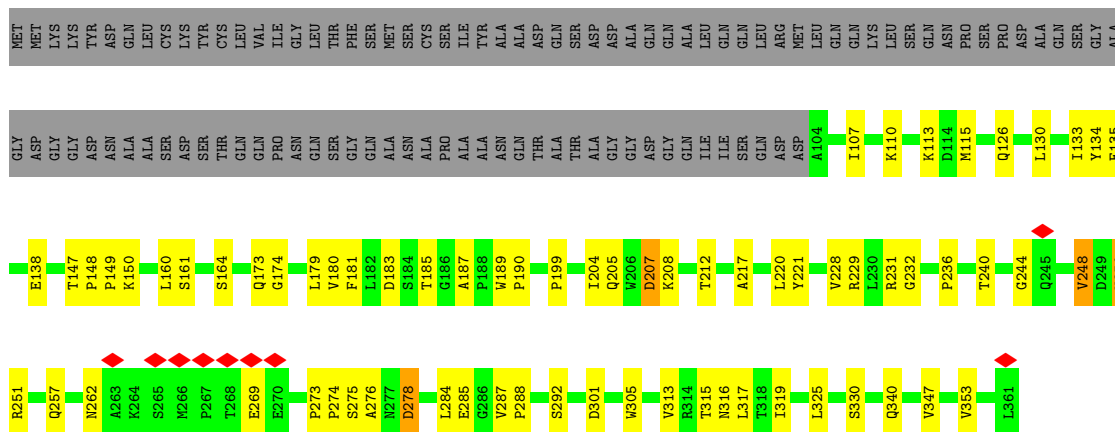
• Molecule 4: Type IV secretion protein IcmK



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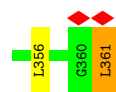


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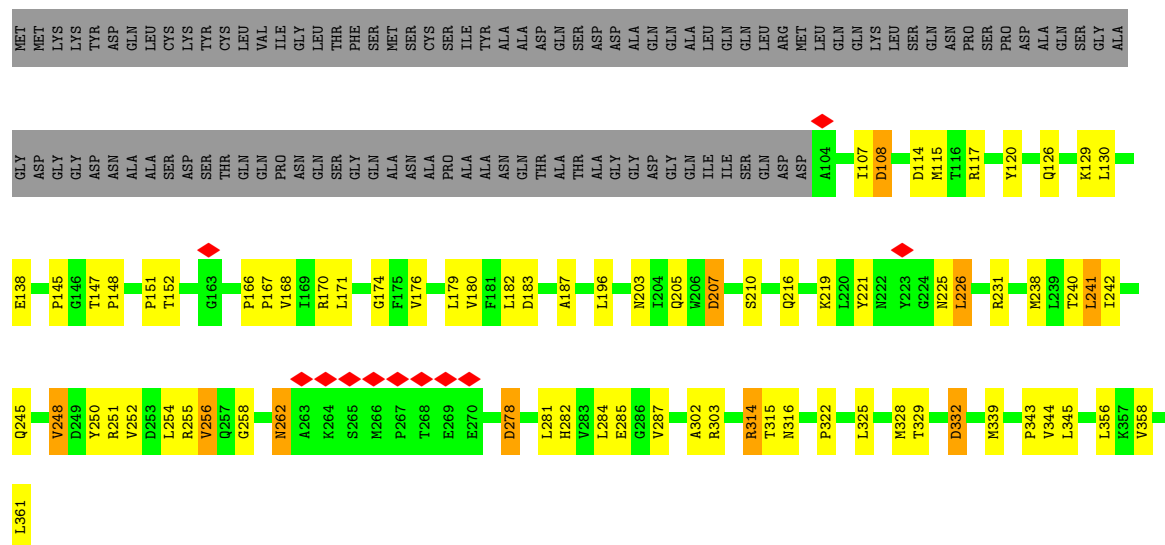
- Molecule 4: Type IV secretion protein IcmK





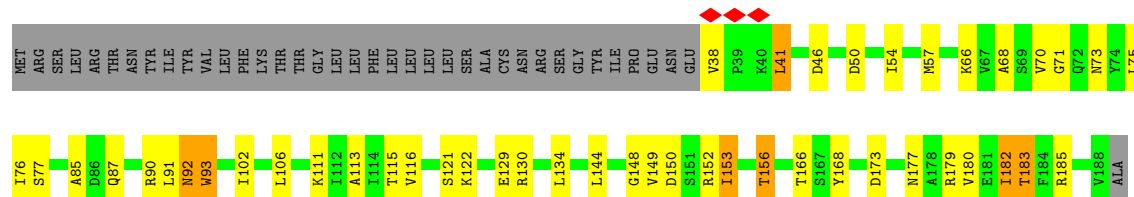
• Molecule 4: Type IV secretion protein IcmK

Chain DH: 51% 18% 29%



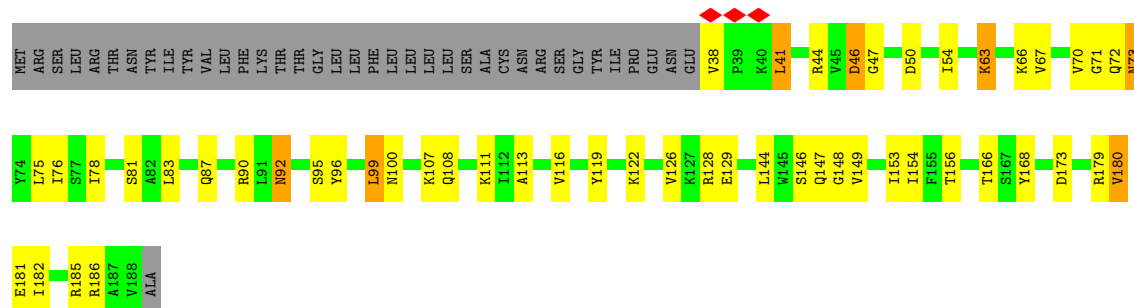
• Molecule 5: Inner membrane lipoprotein YiaD

Chain EK: 55% 21% 20%



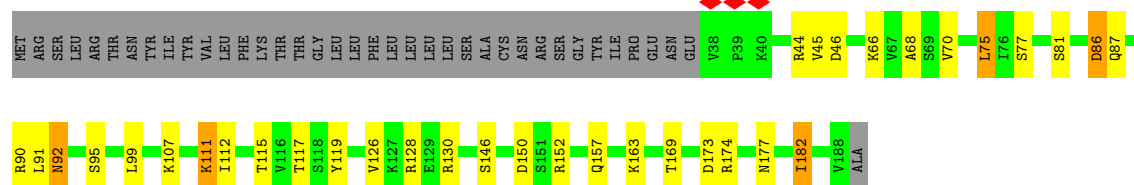
• Molecule 5: Inner membrane lipoprotein YiaD

Chain FK: 52% 24% 20%



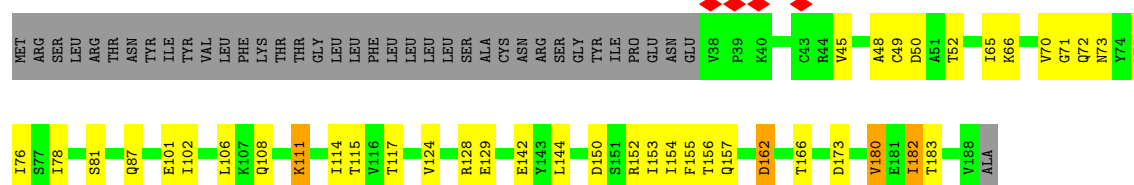
• Molecule 5: Inner membrane lipoprotein YiaD

Chain GK: 



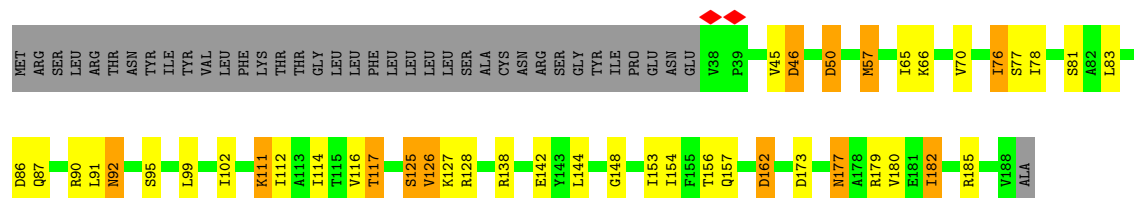
- Molecule 5: Inner membrane lipoprotein YiaD

Chain HK: 



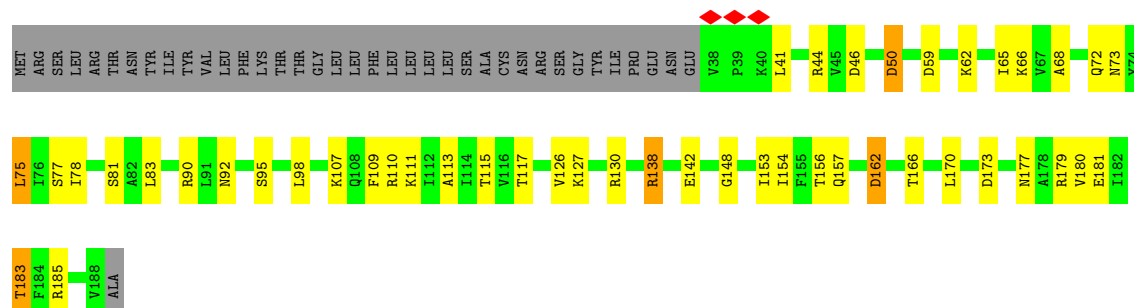
- Molecule 5: Inner membrane lipoprotein YiaD

Chain IK: 



- Molecule 5: Inner membrane lipoprotein YiaD

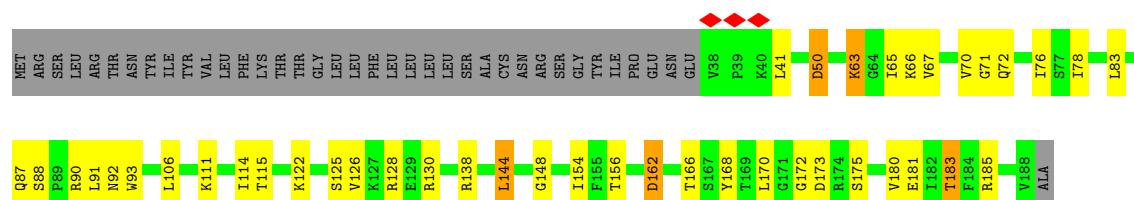
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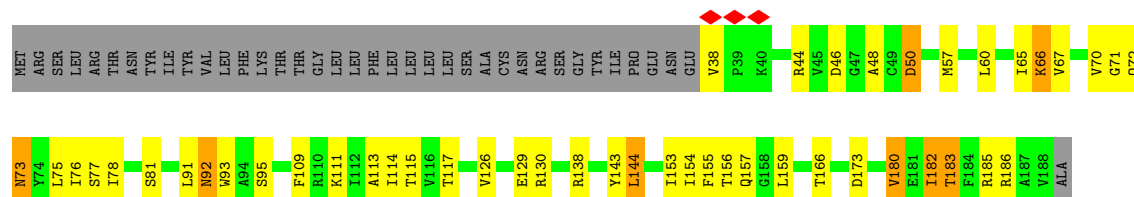
- Molecule 5: Inner membrane lipoprotein YiaD

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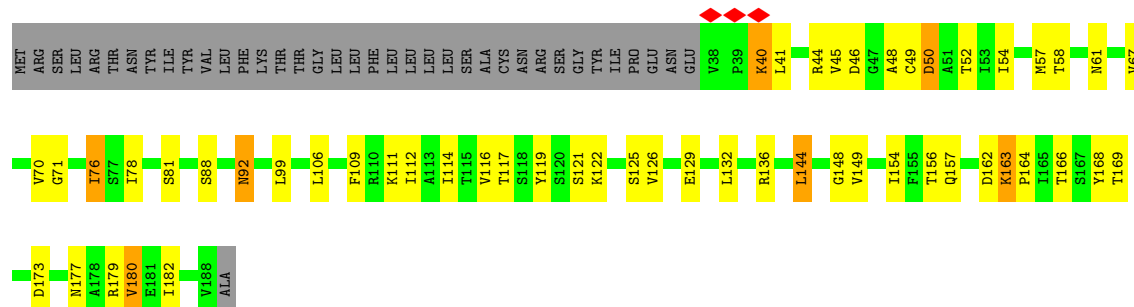




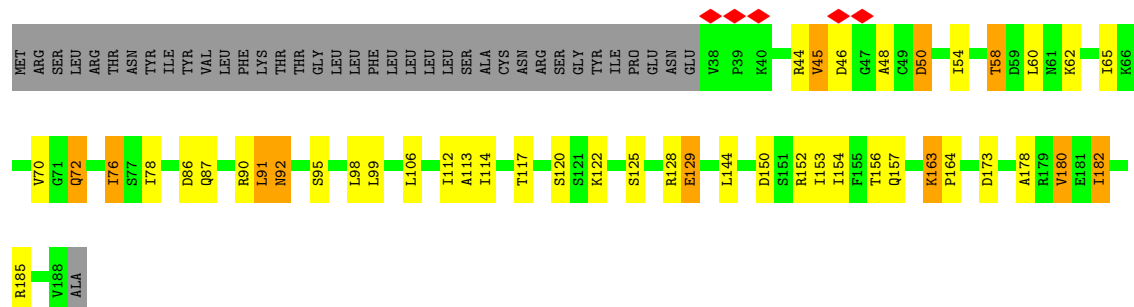
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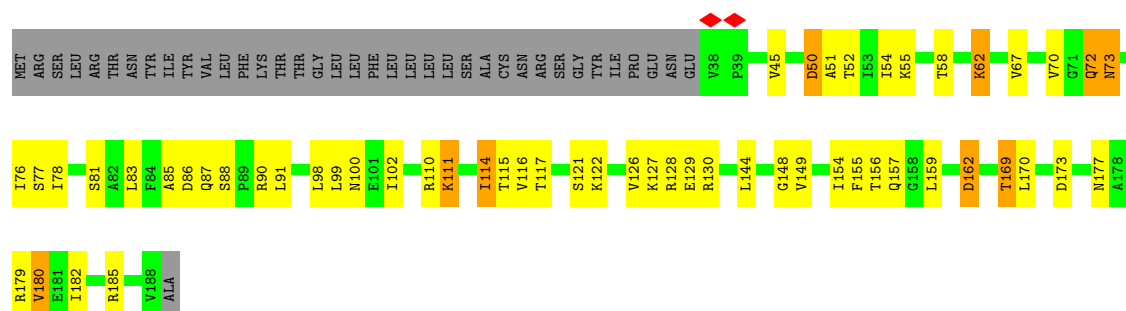


• Molecule 5: Inner membrane lipoprotein YiaD

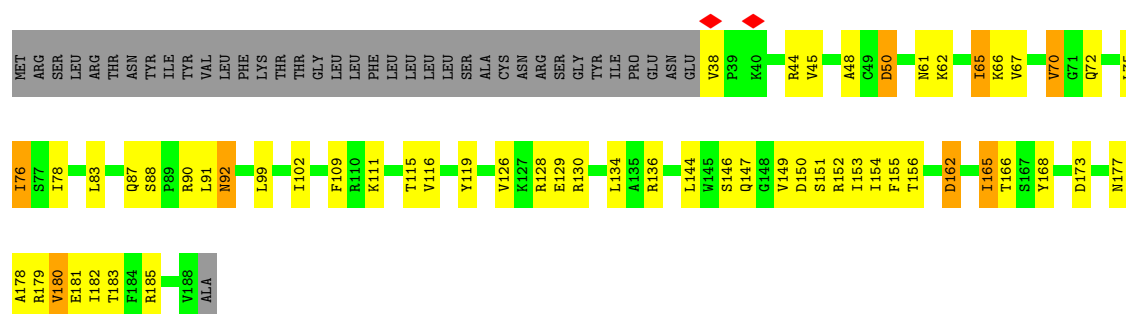


• Molecule 5: Inner membrane lipoprotein YiaD

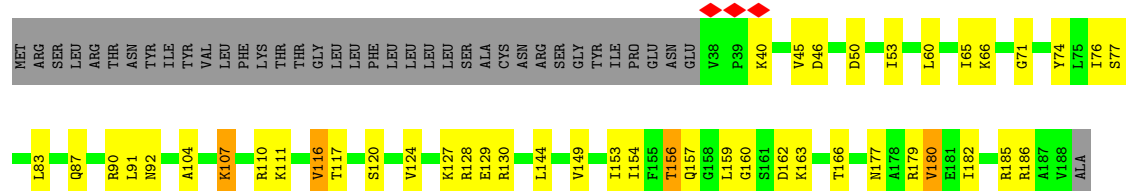




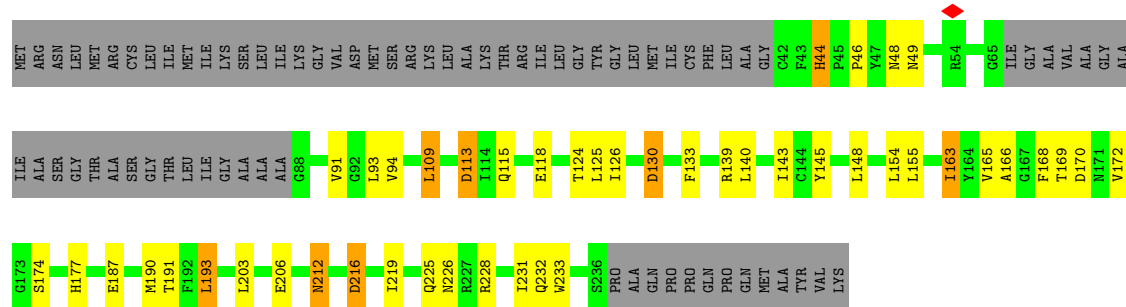
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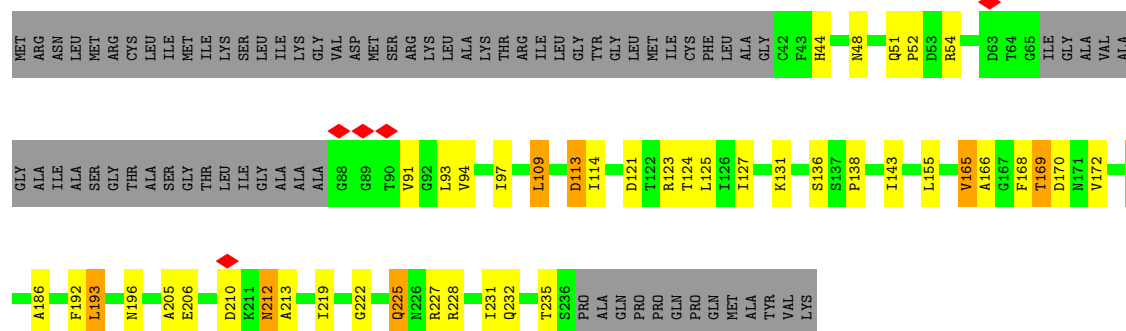


- Molecule 6: Outer membrane protein, OmpA family protein



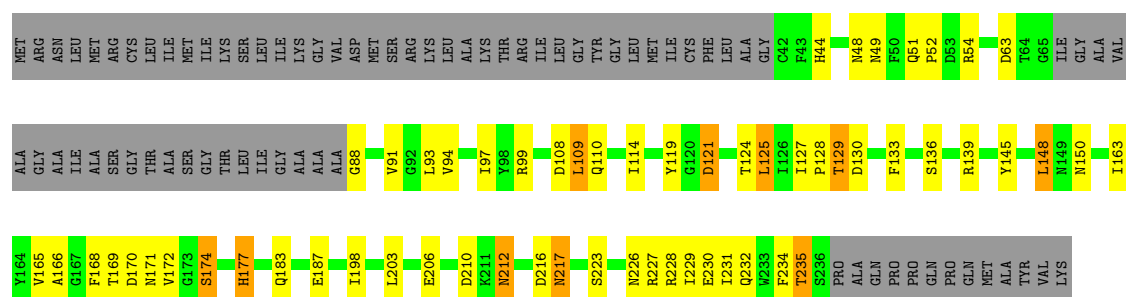
- Molecule 6: Outer membrane protein, OmpA family protein

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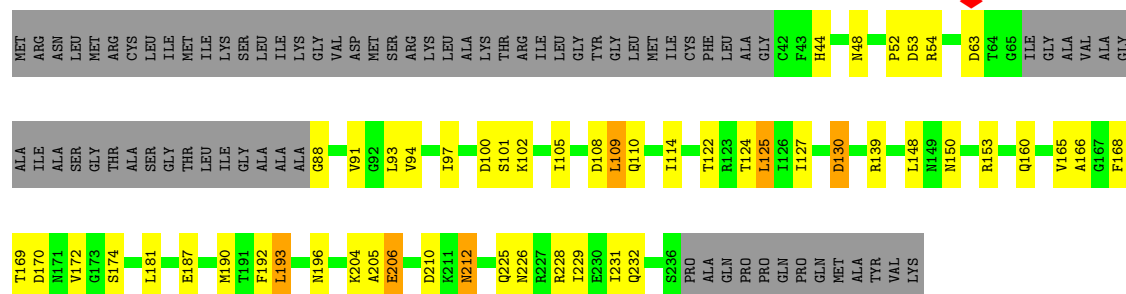
• Molecule 6: Outer membrane protein, OmpA family protein

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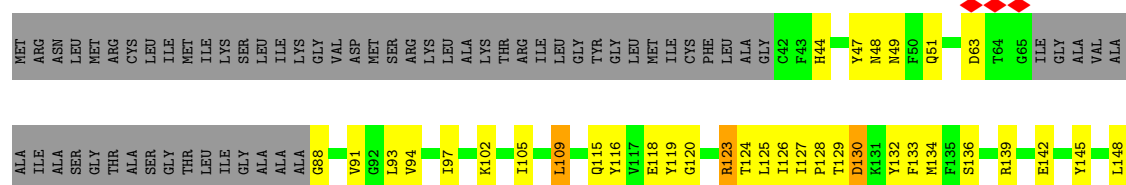
• Molecule 6: Outer membrane protein, OmpA family protein

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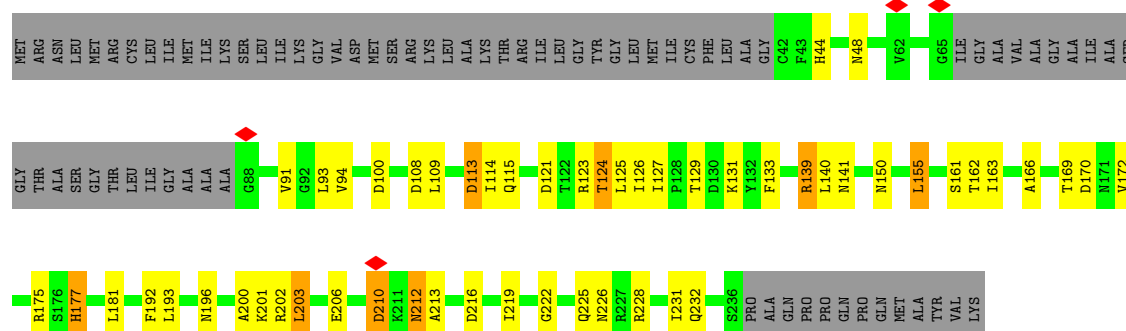
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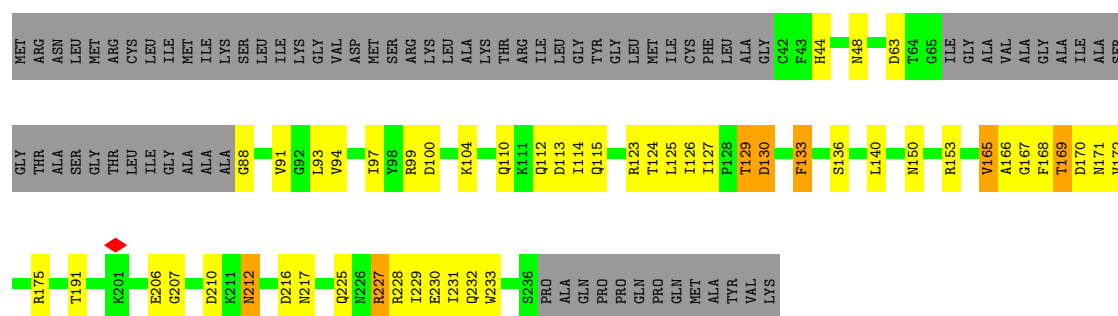




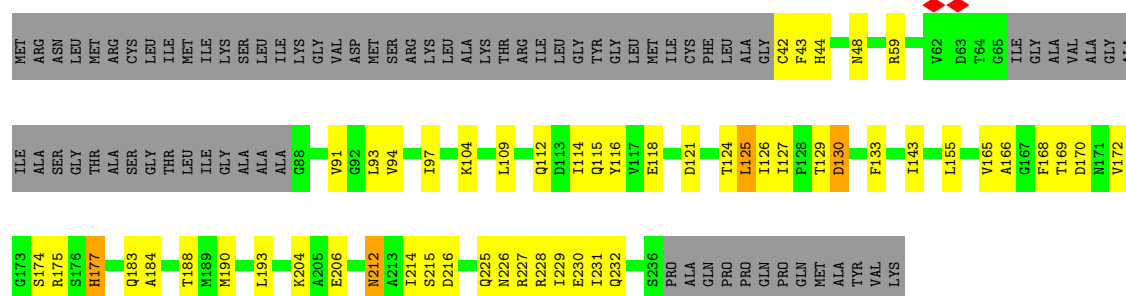
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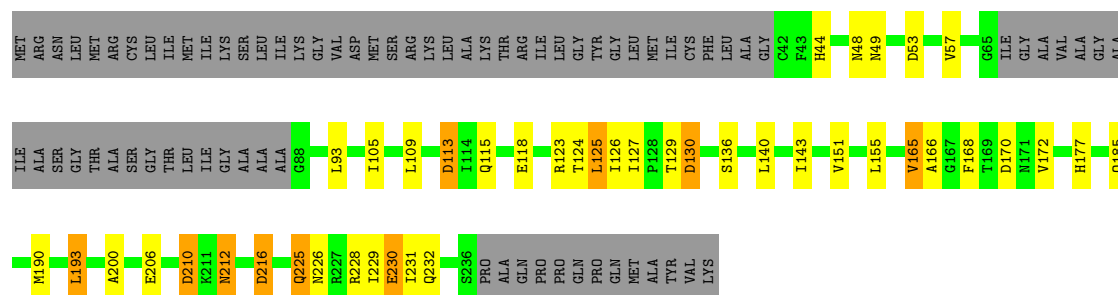


- Molecule 6: Outer membrane protein, OmpA family protein

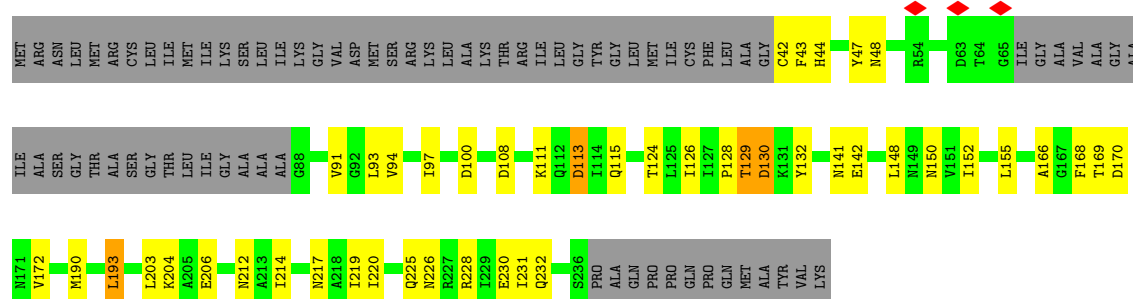


- Molecule 6: Outer membrane protein, OmpA family protein

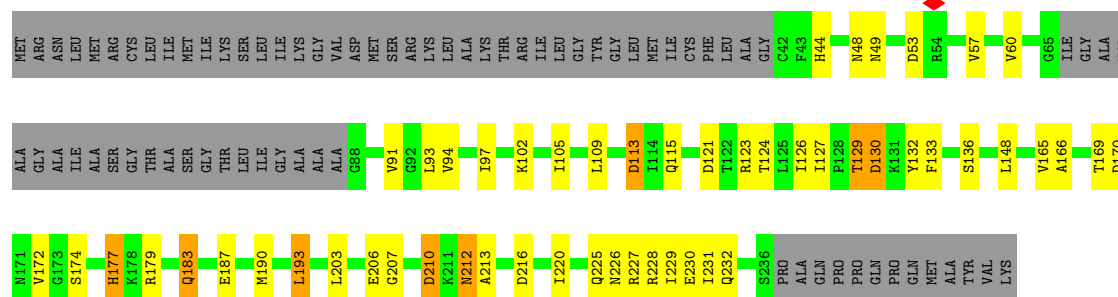




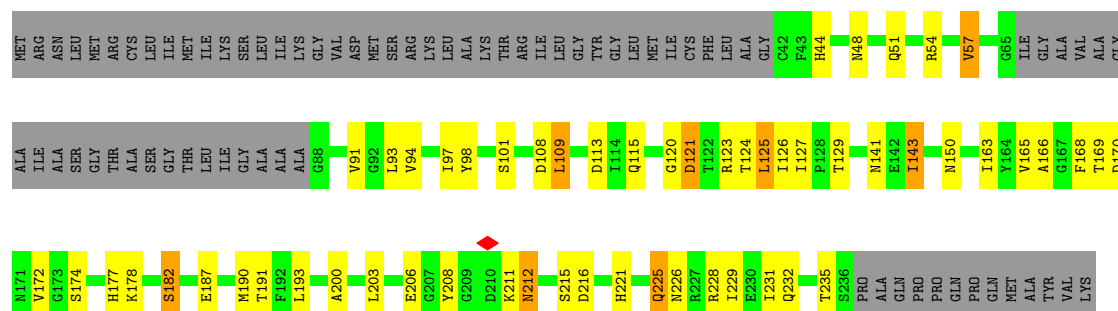
- Molecule 6: Outer membrane protein, OmpA family protein

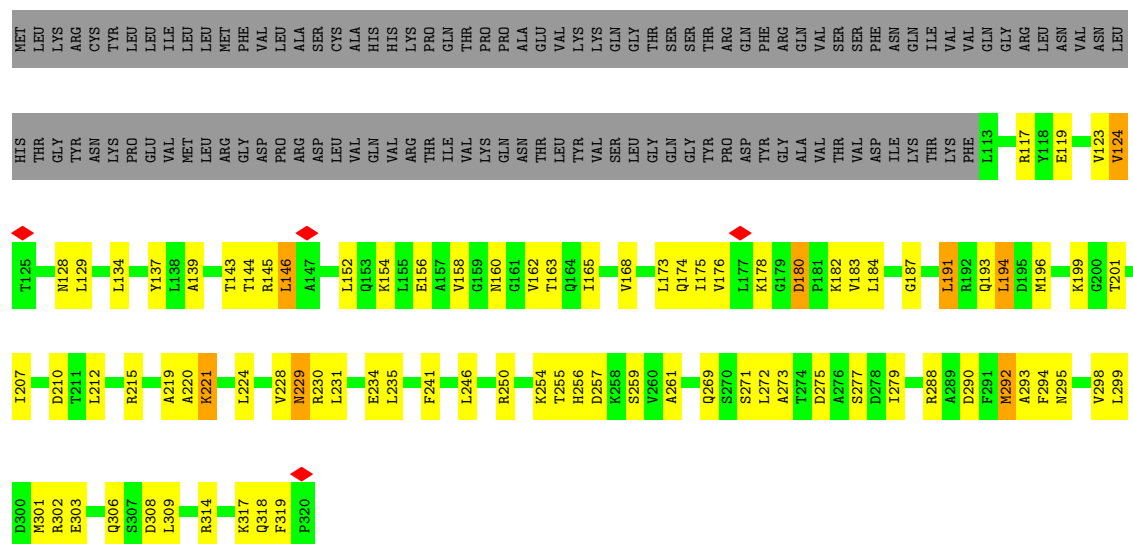


- Molecule 6: Outer membrane protein, OmpA family protein



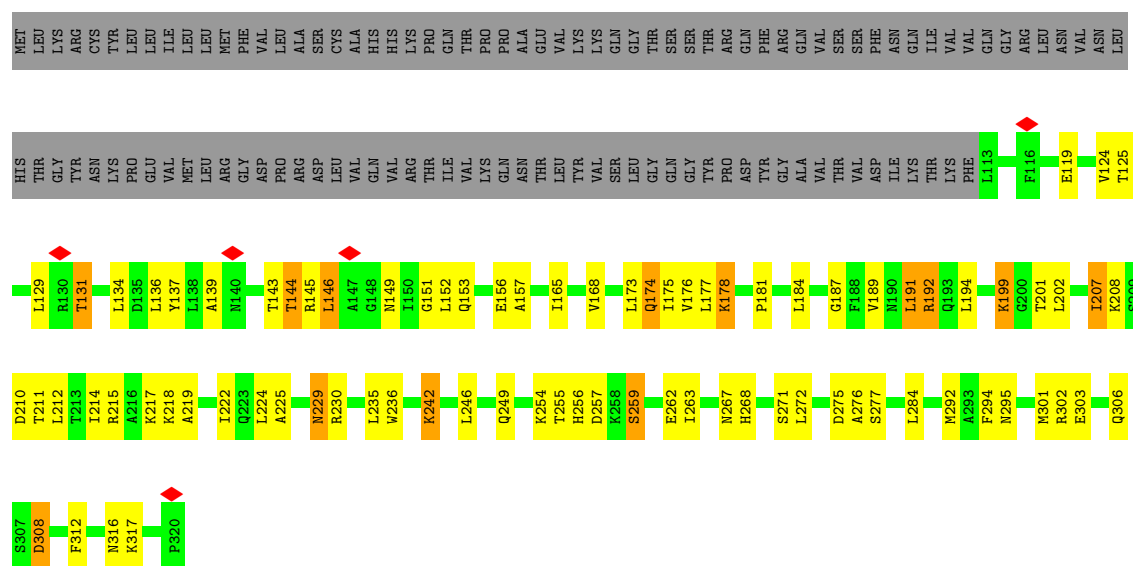
- Molecule 6: Outer membrane protein, OmpA family protein





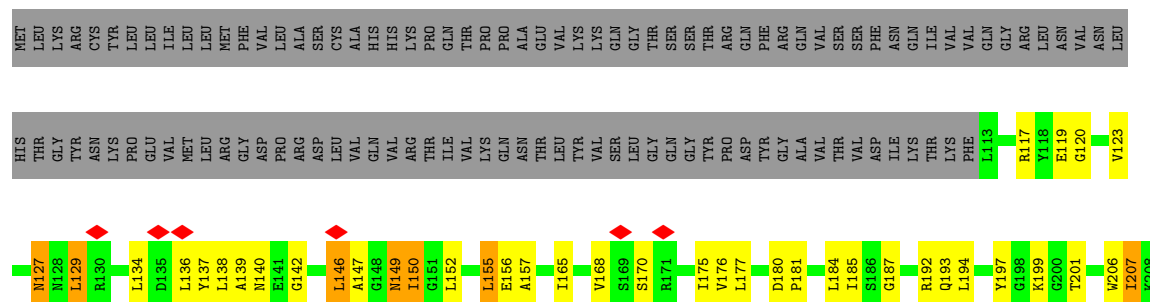
• Molecule 7: DUF2807 domain-containing protein

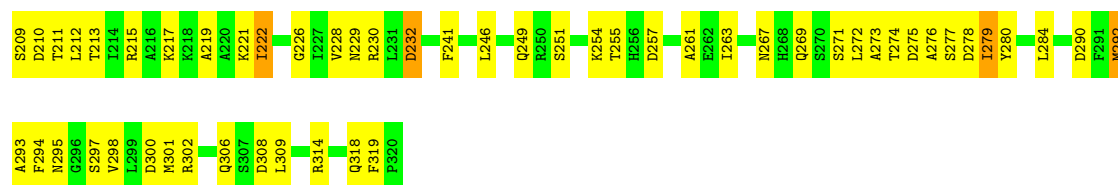
Chain HM: 39% 22% 35%



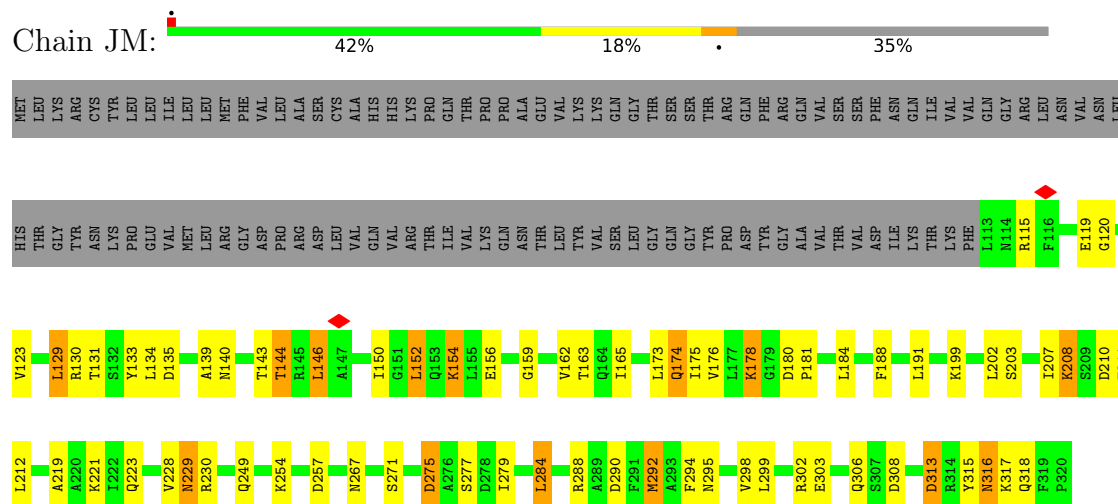
• Molecule 7: DUF2807 domain-containing protein

Chain IM: 36% 26% 35%

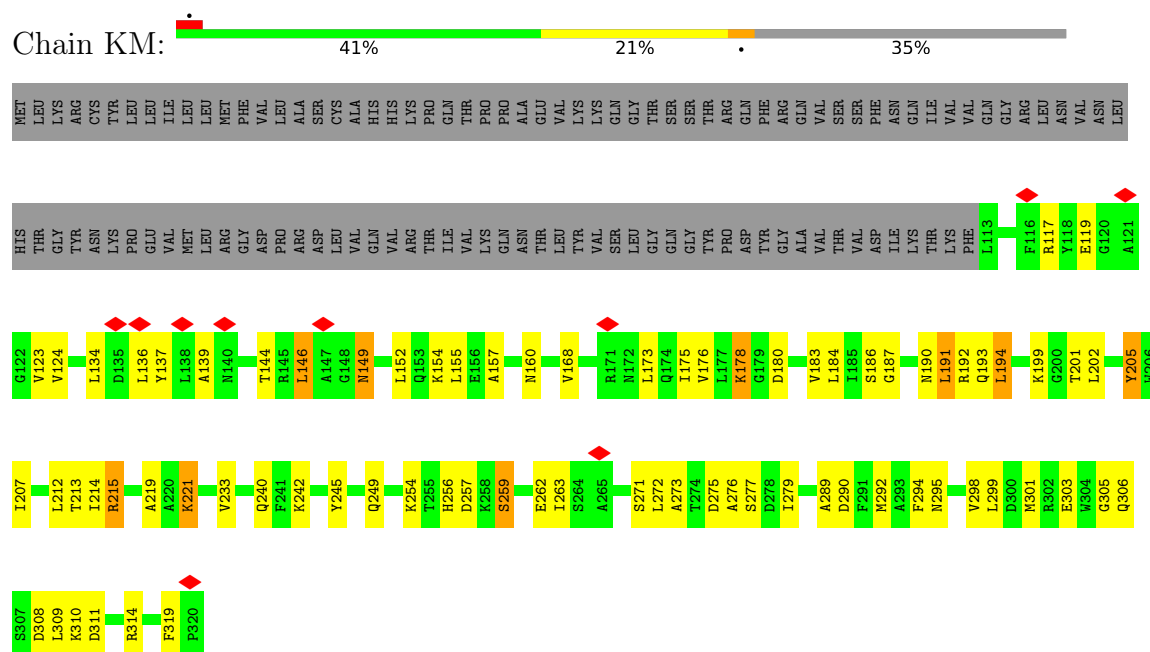




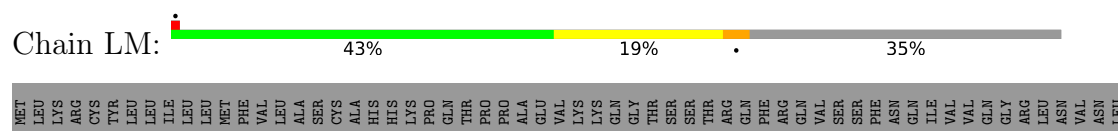
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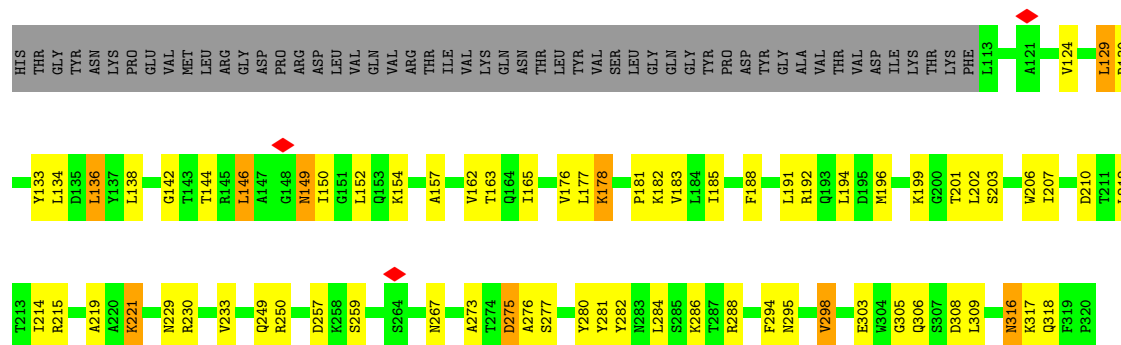


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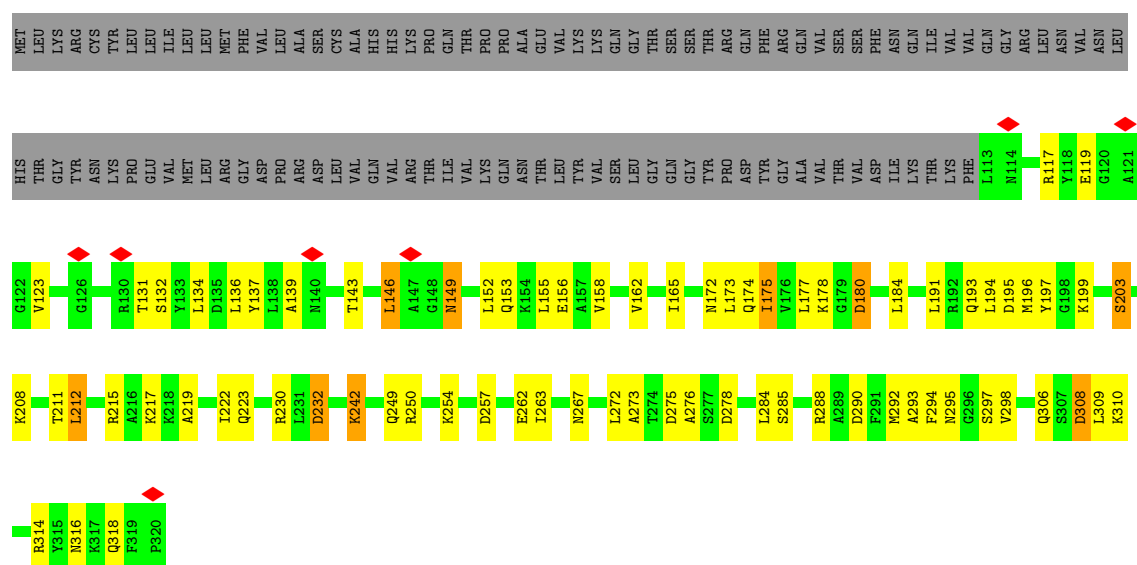


• Molecule 7: DUF2807 domain-containing protein

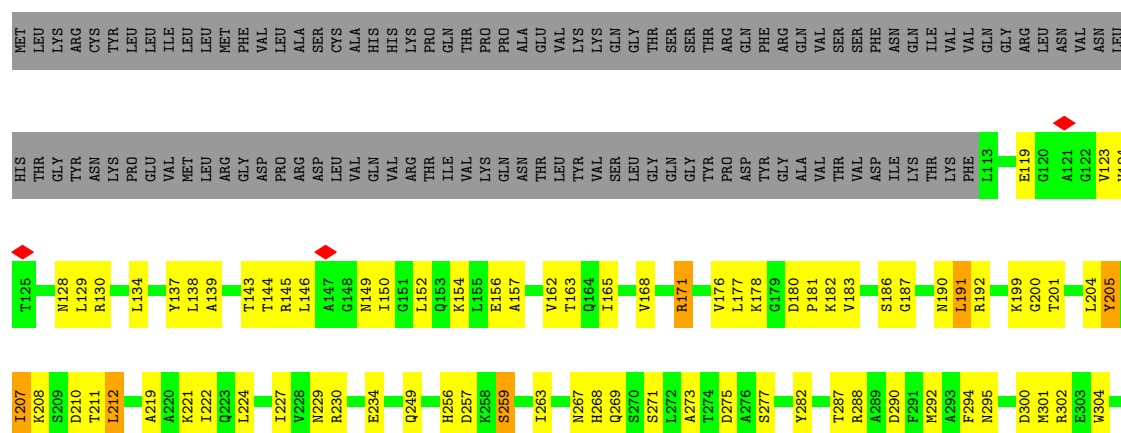


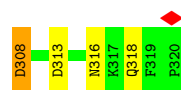


• Molecule 7: DUF2807 domain-containing protein

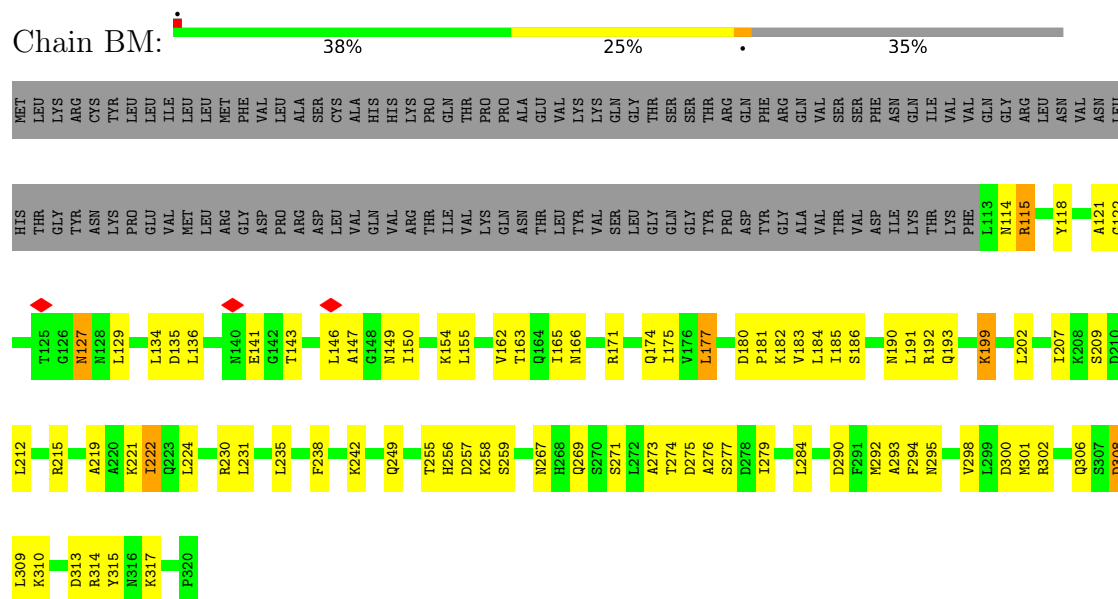


• Molecule 7: DUF2807 domain-containing protein

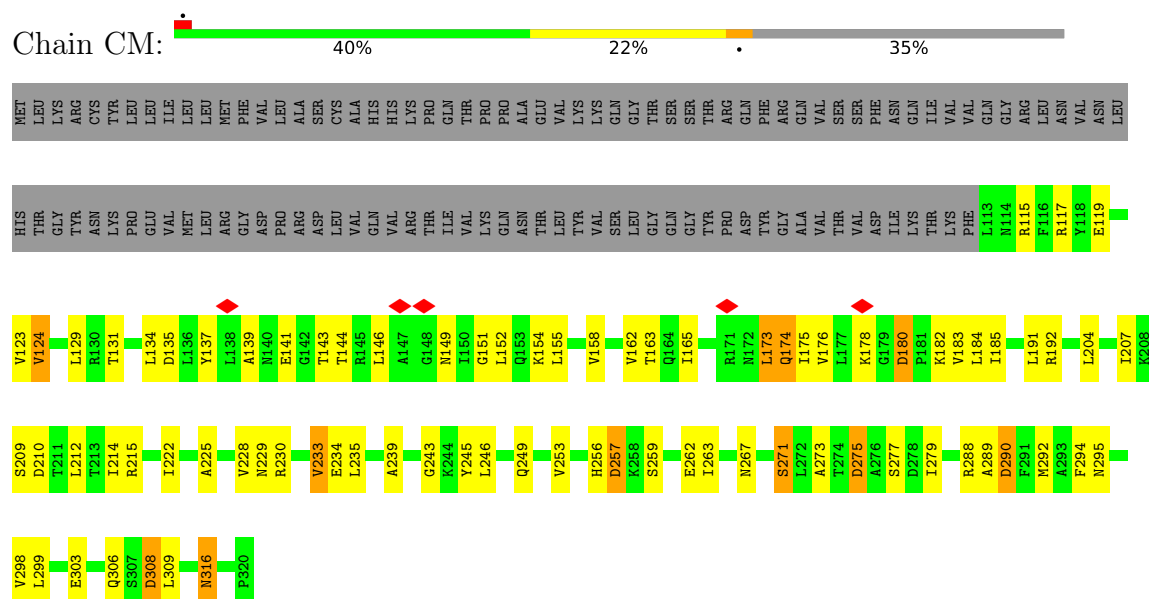




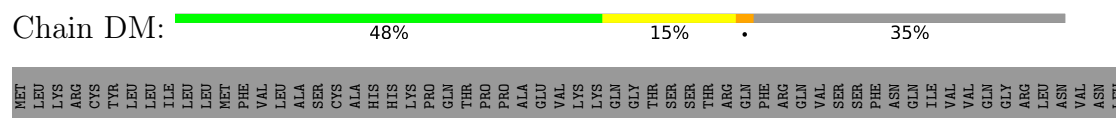
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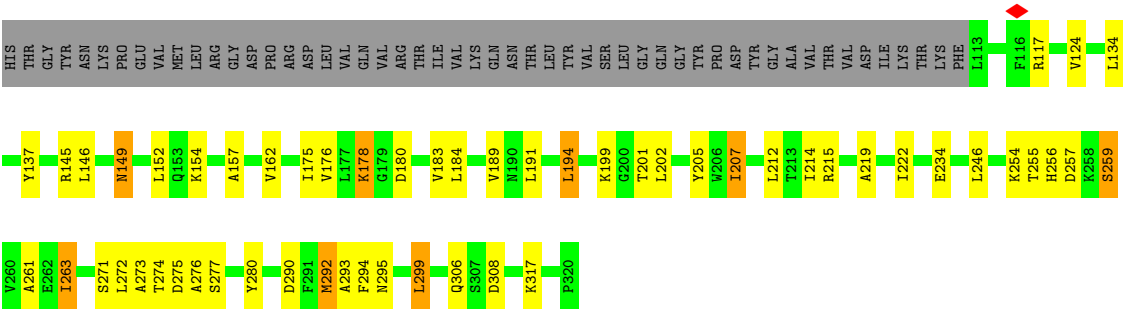


• Molecule 7: DUF2807 domain-containing protein

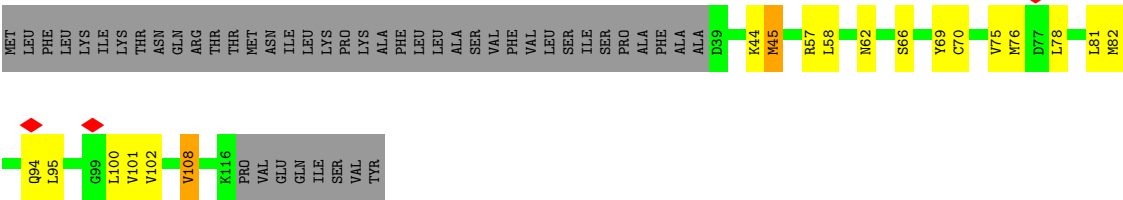


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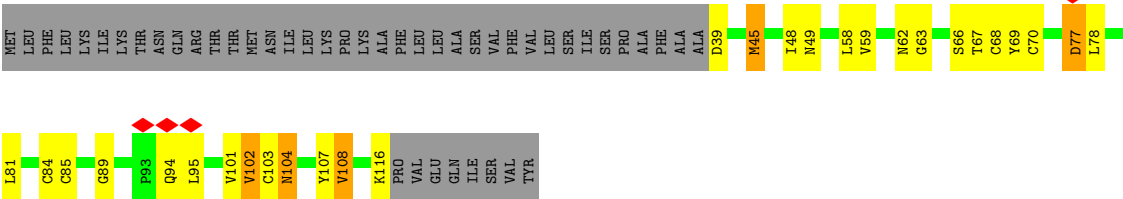




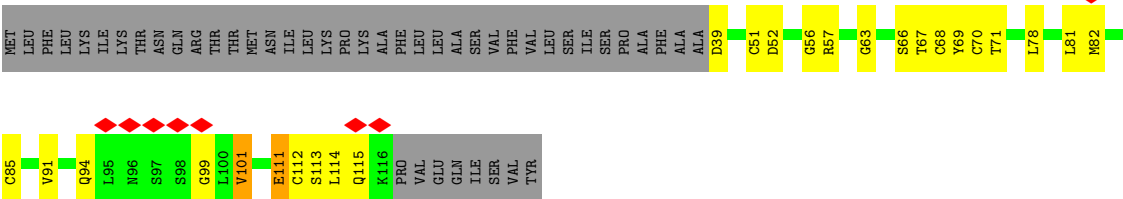
• Molecule 8: Neurogenic locus notch



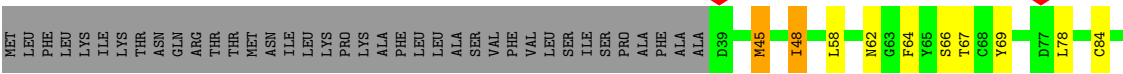
• Molecule 8: Neurogenic locus notch



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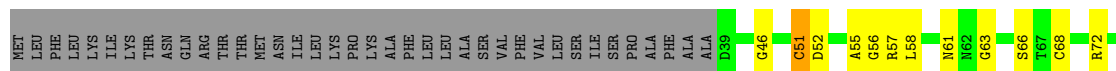


• Molecule 8: Neurogenic locus notch

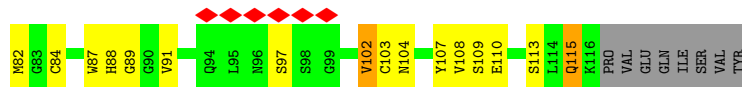
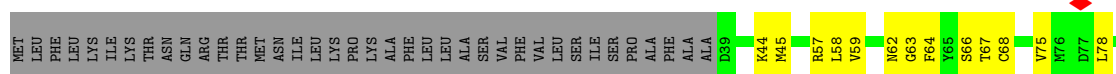
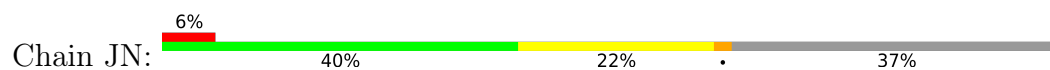




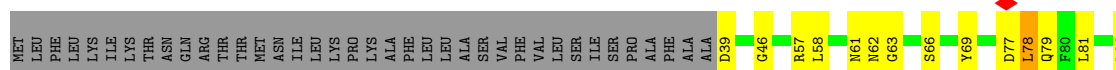
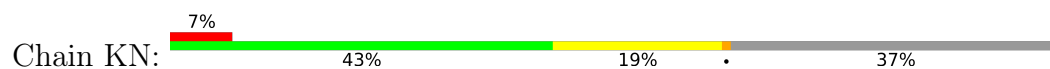
- Molecule 8: Neurogenic locus notch



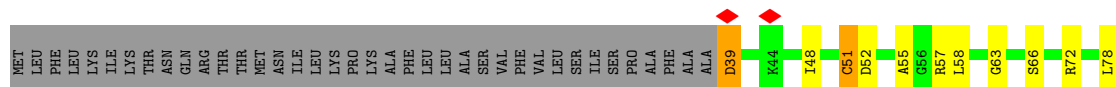
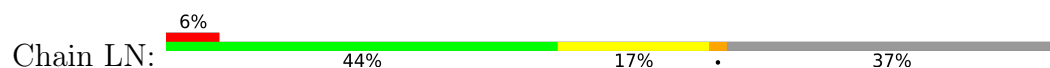
- Molecule 8: Neurogenic locus notch



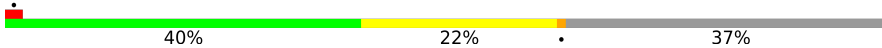
- Molecule 8: Neurogenic locus notch

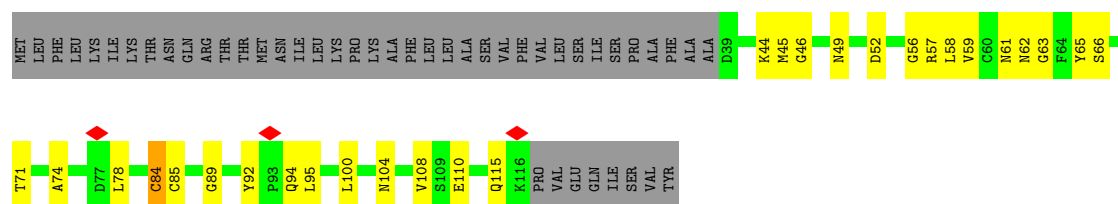


- Molecule 8: Neurogenic locus notch

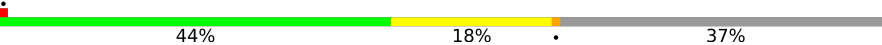


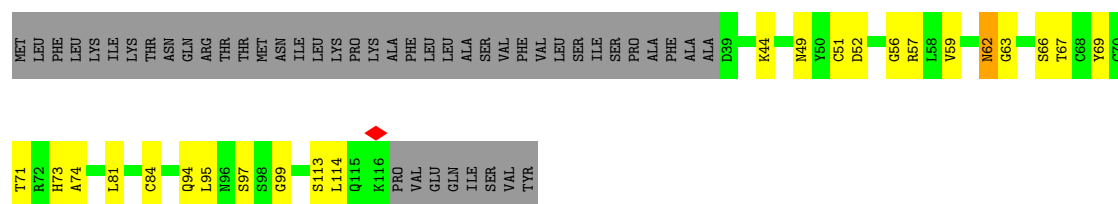
- Molecule 8: Neurogenic locus notch

Chain MN: 

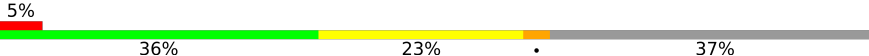


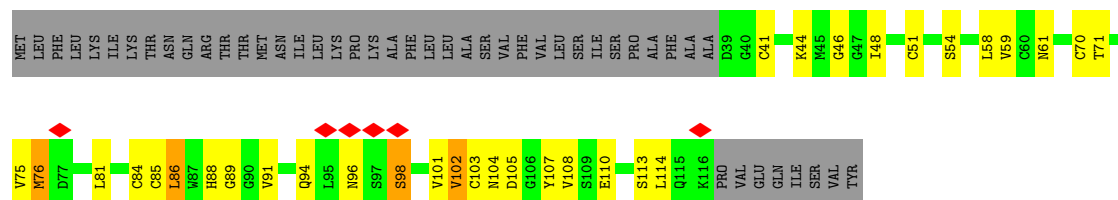
- Molecule 8: Neurogenic locus notch

Chain AN: 



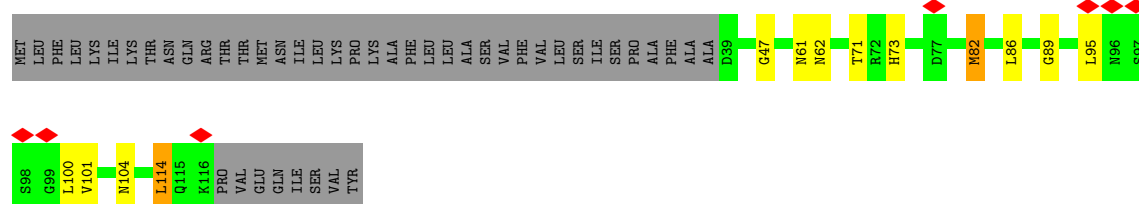
- Molecule 8: Neurogenic locus notch

Chain BN: 

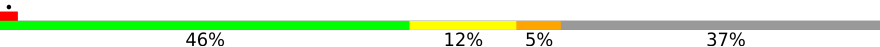


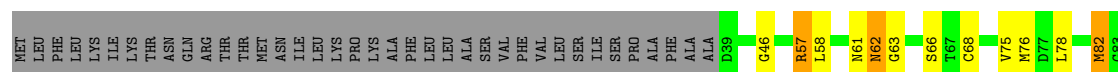
- Molecule 8: Neurogenic locus notch

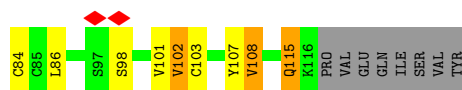
Chain CN: 



- Molecule 8: Neurogenic locus notch

Chain DN: 





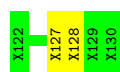
- Molecule 9: Unknown protein fragment

Chain EU: 89% 11%



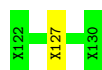
- Molecule 9: Unknown protein fragment

Chain FU: 78% 22%



- Molecule 9: Unknown protein fragment

Chain GU: 89% 11%



- Molecule 9: Unknown protein fragment

Chain HU: 100%

There are no outlier residues recorded for this chain.

- Molecule 9: Unknown protein fragment

Chain IU: 89% 11%



- Molecule 9: Unknown protein fragment

Chain JU: 78% 22%

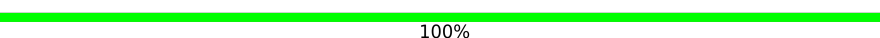


- Molecule 9: Unknown protein fragment

Chain KU: 100%

There are no outlier residues recorded for this chain.

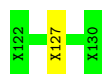
- Molecule 9: Unknown protein fragment

Chain LU:  100%

There are no outlier residues recorded for this chain.

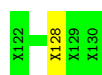
- Molecule 9: Unknown protein fragment

Chain MU:  89% 11%



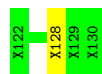
- Molecule 9: Unknown protein fragment

Chain AU:  89% 11%

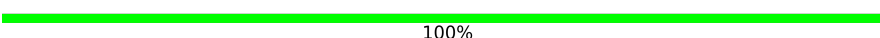


- Molecule 9: Unknown protein fragment

Chain BU:  89% 11%



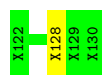
- Molecule 9: Unknown protein fragment

Chain CU:  100%

There are no outlier residues recorded for this chain.

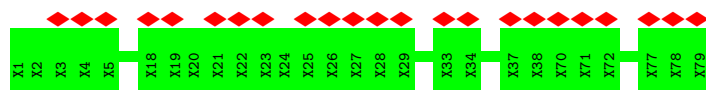
- Molecule 9: Unknown protein fragment

Chain DU:  89% 11%

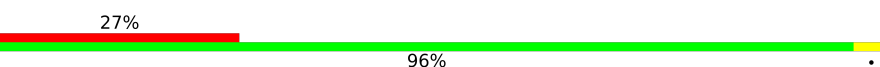


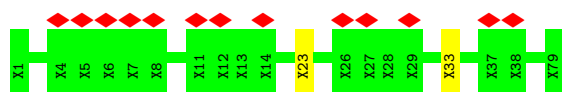
- Molecule 10: Unknown protein fragment

Chain EX:  48% 100%

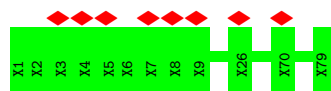


- Molecule 10: Unknown protein fragment

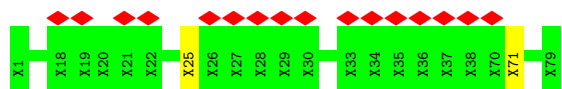
Chain FX:  27% 96%



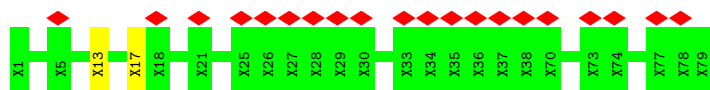
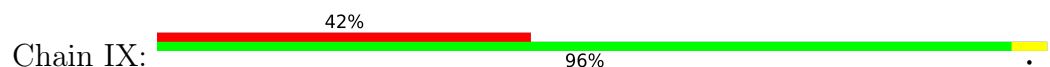
- Molecule 10: Unknown protein fragment



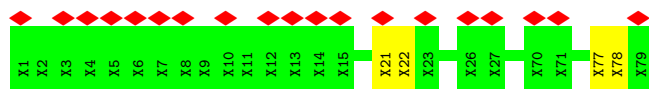
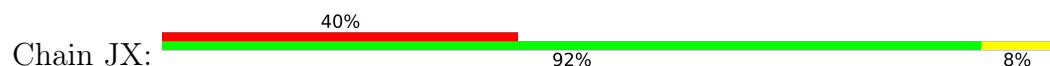
- Molecule 10: Unknown protein fragment



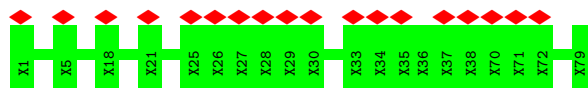
- Molecule 10: Unknown protein fragment



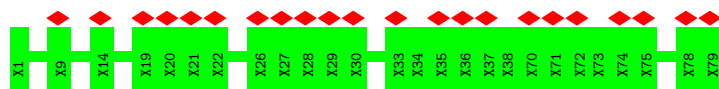
- Molecule 10: Unknown protein fragment



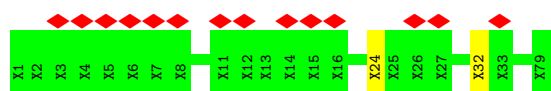
- Molecule 10: Unknown protein fragment



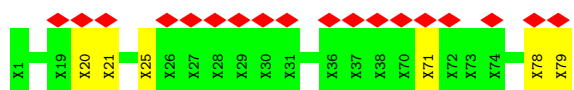
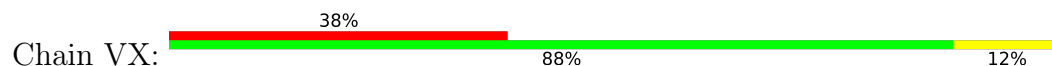
- Molecule 10: Unknown protein fragment



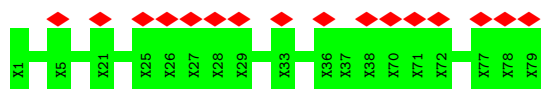
- Molecule 10: Unknown protein fragment



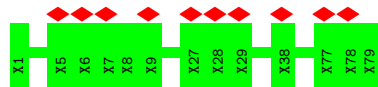
- Molecule 10: Unknown protein fragment



- Molecule 10: Unknown protein fragment



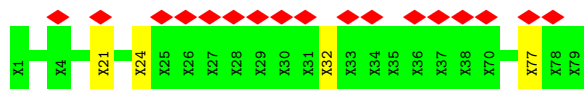
- Molecule 10: Unknown protein fragment



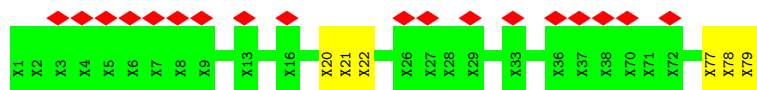
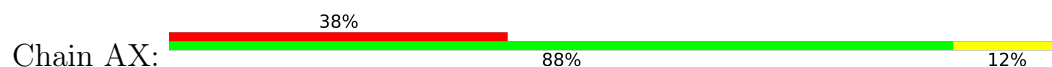
- Molecule 10: Unknown protein fragment



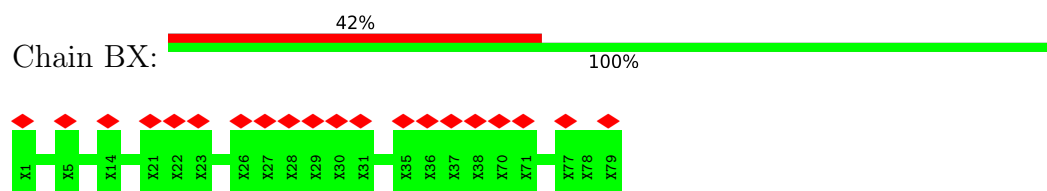
- Molecule 10: Unknown protein fragment



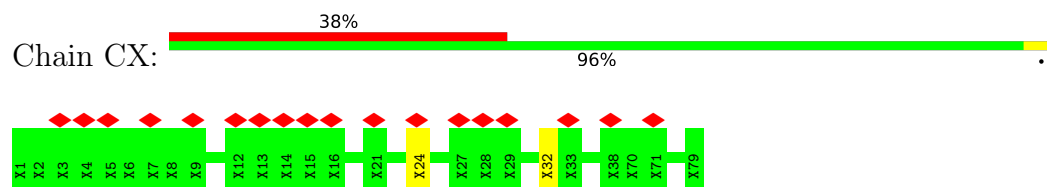
- Molecule 10: Unknown protein fragment



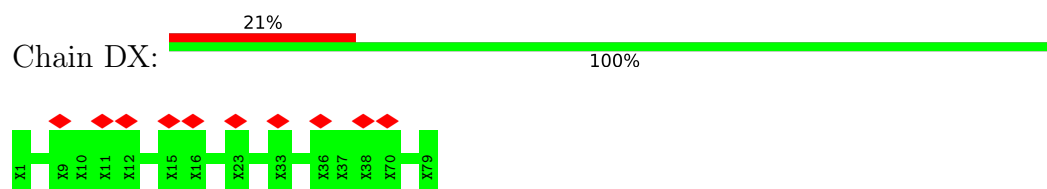
- Molecule 10: Unknown protein fragment



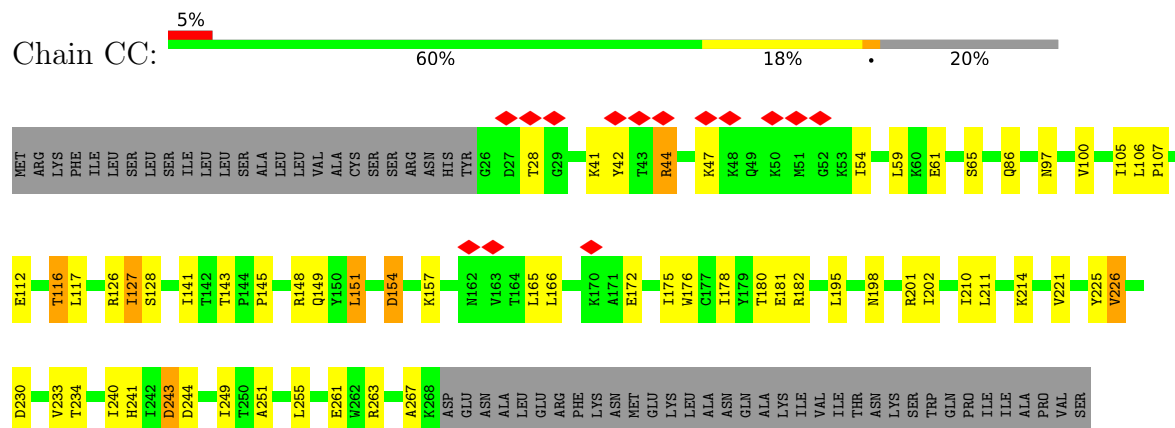
- Molecule 10: Unknown protein fragment



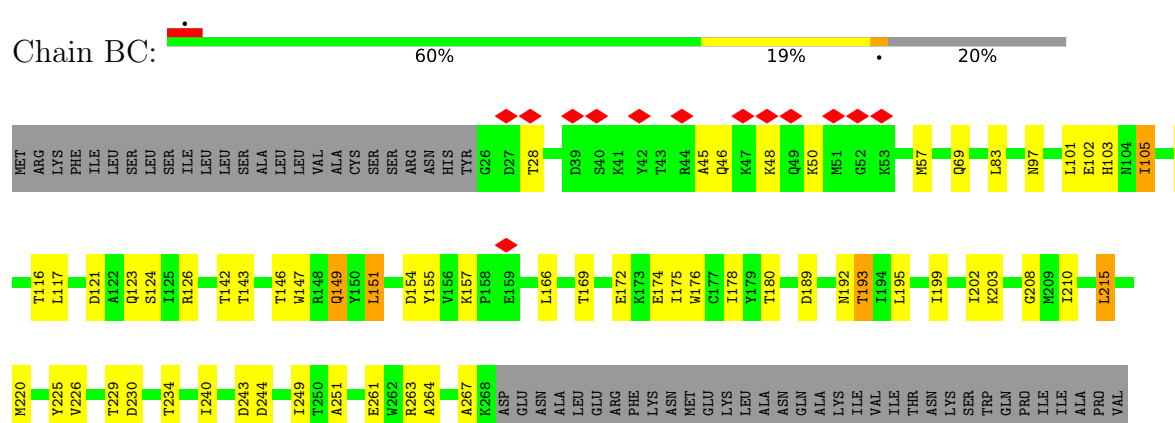
- Molecule 10: Unknown protein fragment



- Molecule 11: DotC

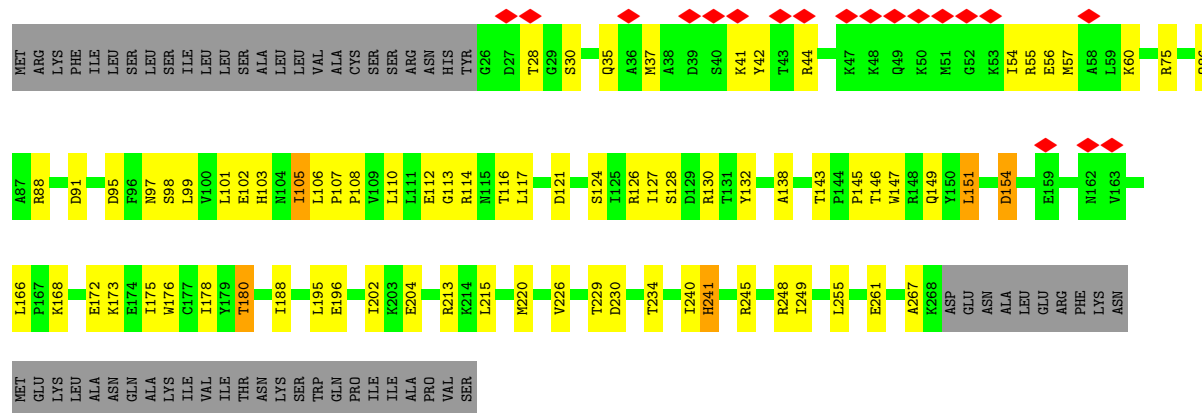


- Molecule 11: DotC

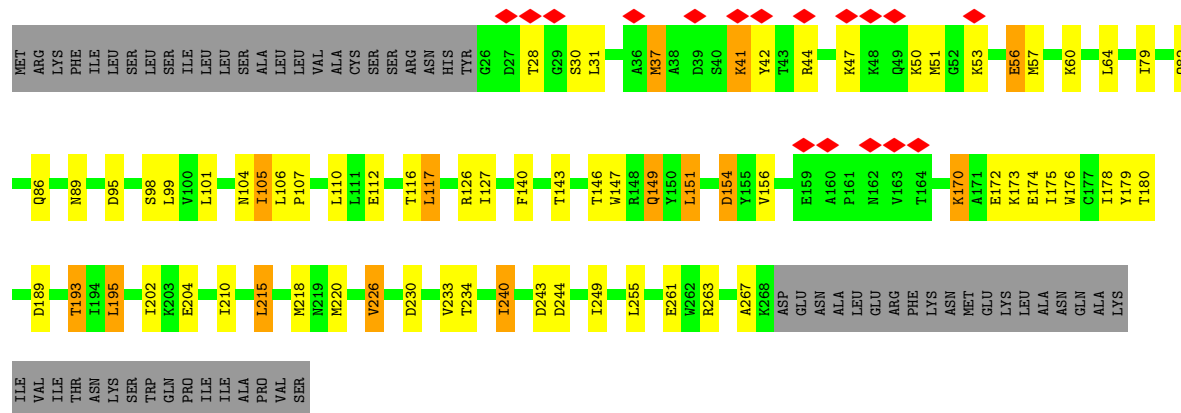


SER

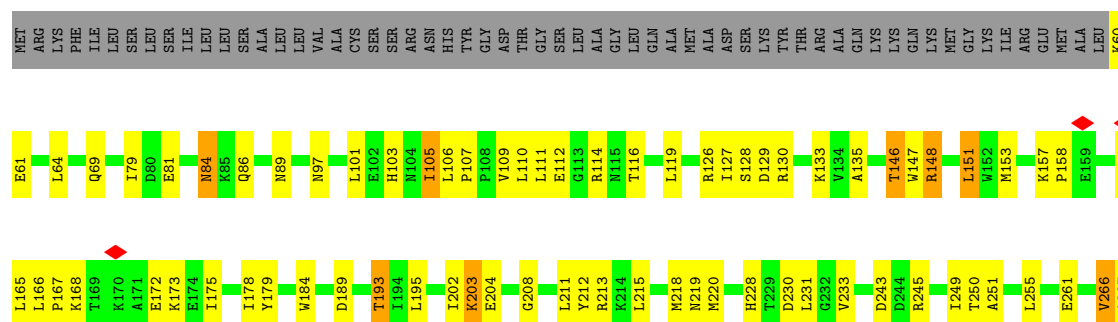
• Molecule 11: DotC



• Molecule 11: DotC



• Molecule 11: DotC



K268
ASP
GLU
ASN
ALA
LEU
GLU
ARG
PHE
LYS
ASN
MET
GLU
LYS
LEU
ALA
ASN
GLN
ALA
LYS
ILE
VAL
ILE
THR
ASN
LYS
SER
TRP
GLN
PRO
ILE
ILE
ALA
VAL
SER

• Molecule 11: DotC



MET	ARG	LYS	PHE	VAL	ILE	LEU	SER	LEU	SER	LEU	ILE	LEU	LEU	SER	ALA	LEU	VAL	ALA	CYS	SER	SER	ARG	ASN	HIS	TYR	GLY	ASP	THR	GLY	ILE	ALA	PRO	VAL	SER
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Q70	W75	I80	K86	R89	D92	L100	E103	H104	N105	I106	L107	P108	T117	L118	D122	S125	I126	R127	I128	T147	W148	R149	L152	D155	K158	P159	E160	A161	V164	L167	P168	K169	E173	K174	E175	W176	C178	I179	W185
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D190	N199	R202	T203	K204	E205	R214	K215	L216	M221	V222	Y226	V227	S228	H229	T230	D231	I241	R246	V247	L248	A252	L256	N257	V258	N259	E262	A266	V267	A268	K269	ASP	GLU	ASN	ALA	LEU	GLU	ARG	PHE	LYS	ASN	MET	GLY	LEU	ALA	ASN	GLN
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

ALA	LYS	ILE	VAL	THR	ASN	LYS	TRP	PRO	ILE	ALA	PRO	VAL	SER
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• Molecule 11: DotC



MET	ARG	LYS	PHE	ILE	LEU	SER	LEU	ILE	LEU	LEU	SER	ALA	LEU	VAL	ALA	CYS	SER	SER	ARG	ASN	HIS	T26	D27	T28	G29	S30	L31	L34	Q35	A36	K37	A38	D39	S40	R44	K47	K48	Q49	K50	M51	G52	K53	F54	R55	E56	I93	N97	L101	E102	H103
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N104	I105	L106	P107	V109	L110	L111	E112	G113	R114	N115	T116	L119	I125	R126	R130	T142	T143	T146	W147	Y150	L151	W152	M153	E159	V163	T169	E172	K173	E174	I175	W176	T180	W184	D189	T193	I194	L195	N198	I199	I202	G208
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

Y212	R213	N221	Y225	V226	D230	L231	G232	V233	T234	E239	I240	H241	I242	D243	D244	R245	L255	R263	A267	K268	ASP	GLU	ASN	ALA	LEU	GLU	ARG	PHE	LYS	ASN	MET	GLU	LYS	LEU	ALA	ASN	GLN	ALA	LYS	ILE	VAL	ILE	THR	ASN	LYS	SER	TRP	GLN	PRO	ILE
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ILE	ALA	PRO	VAL	SER
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• Molecule 11: DotC

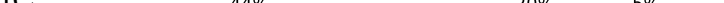


MET	ARG	LYS	PHE	LEU	SER	LEU	ILE	LEU	LEU	SER	ALA	LEU	VAL	ALA	CYS	SER	SER	ARG	ASN	HIS	TYR	GLY	ASP	THR	GLY	LEU	ALA	GLY	LEU	GLN	ALA	MET	ALA	ASP	SER	LYS	TYR	THR	ARG	ALA	GLN	LYS	LYS	MET	GLY	LYS	ILE	ALA	ARG	GLU	MET	ALA	LEU	PRO	K60
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

L64	Q86	A87	R88	N89	L90	N97	S98	L99	I105	V109	L110	L111	M115	T116	L117	N118	L119	Q123	R126	I127	K133	H139	F140	T143	W147	L151	D154	K157	P158	E159	A160	P161	N162	V163	L166	P167	K168	T169	K170	A171	E172
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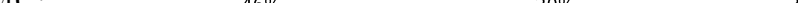
K173	E174	I175	I178	R182	K185	L195	E196	I202	G208	Y212	R213	K214	L215	M220	Y225	V226	V233	H241	T242	D243	R245	I249	T250	A251	L255	N256	E261	Y262	R263	A264	A265	V266	A267	K268	ASP	GLU	ASN	ALA	LEU	GLU	ARG	PHE	T169	LYS	ASN
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	------	-----	-----

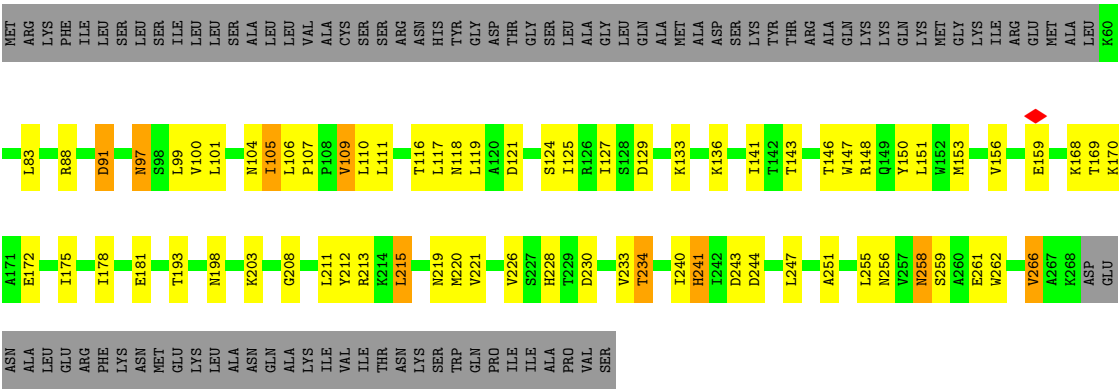
MET	GLU	LYS	LEU	ALA	ASN	GLN	ALA	LYS	THR	ASN	LYS	SER	TRP	GLN	PRO	ILE	ILE	ALA	PRO	VAL	SER
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Chain IC: 

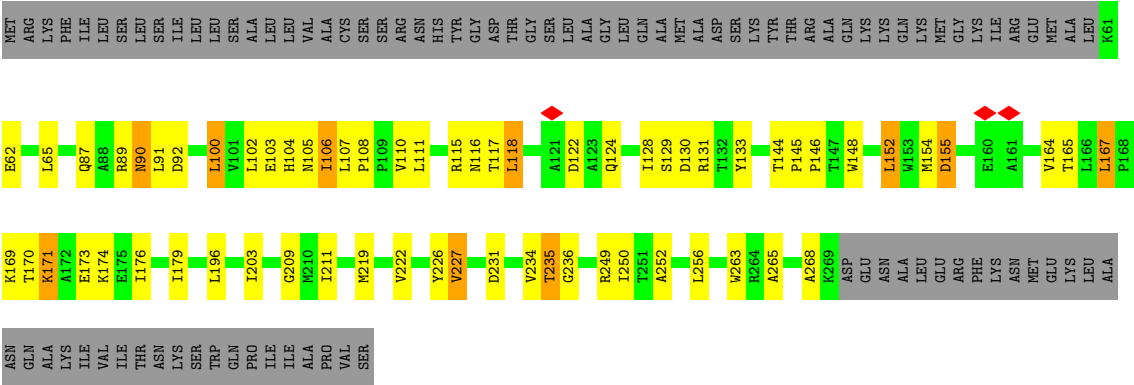
Chain JC:

Chain LC:

Chain MC:  46% 20% . 31%



• Molecule 11: DotC



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	41057	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	7.797	Depositor
Minimum map value	-2.782	Depositor
Average map value	0.094	Depositor
Map value standard deviation	0.545	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	0.22	0/1250	0.53	0/1699
1	Ag	0.16	0/278	0.36	0/377
1	BG	0.23	0/1250	0.57	1/1699 (0.1%)
1	Bg	0.16	0/278	0.35	0/377
1	CG	0.22	0/1250	0.54	0/1699
1	Cg	0.16	0/278	0.40	0/377
1	DG	0.21	0/1250	0.55	1/1699 (0.1%)
1	Dg	0.17	0/278	0.34	0/377
1	EG	0.21	0/1250	0.53	0/1699
1	Eg	0.17	0/278	0.36	0/377
1	FG	0.22	0/1250	0.54	0/1699
1	Fg	0.17	0/278	0.38	0/377
1	GG	0.22	0/1250	0.57	1/1699 (0.1%)
1	Gg	0.17	0/278	0.32	0/377
1	HG	0.22	0/1250	0.54	0/1699
1	Hg	0.16	0/278	0.33	0/377
1	IG	0.22	0/1250	0.53	0/1699
1	Ig	0.16	0/278	0.39	0/377
1	JG	0.22	0/1250	0.57	1/1699 (0.1%)
1	Jg	0.17	0/278	0.36	0/377
1	KG	0.22	0/1250	0.54	0/1699
1	Kg	0.16	0/278	0.35	0/377
1	LG	0.22	0/1250	0.55	0/1699
1	Lg	0.16	0/278	0.36	0/377
1	MG	0.21	0/1250	0.53	0/1699
1	Mg	0.17	0/278	0.36	0/377
1	NG	0.22	0/1250	0.53	0/1699
1	OG	0.21	0/1250	0.54	0/1699
1	PG	0.22	0/1250	0.53	0/1699
1	VG	0.20	0/278	0.53	0/377
1	WG	0.17	0/278	0.47	0/377
1	XG	0.18	0/278	0.45	0/377
1	YG	0.19	0/278	0.44	0/377
1	ZG	0.20	0/278	0.47	0/377

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	AD	0.21	0/1107	0.47	0/1502
2	Ad	0.19	0/1078	0.38	0/1463
2	BD	0.22	0/1107	0.49	0/1502
2	Bd	0.18	0/1078	0.36	0/1463
2	CD	0.20	0/1107	0.46	0/1502
2	Cd	0.19	0/1078	0.42	0/1463
2	DD	0.21	0/1107	0.46	0/1502
2	Dd	0.20	0/1078	0.38	0/1463
2	ED	0.23	0/1107	0.53	0/1502
2	Ed	0.20	0/1078	0.41	0/1463
2	FD	0.22	0/1107	0.48	0/1502
2	Fd	0.18	0/1078	0.40	0/1463
2	GD	0.21	0/1107	0.48	0/1502
2	Gd	0.19	0/1078	0.43	0/1463
2	HD	0.20	0/1107	0.47	0/1502
2	Hd	0.19	0/1078	0.40	0/1463
2	ID	0.22	0/1107	0.50	0/1502
2	Id	0.18	0/1078	0.41	0/1463
2	JD	0.21	0/1107	0.48	0/1502
2	Jd	0.18	0/1078	0.38	0/1463
2	KD	0.21	0/1107	0.47	0/1502
2	Kd	0.19	0/1078	0.40	0/1463
2	LD	0.21	0/1107	0.48	0/1502
2	Ld	0.19	0/1078	0.42	0/1463
2	MD	0.21	0/1107	0.52	0/1502
2	Md	0.19	0/1078	0.39	0/1463
3	AF	0.17	0/490	0.36	0/660
3	Af	0.16	0/456	0.39	0/615
3	BF	0.16	0/490	0.34	0/660
3	Bf	0.16	0/456	0.41	0/615
3	CF	0.14	0/490	0.33	0/660
3	Cf	0.16	0/456	0.36	0/615
3	DF	0.15	0/490	0.35	0/660
3	Df	0.16	0/456	0.36	0/615
3	EF	0.15	0/490	0.35	0/660
3	Ef	0.15	0/456	0.31	0/615
3	FF	0.16	0/490	0.34	0/660
3	Ff	0.16	0/456	0.31	0/615
3	GF	0.15	0/490	0.35	0/660
3	Gf	0.15	0/456	0.37	0/615
3	HF	0.15	0/490	0.35	0/660
3	Hf	0.16	0/456	0.34	0/615
3	IF	0.14	0/490	0.34	0/660

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	If	0.15	0/456	0.35	0/615
3	JF	0.13	0/490	0.32	0/660
3	Jf	0.15	0/456	0.33	0/615
3	KF	0.16	0/490	0.40	0/660
3	Kf	0.15	0/456	0.33	0/615
3	LF	0.15	0/490	0.34	0/660
3	Lf	0.16	0/456	0.33	0/615
3	MF	0.16	0/490	0.32	0/660
3	Mf	0.16	0/456	0.31	0/615
3	VF	0.18	0/490	0.41	0/660
3	WF	0.18	0/490	0.40	0/660
3	XF	0.15	0/490	0.34	0/660
3	YF	0.14	0/490	0.35	0/660
3	ZF	0.16	0/490	0.32	0/660
4	AH	0.18	0/2033	0.40	0/2775
4	BH	0.19	0/2033	0.39	0/2775
4	CH	0.19	0/2033	0.38	0/2775
4	DH	0.18	0/2033	0.38	0/2775
4	EH	0.18	0/2033	0.39	0/2775
4	FH	0.18	0/2033	0.38	0/2775
4	GH	0.19	0/2033	0.41	0/2775
4	HH	0.19	0/2033	0.40	0/2775
4	IH	0.19	0/2033	0.41	0/2775
4	JH	0.18	0/2033	0.38	0/2775
4	KH	0.19	0/2033	0.39	0/2775
4	LH	0.20	0/2033	0.42	0/2775
4	MH	0.19	0/2033	0.40	0/2775
4	VH	0.16	0/1921	0.37	0/2620
4	WH	0.16	0/1921	0.41	0/2620
4	XH	0.17	0/1921	0.39	0/2620
4	YH	0.16	0/1921	0.38	0/2620
4	ZH	0.16	0/1921	0.39	0/2620
5	AK	0.20	0/1195	0.41	0/1616
5	BK	0.22	0/1195	0.43	0/1616
5	CK	0.20	0/1195	0.39	0/1616
5	DK	0.21	0/1195	0.42	0/1616
5	EK	0.20	0/1195	0.40	0/1616
5	FK	0.20	0/1195	0.40	0/1616
5	GK	0.21	0/1195	0.39	0/1616
5	HK	0.23	0/1195	0.41	0/1616
5	IK	0.20	0/1195	0.39	0/1616
5	JK	0.20	0/1195	0.38	0/1616
5	KK	0.21	0/1195	0.41	0/1616

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	LK	0.21	0/1195	0.42	0/1616
5	MK	0.20	0/1195	0.40	0/1616
6	AL	0.19	0/1417	0.43	0/1912
6	BL	0.21	0/1417	0.45	0/1912
6	CL	0.20	0/1417	0.43	0/1912
6	DL	0.21	0/1417	0.43	0/1912
6	EL	0.21	0/1417	0.43	0/1912
6	FL	0.20	0/1417	0.46	0/1912
6	GL	0.20	0/1417	0.45	0/1912
6	HL	0.21	0/1417	0.44	0/1912
6	IL	0.19	0/1417	0.45	0/1912
6	JL	0.20	0/1417	0.43	0/1912
6	KL	0.20	0/1417	0.47	0/1912
6	LL	0.21	0/1417	0.42	0/1912
6	ML	0.21	0/1417	0.45	0/1912
7	AM	0.18	0/1678	0.42	0/2262
7	BM	0.19	0/1678	0.42	0/2262
7	CM	0.18	0/1678	0.42	0/2262
7	DM	0.18	0/1678	0.43	0/2262
7	EM	0.18	0/1678	0.40	0/2262
7	FM	0.18	0/1678	0.43	0/2262
7	GM	0.18	0/1678	0.41	0/2262
7	HM	0.19	0/1678	0.45	0/2262
7	IM	0.19	0/1678	0.43	0/2262
7	JM	0.19	0/1678	0.39	0/2262
7	KM	0.18	0/1678	0.43	0/2262
7	LM	0.18	0/1678	0.43	0/2262
7	MM	0.18	0/1678	0.41	0/2262
8	AN	0.20	0/593	0.44	0/799
8	BN	0.20	0/593	0.46	0/799
8	CN	0.19	0/593	0.37	0/799
8	DN	0.19	0/593	0.40	0/799
8	EN	0.20	0/593	0.40	0/799
8	FN	0.20	0/593	0.38	0/799
8	GN	0.19	0/593	0.41	0/799
8	HN	0.18	0/593	0.40	0/799
8	IN	0.18	0/593	0.38	0/799
8	JN	0.19	0/593	0.39	0/799
8	KN	0.19	0/593	0.36	0/799
8	LN	0.21	0/593	0.37	0/799
8	MN	0.20	0/593	0.39	0/799
11	AC	0.21	0/1702	0.41	0/2315
11	BC	0.20	0/1957	0.41	0/2651

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
11	CC	0.20	0/1957	0.39	0/2651
11	DC	0.21	0/1702	0.43	0/2315
11	EC	0.22	0/1702	0.40	0/2315
11	FC	0.21	0/1957	0.39	0/2651
11	GC	0.20	0/1957	0.39	0/2651
11	HC	0.21	0/1702	0.39	0/2315
11	IC	0.21	0/1702	0.42	0/2315
11	JC	0.22	0/1702	0.40	0/2315
11	KC	0.20	0/1957	0.41	0/2651
11	LC	0.21	0/1702	0.45	0/2315
11	MC	0.21	0/1702	0.42	0/2315
All	All	0.20	0/191071	0.43	4/258997 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	JG	939	THR	N-CA-C	-6.04	106.24	113.97
1	BG	939	THR	N-CA-C	-5.96	106.99	114.56
1	DG	939	THR	N-CA-C	-5.72	107.30	114.56
1	GG	939	THR	N-CA-C	-5.56	107.15	114.04

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	34	0
1	Ag	276	0	263	9	0
1	BG	1229	0	1231	34	0
1	Bg	276	0	263	12	0
1	CG	1229	0	1231	34	0
1	Cg	276	0	263	11	0
1	DG	1229	0	1231	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Dg	276	0	263	8	0
1	EG	1229	0	1231	33	0
1	Eg	276	0	263	9	0
1	FG	1229	0	1231	38	0
1	Fg	276	0	263	9	0
1	GG	1229	0	1231	35	0
1	Gg	276	0	263	10	0
1	HG	1229	0	1231	35	0
1	Hg	276	0	263	7	0
1	IG	1229	0	1231	26	0
1	Ig	276	0	263	10	0
1	JG	1229	0	1231	33	0
1	Jg	276	0	263	9	0
1	KG	1229	0	1231	30	0
1	Kg	276	0	263	8	0
1	LG	1229	0	1231	23	0
1	Lg	276	0	263	6	0
1	MG	1229	0	1231	31	0
1	Mg	276	0	263	8	0
1	NG	1229	0	1231	28	0
1	OG	1229	0	1231	33	0
1	PG	1229	0	1231	26	0
1	VG	276	0	263	6	0
1	WG	276	0	263	7	0
1	XG	276	0	263	6	0
1	YG	276	0	263	10	0
1	ZG	276	0	263	7	0
2	AD	1086	0	1121	28	0
2	Ad	1058	0	1092	27	0
2	BD	1086	0	1121	26	0
2	Bd	1058	0	1092	17	0
2	CD	1086	0	1121	28	0
2	Cd	1058	0	1092	19	0
2	DD	1086	0	1121	25	0
2	Dd	1058	0	1092	21	0
2	ED	1086	0	1121	24	0
2	Ed	1058	0	1092	20	0
2	FD	1086	0	1121	25	0
2	Fd	1058	0	1092	23	0
2	GD	1086	0	1121	32	0
2	Gd	1058	0	1092	21	0
2	HD	1086	0	1121	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	Hd	1058	0	1092	17	0
2	ID	1086	0	1121	30	0
2	Id	1058	0	1092	17	0
2	JD	1086	0	1121	33	0
2	Jd	1058	0	1092	18	0
2	KD	1086	0	1121	28	0
2	Kd	1058	0	1092	25	0
2	LD	1086	0	1121	30	0
2	Ld	1058	0	1092	31	0
2	MD	1086	0	1121	22	0
2	Md	1058	0	1092	22	0
3	AF	483	0	502	9	0
3	Af	449	0	474	13	0
3	BF	483	0	502	8	0
3	Bf	449	0	474	8	0
3	CF	483	0	502	8	0
3	Cf	449	0	474	12	0
3	DF	483	0	502	10	0
3	Df	449	0	474	10	0
3	EF	483	0	502	8	0
3	Ef	449	0	474	5	0
3	FF	483	0	502	18	0
3	Ff	449	0	474	15	0
3	GF	483	0	502	9	0
3	Gf	449	0	474	12	0
3	HF	483	0	502	9	0
3	Hf	449	0	474	8	0
3	IF	483	0	502	12	0
3	If	449	0	474	11	0
3	JF	483	0	502	10	0
3	Jf	449	0	474	9	0
3	KF	483	0	502	10	0
3	Kf	449	0	474	10	0
3	LF	483	0	502	15	0
3	Lf	449	0	474	13	0
3	MF	483	0	502	21	0
3	Mf	449	0	474	15	0
3	VF	483	0	502	15	0
3	WF	483	0	502	14	0
3	XF	483	0	502	13	0
3	YF	483	0	502	15	0
3	ZF	483	0	502	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	AH	1983	0	2009	51	0
4	BH	1983	0	2009	41	0
4	CH	1983	0	2009	51	0
4	DH	1983	0	2009	41	0
4	EH	1983	0	2009	55	0
4	FH	1983	0	2009	34	0
4	GH	1983	0	2009	50	0
4	HH	1983	0	2009	45	0
4	IH	1983	0	2009	31	0
4	JH	1983	0	2009	40	0
4	KH	1983	0	2009	40	0
4	LH	1983	0	2009	55	0
4	MH	1983	0	2009	42	0
4	VH	1875	0	1900	50	0
4	WH	1875	0	1900	36	0
4	XH	1875	0	1900	35	0
4	YH	1875	0	1900	37	0
4	ZH	1875	0	1900	43	0
5	AK	1175	0	1221	28	0
5	BK	1175	0	1221	31	0
5	CK	1175	0	1221	32	0
5	DK	1175	0	1221	31	0
5	EK	1175	0	1221	28	0
5	FK	1175	0	1221	32	0
5	GK	1175	0	1221	25	0
5	HK	1175	0	1221	25	0
5	IK	1175	0	1221	27	0
5	JK	1175	0	1221	31	0
5	KK	1175	0	1221	23	0
5	LK	1175	0	1221	29	0
5	MK	1175	0	1221	24	0
6	AL	1388	0	1378	28	0
6	BL	1388	0	1378	34	0
6	CL	1388	0	1378	33	0
6	DL	1388	0	1378	28	0
6	EL	1388	0	1378	29	0
6	FL	1388	0	1378	30	0
6	GL	1388	0	1378	38	0
6	HL	1388	0	1378	32	0
6	IL	1388	0	1378	39	0
6	JL	1388	0	1378	31	0
6	KL	1388	0	1378	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	LL	1388	0	1378	34	0
6	ML	1388	0	1378	30	0
7	AM	1650	0	1658	43	0
7	BM	1650	0	1658	44	0
7	CM	1650	0	1658	48	0
7	DM	1650	0	1658	28	0
7	EM	1650	0	1658	33	0
7	FM	1650	0	1658	41	0
7	GM	1650	0	1658	51	0
7	HM	1650	0	1658	43	0
7	IM	1650	0	1658	51	0
7	JM	1650	0	1658	35	0
7	KM	1650	0	1658	42	0
7	LM	1650	0	1658	33	0
7	MM	1650	0	1658	46	0
8	AN	582	0	530	12	0
8	BN	582	0	530	19	0
8	CN	582	0	530	6	0
8	DN	582	0	530	11	0
8	EN	582	0	530	7	0
8	FN	582	0	530	16	0
8	GN	582	0	530	13	0
8	HN	582	0	530	6	0
8	IN	582	0	530	8	0
8	JN	582	0	530	19	0
8	KN	582	0	530	12	0
8	LN	582	0	530	13	0
8	MN	582	0	530	15	0
9	AU	45	0	12	1	0
9	BU	45	0	12	1	0
9	CU	45	0	13	0	0
9	DU	45	0	12	1	0
9	EU	45	0	12	1	0
9	FU	45	0	12	2	0
9	GU	45	0	12	1	0
9	HU	45	0	12	0	0
9	IU	45	0	12	1	0
9	JU	45	0	13	2	0
9	KU	45	0	12	0	0
9	LU	45	0	13	0	0
9	MU	45	0	12	1	0
10	AX	240	0	55	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	BX	240	0	56	0	0
10	CX	240	0	54	1	0
10	DX	240	0	56	0	0
10	EX	240	0	56	0	0
10	FX	240	0	57	1	0
10	GX	240	0	53	0	0
10	HX	240	0	56	1	0
10	IX	240	0	56	1	0
10	JX	240	0	56	2	0
10	KX	240	0	56	0	0
10	LX	240	0	53	0	0
10	MX	240	0	55	1	0
10	VX	240	0	58	3	0
10	WX	240	0	58	0	0
10	XX	240	0	55	0	0
10	YX	240	0	55	1	0
10	ZX	240	0	57	2	0
11	AC	1667	0	1682	41	0
11	BC	1921	0	1952	33	0
11	CC	1921	0	1952	33	0
11	DC	1667	0	1682	43	0
11	EC	1667	0	1682	38	0
11	FC	1921	0	1952	45	0
11	GC	1921	0	1952	50	0
11	HC	1667	0	1682	39	0
11	IC	1667	0	1682	43	0
11	JC	1667	0	1682	28	0
11	KC	1921	0	1952	39	0
11	LC	1667	0	1682	32	0
11	MC	1667	0	1682	41	0
All	All	192370	0	190622	3839	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 10.

All (3839) 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)
6:DL:129:THR:O	6:DL:133:PHE:HB2	1.71	0.91
6:KL:129:THR:O	6:KL:133:PHE:HB2	1.73	0.89
6:BL:166:ALA:HA	6:BL:206:GLU:O	1.75	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:KL:166:ALA:HA	6:KL:206:GLU:O	1.76	0.85
6:JL:166:ALA:HA	6:JL:206:GLU:O	1.77	0.85
6:FL:166:ALA:HA	6:FL:206:GLU:O	1.82	0.79
5:HK:117:THR:HA	5:HK:157:GLN:O	1.84	0.78
6:CL:166:ALA:HA	6:CL:206:GLU:O	1.85	0.77
6:GL:166:ALA:HA	6:GL:206:GLU:O	1.84	0.76
6:AL:166:ALA:HA	6:AL:206:GLU:O	1.89	0.73
4:AH:176:VAL:H	4:ZH:225:ASN:HD21	1.39	0.71
6:IL:166:ALA:HA	6:IL:206:GLU:O	1.91	0.70
6:DL:166:ALA:HA	6:DL:206:GLU:O	1.91	0.70
5:IK:87:GLN:HB3	5:IK:128:ARG:HH12	1.56	0.70
6:BL:129:THR:O	6:BL:133:PHE:HB2	1.90	0.69
1:IG:947:ARG:H	1:IG:947:ARG:HE	1.38	0.69
11:KC:267:ALA:HB3	2:Bd:84:SER:H	1.57	0.69
6:LL:166:ALA:HA	6:LL:206:GLU:O	1.92	0.69
6:AL:44:HIS:HB3	6:AL:48:ASN:HA	1.75	0.69
4:WH:202:PHE:HB3	4:WH:215:ILE:HD11	1.75	0.69
7:BM:276:ALA:H	7:BM:295:ASN:HB2	1.57	0.69
7:JM:275:ASP:HB3	7:JM:294:PHE:HB2	1.75	0.68
6:HL:166:ALA:HA	6:HL:206:GLU:O	1.92	0.68
7:IM:276:ALA:H	7:IM:295:ASN:HB2	1.59	0.68
4:WH:226:LEU:O	4:WH:238:MET:HA	1.93	0.68
2:JD:29:PRO:HG2	6:JL:225:GLN:HA	1.76	0.68
3:HF:254:ILE:O	3:HF:261:VAL:HA	1.93	0.67
2:HD:52:MET:HG2	2:Hd:48:VAL:HG23	1.76	0.67
7:LM:275:ASP:HB3	7:LM:294:PHE:HB2	1.77	0.67
7:CM:275:ASP:HB3	7:CM:294:PHE:HB2	1.77	0.67
1:CG:1019:ALA:O	1:CG:1023:PHE:HB2	1.95	0.66
6:ML:124:THR:HA	6:ML:231:ILE:O	1.94	0.66
1:LG:972:PHE:HB3	1:LG:1005:VAL:HG22	1.78	0.66
2:Fd:84:SER:H	11:BC:267:ALA:HB3	1.60	0.66
1:PG:1019:ALA:O	1:PG:1023:PHE:HB2	1.95	0.66
1:DG:875:THR:HA	1:EG:940:ALA:HB1	1.78	0.65
3:ZF:208:ILE:HG13	3:ZF:225:SER:H	1.62	0.65
7:HM:276:ALA:H	7:HM:295:ASN:HB2	1.61	0.65
7:DM:275:ASP:HB3	7:DM:294:PHE:HB2	1.79	0.65
2:Ed:141:LYS:H	2:Ed:141:LYS:HZ3	1.43	0.65
11:CC:267:ALA:HB3	2:Gd:84:SER:H	1.62	0.65
5:LK:73:ASN:HD21	5:LK:185:ARG:HH21	1.43	0.65
7:MM:275:ASP:HB3	7:MM:294:PHE:HB2	1.79	0.65
1:YG:818:GLN:HG3	4:YH:205:GLN:HE21	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:GH:190:PRO:HB2	4:GH:231:ARG:HD3	1.79	0.65
3:Kf:254:ILE:O	3:Kf:261:VAL:HA	1.97	0.65
1:ZG:810:GLN:HA	1:ZG:813:LYS:HG2	1.80	0.64
6:FL:44:HIS:HB3	6:FL:48:ASN:HA	1.79	0.64
2:ID:105:ARG:HB3	2:ID:153:VAL:HG12	1.78	0.64
6:ML:166:ALA:HA	6:ML:206:GLU:O	1.98	0.64
1:IG:875:THR:HA	1:JG:940:ALA:HB1	1.79	0.64
4:ZH:311:MET:HE1	4:ZH:342:SER:H	1.63	0.64
3:DF:241:TYR:HB3	3:DF:256:THR:HG21	1.78	0.64
7:AM:211:THR:HA	7:AM:230:ARG:O	1.98	0.64
11:LC:266:VAL:HB	2:Cd:97:ARG:HH21	1.63	0.64
11:MC:109:VAL:HG23	11:MC:208:GLY:HA3	1.78	0.64
6:IL:124:THR:HA	6:IL:231:ILE:O	1.98	0.64
7:BM:275:ASP:HB3	7:BM:294:PHE:HB2	1.79	0.64
11:LC:109:VAL:HG23	11:LC:208:GLY:HA3	1.80	0.63
7:HM:275:ASP:HB3	7:HM:294:PHE:HB2	1.81	0.63
7:HM:308:ASP:N	7:HM:308:ASP:OD1	2.31	0.63
7:MM:211:THR:HA	7:MM:230:ARG:O	1.99	0.63
2:Md:84:SER:H	11:IC:267:ALA:HB3	1.62	0.63
3:DF:245:LYS:HE3	3:DF:257:SER:HA	1.81	0.63
8:JN:97:SER:HB2	1:FG:923:GLY:HA2	1.79	0.63
4:VH:183:ASP:HA	4:VH:256:VAL:HB	1.81	0.63
1:HG:899:LEU:HD13	1:HG:919:MET:HG2	1.80	0.63
4:FH:229:ARG:HG2	4:FH:236:PRO:HB3	1.80	0.63
6:KL:44:HIS:HB2	6:KL:48:ASN:HA	1.80	0.63
4:XH:230:LEU:HB2	4:XH:233:LEU:HB2	1.80	0.63
4:CH:230:LEU:HB2	4:CH:233:LEU:HB2	1.81	0.63
3:MF:222:LEU:O	3:MF:229:THR:HA	1.98	0.63
1:NG:871:ALA:HB2	1:NG:889:ILE:HD13	1.81	0.63
4:GH:251:ARG:HB2	4:WH:238:MET:HE1	1.79	0.63
6:ML:44:HIS:HB2	6:ML:48:ASN:HA	1.81	0.63
1:WG:818:GLN:HG3	4:WH:205:GLN:HE21	1.64	0.63
7:LM:306:GLN:HG2	7:LM:308:ASP:H	1.63	0.63
4:MH:108:ASP:N	4:MH:108:ASP:OD1	2.31	0.63
4:XH:168:VAL:HA	4:XH:240:THR:O	1.99	0.63
1:NG:899:LEU:HD13	1:NG:919:MET:HG2	1.79	0.63
2:AD:105:ARG:HB3	2:AD:153:VAL:HG12	1.80	0.63
11:GC:240:ILE:HG12	11:HC:255:LEU:HD13	1.81	0.62
5:JK:50:ASP:OD1	5:JK:50:ASP:N	2.32	0.62
2:Jd:97:ARG:HB2	11:FC:263:ARG:HH12	1.64	0.62
3:Bf:246:LEU:HB3	3:Bf:255:LEU:HB2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CL:115:GLN:HB3	6:CL:126:ILE:HB	1.81	0.62
7:JM:115:ARG:HG3	7:JM:135:ASP:HB3	1.80	0.62
3:ZF:222:LEU:O	3:ZF:229:THR:HA	1.98	0.62
2:JD:23:MET:N	2:JD:23:MET:SD	2.72	0.62
7:HM:131:THR:HG23	7:HM:151:GLY:H	1.64	0.62
11:GC:55:ARG:HH11	1:HG:1034:GLY:HA2	1.64	0.62
1:FG:899:LEU:HD13	1:FG:919:MET:HG2	1.82	0.62
6:GL:139:ARG:HH21	7:GM:319:PHE:HB2	1.65	0.62
6:EL:166:ALA:HA	6:EL:206:GLU:O	2.00	0.62
7:GM:117:ARG:HG2	7:GM:137:TYR:HB3	1.82	0.62
11:AC:62:GLU:HA	11:AC:65:LEU:HD12	1.82	0.62
6:IL:127:ILE:HB	6:IL:229:ILE:HB	1.81	0.62
3:Ff:221:TRP:HE1	3:Ff:229:THR:HB	1.64	0.62
1:CG:899:LEU:HD13	1:CG:919:MET:HG2	1.79	0.62
5:LK:50:ASP:N	5:LK:50:ASP:OD1	2.33	0.62
11:IC:214:LYS:HG3	2:AD:55:MET:HB3	1.82	0.62
1:OG:872:VAL:HA	1:OG:1036:GLY:HA2	1.80	0.62
7:IM:119:GLU:HG3	7:IM:139:ALA:HB3	1.81	0.61
11:DC:146:THR:OG1	11:DC:147:TRP:N	2.32	0.61
3:JF:210:TYR:HA	3:JF:224:GLY:HA2	1.82	0.61
3:VF:235:GLY:HA2	3:VF:243:MET:HE1	1.82	0.61
4:HH:238:MET:HG3	4:XH:250:TYR:HB3	1.83	0.61
6:JL:192:PHE:O	6:JL:196:ASN:ND2	2.33	0.61
7:JM:133:TYR:HA	7:JM:152:LEU:HA	1.81	0.61
3:Kf:237:LYS:HE2	3:Kf:242:GLY:HA2	1.82	0.61
6:LL:127:ILE:HB	6:LL:229:ILE:HB	1.83	0.61
7:AM:304:TRP:HB3	2:AD:80:GLN:HG3	1.82	0.61
7:BM:211:THR:HA	7:BM:230:ARG:O	2.01	0.61
2:Cd:94:LEU:HD12	2:Cd:97:ARG:HH12	1.66	0.61
4:DH:182:LEU:HB2	4:DH:255:ARG:HG3	1.81	0.61
1:KG:947:ARG:NH2	1:KG:1030:GLU:OE1	2.31	0.61
11:BC:101:LEU:HB2	11:BC:105:ILE:HG23	1.82	0.61
4:HH:192:ALA:HB2	4:HH:231:ARG:HG2	1.81	0.61
3:IF:230:LEU:HA	4:IH:165:THR:HG21	1.81	0.61
7:IM:275:ASP:HB3	7:IM:294:PHE:HB2	1.81	0.61
5:JK:65:ILE:HD12	5:JK:78:ILE:HG12	1.82	0.61
1:EG:899:LEU:HD13	1:EG:919:MET:HG2	1.82	0.61
2:Ad:73:ILE:HG12	2:Ad:75:ASN:H	1.64	0.61
3:FF:246:LEU:HD23	3:FF:255:LEU:HD12	1.83	0.61
1:CG:876:SER:HB3	1:DG:941:ARG:HG2	1.81	0.61
4:LH:190:PRO:HB2	4:LH:231:ARG:HG3	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:BC:146:THR:O	11:BC:149:GLN:NE2	2.33	0.61
1:GG:886:LEU:HA	1:GG:899:LEU:O	2.00	0.61
4:GH:326:ALA:HB3	4:GH:338:GLU:HB3	1.81	0.61
11:KC:146:THR:O	11:KC:149:GLN:NE2	2.33	0.61
1:EG:885:ILE:O	1:EG:900:ILE:HA	2.01	0.61
5:DK:117:THR:HG23	5:DK:157:GLN:HG3	1.83	0.61
2:LD:105:ARG:HB2	2:LD:153:VAL:HG12	1.83	0.61
11:LC:267:ALA:HB3	2:Cd:84:SER:H	1.66	0.61
1:BG:899:LEU:HD13	1:BG:919:MET:HG2	1.83	0.60
7:GM:275:ASP:HB3	7:GM:294:PHE:HB2	1.82	0.60
4:WH:229:ARG:HG2	4:WH:236:PRO:HB3	1.83	0.60
4:ZH:238:MET:N	4:ZH:238:MET:SD	2.74	0.60
3:FF:265:SER:HB3	3:FF:268:ASP:HB3	1.82	0.60
1:DG:900:ILE:HD11	1:EG:865:THR:HG22	1.83	0.60
6:ML:118:GLU:HG2	6:ML:123:ARG:HG2	1.83	0.60
7:AM:119:GLU:HG3	7:AM:139:ALA:HB3	1.83	0.60
1:GG:876:SER:HB3	1:HG:941:ARG:HG2	1.83	0.60
5:DK:117:THR:HA	5:DK:157:GLN:O	2.01	0.60
5:FK:90:ARG:HD3	7:FM:292:MET:HB2	1.82	0.60
5:HK:115:THR:HG1	5:HK:183:THR:HG1	1.48	0.60
2:Jd:84:SER:H	11:FC:267:ALA:HB3	1.66	0.60
3:MF:246:LEU:HB3	3:MF:255:LEU:HB2	1.83	0.60
11:IC:146:THR:OG1	11:IC:147:TRP:N	2.32	0.60
1:PG:912:MET:HB3	1:PG:944:LEU:HB2	1.82	0.60
1:Gg:806:THR:O	1:Gg:810:GLN:NE2	2.34	0.60
7:IM:120:GLY:H	7:IM:140:ASN:HB2	1.66	0.60
6:DL:115:GLN:HB3	6:DL:126:ILE:HB	1.82	0.60
4:AH:216:GLN:HB3	1:Ag:818:GLN:HE21	1.65	0.60
7:KM:240:GLN:HB3	7:KM:242:LYS:HE3	1.84	0.60
3:Af:210:TYR:HB3	3:Af:222:LEU:HD11	1.82	0.60
1:OG:871:ALA:HB2	1:OG:889:ILE:HD13	1.81	0.60
3:If:244:VAL:HA	3:If:256:THR:HA	1.82	0.60
4:YH:189:TRP:HE1	4:YH:232:GLY:H	1.49	0.60
11:DC:133:LYS:HE2	11:DC:135:ALA:HA	1.83	0.60
5:BK:117:THR:HA	5:BK:157:GLN:O	2.02	0.60
7:BM:306:GLN:HB3	7:BM:309:LEU:HB2	1.82	0.60
4:CH:183:ASP:HA	4:CH:256:VAL:HG22	1.82	0.60
5:DK:66:LYS:HB3	5:DK:77:SER:HB3	1.83	0.60
6:EL:49:ASN:HB3	7:EM:293:ALA:HB1	1.84	0.60
3:Ff:212:ILE:HG22	3:Ff:222:LEU:HD22	1.84	0.60
1:BG:876:SER:HB3	1:CG:941:ARG:HG2	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:IL:130:ASP:OD1	6:IL:130:ASP:N	2.34	0.60
6:JL:115:GLN:HB3	6:JL:126:ILE:HB	1.83	0.60
3:Lf:241:TYR:HB3	3:Lf:256:THR:HG21	1.84	0.60
1:BG:871:ALA:HB2	1:BG:889:ILE:HD13	1.84	0.60
5:IK:177:ASN:O	5:IK:179:ARG:NH1	2.35	0.60
2:Id:29:PRO:HB2	2:Id:32:ASN:HB2	1.83	0.60
4:XH:183:ASP:HA	4:XH:256:VAL:HG12	1.82	0.60
2:Ed:148:TYR:HB2	2:Ed:153:VAL:HG12	1.84	0.60
1:WG:797:ARG:NH2	1:WG:798:THR:OG1	2.35	0.60
5:BK:50:ASP:OD1	5:BK:50:ASP:N	2.34	0.60
11:CC:225:TYR:HB3	11:CC:251:ALA:HB3	1.83	0.60
1:CG:900:ILE:HD11	1:DG:865:THR:HG22	1.84	0.60
6:LL:124:THR:HA	6:LL:231:ILE:O	2.02	0.60
7:MM:199:LYS:HA	7:MM:219:ALA:HB3	1.84	0.60
3:VF:241:TYR:HB3	3:VF:256:THR:HG21	1.83	0.60
7:AM:146:LEU:HD23	7:AM:165:ILE:HG12	1.83	0.60
4:GH:345:LEU:HB2	4:GH:356:LEU:HB2	1.84	0.59
6:IL:49:ASN:HB3	7:IM:293:ALA:HB1	1.84	0.59
2:CD:77:TYR:O	2:CD:78:ASN:ND2	2.35	0.59
2:MD:105:ARG:HB3	2:MD:153:VAL:HG22	1.84	0.59
5:CK:50:ASP:N	5:CK:50:ASP:OD1	2.35	0.59
1:JG:899:LEU:HD13	1:JG:919:MET:HG2	1.83	0.59
7:FM:143:THR:HG22	7:FM:145:ARG:HH12	1.67	0.59
5:GK:90:ARG:HD3	7:GM:292:MET:HB2	1.84	0.59
2:Ad:76:ALA:HB3	2:Ad:79:LEU:HD23	1.84	0.59
7:IM:146:LEU:HD23	7:IM:165:ILE:HG12	1.84	0.59
2:DD:83:ALA:HA	5:DK:154:ILE:O	2.03	0.59
5:JK:117:THR:HA	5:JK:157:GLN:O	2.02	0.59
8:JN:63:GLY:HA3	2:KD:27:LYS:HB2	1.85	0.59
3:WF:237:LYS:NZ	3:WF:243:MET:SD	2.75	0.59
7:AM:308:ASP:N	7:AM:308:ASP:OD1	2.34	0.59
2:GD:105:ARG:HB2	2:GD:153:VAL:HG12	1.83	0.59
8:IN:57:ARG:NH1	8:IN:66:SER:O	2.35	0.59
8:KN:99:GLY:HA3	8:KN:114:LEU:HB3	1.84	0.59
4:WH:343:PRO:HA	4:WH:358:VAL:HG12	1.85	0.59
11:KC:51:MET:HE3	1:MG:938:ASN:HB2	1.85	0.59
6:ML:170:ASP:OD1	6:ML:170:ASP:N	2.36	0.59
1:WG:821:THR:OG1	1:WG:822:GLU:N	2.35	0.59
8:DN:57:ARG:NH1	8:DN:66:SER:O	2.36	0.59
6:EL:130:ASP:N	6:EL:130:ASP:OD1	2.36	0.59
2:Fd:76:ALA:HB3	2:Fd:79:LEU:HD23	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:LL:165:VAL:HG12	6:LL:231:ILE:HG12	1.85	0.59
3:ZF:230:LEU:HA	4:ZH:165:THR:HG21	1.85	0.59
1:LG:886:LEU:HA	1:LG:899:LEU:O	2.03	0.59
6:GL:44:HIS:HB2	6:GL:48:ASN:HA	1.85	0.59
4:IH:311:MET:HE3	4:IH:341:LYS:HA	1.85	0.59
4:IH:326:ALA:HB3	4:IH:338:GLU:HB3	1.85	0.59
5:AK:50:ASP:N	5:AK:50:ASP:OD1	2.35	0.59
1:EG:972:PHE:HB3	1:EG:1005:VAL:HG22	1.85	0.59
7:CM:146:LEU:HD23	7:CM:165:ILE:HG12	1.84	0.59
7:FM:313:ASP:OD1	7:FM:316:ASN:ND2	2.36	0.59
4:IH:229:ARG:NH2	4:IH:234:ASN:O	2.36	0.59
3:If:221:TRP:HE1	3:If:229:THR:HB	1.68	0.59
3:JF:254:ILE:HB	3:JF:262:ILE:HB	1.84	0.59
4:JH:324:TRP:HA	4:JH:339:MET:HB3	1.85	0.59
4:AH:273:PRO:O	11:IC:126:ARG:NH1	2.36	0.59
4:AH:326:ALA:HB3	4:AH:338:GLU:HB3	1.84	0.59
4:LH:192:ALA:HA	4:LH:231:ARG:HH11	1.67	0.59
7:MM:119:GLU:HG3	7:MM:139:ALA:HB3	1.85	0.59
3:Af:254:ILE:HB	3:Af:262:ILE:HB	1.84	0.59
6:DL:44:HIS:HB2	6:DL:48:ASN:HA	1.84	0.59
8:JN:45:MET:SD	8:JN:62:ASN:ND2	2.75	0.58
3:Jf:241:TYR:HB3	3:Jf:256:THR:HG21	1.85	0.58
4:AH:150:LYS:H	4:AH:247:ALA:HA	1.68	0.58
2:GD:124:LYS:O	7:GM:317:LYS:NZ	2.35	0.58
4:VH:230:LEU:HD12	4:VH:233:LEU:HD12	1.84	0.58
7:AM:145:ARG:HH22	7:AM:162:VAL:HG23	1.68	0.58
11:LC:247:LEU:HD21	2:DD:162:TYR:HB3	1.84	0.58
4:DH:183:ASP:HA	4:DH:256:VAL:HG12	1.85	0.58
1:Ig:797:ARG:HH12	4:JH:121:PRO:HB3	1.69	0.58
7:MM:288:ARG:O	7:MM:318:GLN:NE2	2.37	0.58
7:BM:308:ASP:OD1	7:BM:308:ASP:N	2.36	0.58
1:IG:912:MET:HB3	1:IG:944:LEU:HB2	1.85	0.58
2:AD:73:ILE:O	2:AD:133:ARG:NH2	2.36	0.58
1:AG:865:THR:HG22	1:PG:900:ILE:HD11	1.86	0.58
2:Hd:107:ARG:O	2:Hd:155:GLU:HA	2.03	0.58
2:Kd:29:PRO:O	2:Kd:32:ASN:ND2	2.36	0.58
1:WG:818:GLN:NE2	4:WH:203:ASN:O	2.37	0.58
6:HL:52:PRO:HB2	6:HL:54:ARG:HH12	1.68	0.58
1:Jg:811:ASP:O	1:Jg:814:GLN:NE2	2.36	0.58
7:KM:275:ASP:HB3	7:KM:294:PHE:HB2	1.85	0.58
5:MK:117:THR:HA	5:MK:157:GLN:O	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:WH:189:TRP:HE1	4:WH:232:GLY:H	1.50	0.58
1:OG:912:MET:HB3	1:OG:944:LEU:HB2	1.85	0.58
1:AG:941:ARG:HG2	1:PG:876:SER:HB3	1.85	0.58
3:FF:231:THR:HG23	4:WH:150:LYS:HE3	1.86	0.58
11:DC:114:ARG:HG2	11:DC:130:ARG:HG2	1.86	0.58
8:AN:62:ASN:OD1	8:AN:62:ASN:N	2.33	0.58
2:Ad:87:TRP:NE1	2:Ad:90:PRO:O	2.36	0.58
8:JN:57:ARG:NH1	8:JN:66:SER:O	2.37	0.58
5:LK:75:LEU:HD12	5:LK:183:THR:HB	1.86	0.58
5:AK:166:THR:HG22	5:AK:168:TYR:H	1.68	0.58
7:MM:285:SER:O	7:MM:316:ASN:ND2	2.36	0.58
5:EK:85:ALA:HB2	5:EK:90:ARG:HH21	1.68	0.58
2:FD:29:PRO:HG2	6:FL:225:GLN:HA	1.85	0.58
5:FK:46:ASP:OD1	5:FK:46:ASP:N	2.37	0.58
4:HH:230:LEU:HB2	4:HH:233:LEU:HB2	1.84	0.58
3:IF:231:THR:HG23	4:JH:150:LYS:HE3	1.85	0.58
9:JU:127:UNK:O	6:KL:232:GLN:NE2	2.37	0.58
5:BK:78:ILE:HB	5:BK:180:VAL:HG23	1.85	0.58
6:DL:127:ILE:HB	6:DL:229:ILE:HB	1.84	0.58
8:DN:82:MET:N	8:DN:82:MET:SD	2.76	0.58
8:FN:84:CYS:HA	11:AC:155:ASP:HB3	1.85	0.58
7:HM:214:ILE:O	7:HM:215:ARG:NH1	2.36	0.58
6:JL:210:ASP:N	6:JL:210:ASP:OD1	2.35	0.58
2:Kd:55:MET:SD	11:FC:213:ARG:NH1	2.77	0.58
3:MF:209:ILE:H	3:MF:225:SER:HB3	1.69	0.58
11:DC:167:PRO:HB2	11:DC:173:LYS:HG2	1.86	0.58
7:AM:275:ASP:HB3	7:AM:294:PHE:HB2	1.86	0.58
2:BD:39:ILE:HD12	6:BL:220:ILE:HG13	1.85	0.58
1:OG:899:LEU:HD13	1:OG:919:MET:HG2	1.86	0.58
1:PG:900:ILE:HG13	1:PG:918:THR:HB	1.84	0.58
7:FM:276:ALA:H	7:FM:295:ASN:HB2	1.69	0.58
6:HL:192:PHE:O	6:HL:196:ASN:ND2	2.36	0.58
2:Jd:55:MET:SD	11:EC:214:ARG:NH1	2.76	0.58
5:KK:115:THR:HB	5:KK:183:THR:HG23	1.86	0.58
6:KL:124:THR:HA	6:KL:231:ILE:O	2.03	0.58
7:MM:292:MET:SD	7:MM:292:MET:N	2.77	0.58
11:MC:266:VAL:HB	2:Dd:97:ARG:HH22	1.68	0.58
2:DD:85:VAL:HG12	5:DK:153:ILE:HG23	1.86	0.58
1:LG:1044:ASP:N	1:LG:1044:ASP:OD1	2.37	0.58
7:EM:119:GLU:HG3	7:EM:139:ALA:HB3	1.85	0.57
4:GH:189:TRP:HE1	4:GH:232:GLY:H	1.51	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GM:306:GLN:HB3	7:GM:309:LEU:HB2	1.86	0.57
2:Hd:64:PRO:HG2	2:Hd:67:LYS:HB2	1.85	0.57
5:JK:109:PHE:O	5:JK:111:LYS:NZ	2.37	0.57
8:JN:89:GLY:HA3	8:JN:104:ASN:HB2	1.85	0.57
1:DG:899:LEU:HD13	1:DG:919:MET:HG2	1.86	0.57
7:KM:124:VAL:HB	7:KM:144:THR:HG23	1.85	0.57
2:Kd:36:ASP:N	2:Kd:36:ASP:OD1	2.36	0.57
3:LF:254:ILE:HB	3:LF:262:ILE:HB	1.86	0.57
3:VF:254:ILE:HB	3:VF:262:ILE:HB	1.86	0.57
4:VH:324:TRP:HA	4:VH:339:MET:HB3	1.86	0.57
8:EN:82:MET:N	8:EN:82:MET:SD	2.76	0.57
2:MD:23:MET:N	2:MD:23:MET:SD	2.77	0.57
7:MM:308:ASP:OD1	7:MM:308:ASP:N	2.36	0.57
6:AL:130:ASP:OD1	6:AL:130:ASP:N	2.36	0.57
4:YH:108:ASP:OD1	4:YH:108:ASP:N	2.36	0.57
2:BD:117:VAL:HG22	2:BD:142:LYS:HD3	1.86	0.57
1:GG:871:ALA:HB2	1:GG:889:ILE:HD13	1.86	0.57
1:MG:899:LEU:HD13	1:MG:919:MET:HG2	1.86	0.57
5:EK:90:ARG:NH2	5:EK:92:ASN:OD1	2.38	0.57
7:FM:310:LYS:NZ	7:FM:311:ASP:O	2.37	0.57
6:HL:130:ASP:OD1	6:HL:130:ASP:N	2.37	0.57
6:IL:190:MET:HA	6:IL:193:LEU:HD23	1.85	0.57
7:IM:138:LEU:HD11	7:IM:142:GLY:HA3	1.86	0.57
3:If:235:GLY:HA2	3:If:243:MET:HE1	1.86	0.57
3:JF:245:LYS:HD3	3:JF:257:SER:HA	1.86	0.57
2:KD:41:LEU:HD12	11:FC:199:ILE:HD12	1.86	0.57
7:MM:242:LYS:HA	7:MM:262:GLU:HB3	1.85	0.57
1:FG:972:PHE:HB3	1:FG:1005:VAL:HG22	1.85	0.57
7:AM:191:LEU:HB3	7:AM:212:LEU:HD21	1.86	0.57
1:JG:972:PHE:HB3	1:JG:1005:VAL:HG22	1.86	0.57
3:If:210:TYR:HB3	3:If:222:LEU:HD12	1.86	0.57
4:AH:251:ARG:HH22	4:ZH:236:PRO:HD2	1.70	0.57
6:ML:127:ILE:HB	6:ML:229:ILE:HB	1.87	0.57
3:Mf:221:TRP:HE1	3:Mf:229:THR:HB	1.67	0.57
1:YG:798:THR:O	1:YG:802:LEU:HB2	2.04	0.57
2:BD:82:ARG:HH21	2:BD:126:GLU:HA	1.69	0.57
4:BH:273:PRO:O	11:JC:127:ARG:NH1	2.38	0.57
6:CL:226:ASN:O	6:CL:228:ARG:NH1	2.36	0.57
7:CM:273:ALA:HB1	7:CM:277:SER:HB2	1.85	0.57
1:OG:869:MET:HG2	1:OG:889:ILE:HD12	1.87	0.57
3:Df:218:GLY:H	3:Df:247:ILE:HD11	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:FK:96:TYR:O	5:FK:100:ASN:ND2	2.37	0.57
7:LM:276:ALA:H	7:LM:295:ASN:HB2	1.69	0.57
2:Ld:68:ASP:OD1	2:Ld:68:ASP:N	2.37	0.57
4:MH:188:PRO:O	4:MH:262:ASN:ND2	2.37	0.57
4:MH:230:LEU:HB2	4:MH:233:LEU:HB2	1.86	0.57
4:EH:271:GLY:O	11:LC:248:ARG:NH2	2.37	0.57
4:LH:106:VAL:HA	4:LH:109:LYS:HE2	1.86	0.57
2:DD:23:MET:SD	2:DD:23:MET:N	2.78	0.57
1:LG:867:ASP:OD1	1:LG:867:ASP:N	2.38	0.57
1:LG:900:ILE:HB	1:LG:918:THR:HB	1.87	0.57
1:OG:1003:ASN:HA	1:OG:1006:ILE:HD12	1.87	0.57
1:Eg:800:ASP:N	1:Eg:800:ASP:OD1	2.37	0.57
6:GL:212:ASN:N	6:GL:212:ASN:OD1	2.37	0.57
5:IK:162:ASP:OD1	5:IK:162:ASP:N	2.37	0.57
5:JK:44:ARG:HB2	8:JN:67:THR:HG22	1.86	0.57
8:MN:57:ARG:NH1	8:MN:66:SER:O	2.37	0.57
6:BL:44:HIS:HB2	6:BL:48:ASN:HA	1.85	0.57
2:CD:85:VAL:HG13	2:CD:123:THR:H	1.69	0.57
5:IK:125:SER:OG	5:IK:126:VAL:N	2.37	0.57
2:Kd:78:ASN:OD1	2:Kd:78:ASN:N	2.37	0.57
3:LF:233:ARG:HH22	3:MF:266:GLN:HA	1.69	0.57
4:MH:225:ASN:HD21	4:ZH:176:VAL:H	1.50	0.57
4:ZH:170:ARG:HA	4:ZH:242:ILE:O	2.05	0.57
4:ZH:207:ASP:N	4:ZH:207:ASP:OD1	2.38	0.57
11:EC:167:LEU:HB3	11:EC:169:LYS:HE2	1.87	0.57
11:IC:89:ASN:N	11:IC:89:ASN:OD1	2.38	0.57
8:CN:71:THR:HG22	8:CN:73:HIS:H	1.69	0.57
6:EL:115:GLN:HB3	6:EL:126:ILE:HB	1.85	0.57
1:Fg:804:ALA:O	1:Fg:807:GLN:NE2	2.38	0.57
6:FL:136:SER:O	7:FM:314:ARG:NH1	2.38	0.57
4:GH:230:LEU:HB2	4:GH:233:LEU:HB2	1.86	0.57
1:CG:951:HIS:H	1:CG:1027:THR:HG22	1.69	0.57
2:Id:110:GLY:HA3	2:Id:158:TYR:HB2	1.87	0.57
4:KH:208:LYS:HG3	1:YG:823:GLY:HA2	1.86	0.57
5:KK:66:LYS:NZ	6:LL:118:GLU:O	2.36	0.57
2:Kd:48:VAL:HG11	11:FC:93:ILE:HA	1.87	0.57
7:MM:306:GLN:HB3	7:MM:309:LEU:HB2	1.86	0.57
4:VH:238:MET:N	4:VH:238:MET:SD	2.77	0.57
5:BK:72:GLN:HB2	5:BK:185:ARG:HG3	1.87	0.57
11:IC:263:ARG:HD3	2:AD:62:ILE:HD11	1.87	0.57
3:HF:265:SER:HB3	3:HF:268:ASP:HB3	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:IF:220:ALA:O	3:IF:231:THR:HA	2.05	0.57
1:Ig:799:SER:HA	1:Ig:802:LEU:HD12	1.87	0.57
4:AH:251:ARG:NH1	4:ZH:236:PRO:O	2.38	0.57
2:LD:77:TYR:OH	5:LK:130:ARG:NH1	2.38	0.57
4:LH:332:ASP:OD1	4:LH:332:ASP:N	2.38	0.57
5:AK:163:LYS:NZ	5:AK:164:PRO:O	2.37	0.57
7:MM:276:ALA:H	7:MM:295:ASN:HB2	1.68	0.57
4:WH:344:VAL:HG13	4:WH:355:GLN:HE21	1.68	0.57
11:JC:103:GLU:OE2	11:JC:104:HIS:ND1	2.37	0.57
4:EH:114:ASP:HB3	1:VG:801:MET:HE1	1.86	0.56
2:Fd:97:ARG:HD3	11:BC:264:ALA:HB3	1.87	0.56
5:IK:111:LYS:HD3	5:IK:114:ILE:HD11	1.87	0.56
7:IM:149:ASN:OD1	7:IM:149:ASN:N	2.38	0.56
4:JH:238:MET:SD	4:JH:238:MET:N	2.77	0.56
4:KH:320:LEU:HB2	4:KH:346:LEU:HB3	1.87	0.56
7:KM:201:THR:HG22	7:KM:221:LYS:HB2	1.86	0.56
6:ML:130:ASP:N	6:ML:130:ASP:OD1	2.36	0.56
6:ML:210:ASP:N	6:ML:210:ASP:OD1	2.37	0.56
4:VH:230:LEU:HB2	4:VH:233:LEU:HB2	1.87	0.56
4:XH:178:SER:HA	4:XH:213:LEU:O	2.04	0.56
3:BF:254:ILE:HB	3:BF:262:ILE:HB	1.86	0.56
5:BK:127:LYS:HE3	7:BM:301:MET:HB2	1.86	0.56
6:CL:221:HIS:O	6:CL:225:GLN:NE2	2.37	0.56
4:DH:174:GLY:HA2	4:DH:216:GLN:HE21	1.69	0.56
1:IG:947:ARG:HH22	1:IG:1030:GLU:HB3	1.70	0.56
1:AG:875:THR:HA	1:BG:940:ALA:HB1	1.87	0.56
5:EK:66:LYS:HB3	5:EK:77:SER:HB3	1.87	0.56
6:GL:49:ASN:ND2	7:GM:293:ALA:O	2.38	0.56
4:IH:183:ASP:O	4:IH:255:ARG:NH1	2.38	0.56
11:KC:146:THR:OG1	11:KC:147:TRP:N	2.37	0.56
8:KN:57:ARG:NH1	8:KN:66:SER:O	2.38	0.56
2:Ld:105:ARG:HB2	2:Ld:153:VAL:HG23	1.87	0.56
3:VF:254:ILE:O	3:VF:261:VAL:HA	2.05	0.56
11:FC:34:LEU:HA	11:FC:37:MET:HB2	1.87	0.56
5:CK:150:ASP:O	5:CK:152:ARG:NH1	2.38	0.56
1:OG:900:ILE:HG13	1:OG:918:THR:HB	1.87	0.56
1:AG:951:HIS:H	1:AG:1027:THR:HG22	1.70	0.56
6:EL:169:THR:OG1	6:EL:170:ASP:N	2.37	0.56
4:FH:172:SER:HB2	4:FH:248:VAL:HG11	1.87	0.56
5:HK:87:GLN:HB3	5:HK:128:ARG:HH12	1.70	0.56
6:HL:124:THR:HG22	6:HL:232:GLN:HG2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:IH:192:ALA:HA	4:IH:231:ARG:HH11	1.71	0.56
4:IH:278:ASP:N	4:IH:278:ASP:OD1	2.37	0.56
7:IM:197:TYR:HA	7:IM:217:LYS:HB3	1.87	0.56
11:KC:126:ARG:NH1	4:CH:273:PRO:O	2.37	0.56
8:JN:62:ASN:HD22	8:JN:64:PHE:HD2	1.53	0.56
3:Jf:210:TYR:HB3	3:Jf:222:LEU:HD11	1.87	0.56
2:KD:26:LYS:NZ	6:KL:112:GLN:O	2.39	0.56
4:KH:225:ASN:HD21	4:YH:176:VAL:H	1.53	0.56
2:LD:23:MET:N	2:LD:23:MET:SD	2.78	0.56
1:Lg:804:ALA:O	1:Lg:807:GLN:NE2	2.38	0.56
5:LK:72:GLN:HE22	6:ML:216:ASP:H	1.52	0.56
8:LN:57:ARG:NH1	8:LN:66:SER:O	2.39	0.56
4:XH:200:SER:OG	4:XH:219:LYS:NZ	2.38	0.56
3:ZF:214:ALA:HB3	3:ZF:221:TRP:HB2	1.87	0.56
3:ZF:254:ILE:HB	3:ZF:262:ILE:HB	1.88	0.56
5:BK:87:GLN:HB3	5:BK:128:ARG:HH12	1.69	0.56
7:BM:163:THR:HB	7:BM:183:VAL:HG12	1.86	0.56
11:MC:240:ILE:HG22	11:AC:133:TYR:HB2	1.86	0.56
6:CL:141:ASN:HD21	6:CL:143:ILE:HB	1.69	0.56
1:PG:899:LEU:HD13	1:PG:919:MET:HG2	1.86	0.56
2:AD:36:ASP:N	2:AD:36:ASP:OD1	2.35	0.56
2:ED:105:ARG:HB2	2:ED:153:VAL:HG22	1.87	0.56
11:GC:151:LEU:HD21	11:GC:202:ILE:HG21	1.87	0.56
5:HK:66:LYS:HE2	6:IL:119:TYR:HB2	1.88	0.56
7:JM:154:LYS:HE2	7:JM:174:GLN:HB3	1.88	0.56
2:KD:77:TYR:OH	5:KK:130:ARG:NH1	2.38	0.56
4:XH:283:VAL:O	4:XH:314:ARG:NH1	2.39	0.56
4:YH:106:VAL:HA	4:YH:109:LYS:HE2	1.87	0.56
11:FC:142:THR:HG22	11:FC:143:THR:HG23	1.87	0.56
1:Dg:807:GLN:O	1:Dg:810:GLN:NE2	2.39	0.56
5:DK:90:ARG:NH2	5:DK:92:ASN:OD1	2.39	0.56
7:DM:202:LEU:HB2	7:DM:222:ILE:HG23	1.87	0.56
3:Ff:218:GLY:H	3:Ff:247:ILE:HD11	1.70	0.56
5:GK:66:LYS:HB3	5:GK:77:SER:HB3	1.87	0.56
6:BL:187:GLU:HG3	6:BL:190:MET:HE3	1.85	0.56
7:BM:279:ILE:HB	7:BM:298:VAL:HG22	1.87	0.56
7:BM:306:GLN:HG3	7:BM:308:ASP:H	1.70	0.56
3:Df:213:GLN:HB2	3:Df:221:TRP:HD1	1.70	0.56
5:FK:47:GLY:O	5:FK:108:GLN:NE2	2.39	0.56
5:FK:107:LYS:NZ	5:FK:148:GLY:O	2.39	0.56
7:GM:199:LYS:HA	7:GM:219:ALA:HB3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:HD:82:ARG:NH2	2:HD:125:ASP:O	2.37	0.56
2:ID:82:ARG:HD3	2:ID:125:ASP:HB2	1.88	0.56
5:IK:185:ARG:NH1	6:JL:216:ASP:OD1	2.39	0.56
3:MF:231:THR:HG23	4:ZH:150:LYS:HE3	1.88	0.56
4:MH:268:THR:HG23	4:ZH:329:THR:HG23	1.87	0.56
11:LC:146:THR:OG1	11:LC:147:TRP:N	2.36	0.56
4:DH:284:LEU:O	4:DH:314:ARG:NH2	2.39	0.56
1:PG:910:ASP:OD1	1:PG:910:ASP:N	2.39	0.56
7:EM:275:ASP:HB3	7:EM:294:PHE:HB2	1.87	0.56
2:Ed:68:ASP:N	2:Ed:68:ASP:OD1	2.38	0.56
2:GD:77:TYR:OH	5:GK:130:ARG:NH1	2.39	0.56
5:GK:87:GLN:HB3	5:GK:128:ARG:HH12	1.70	0.56
4:HH:230:LEU:HD12	4:HH:233:LEU:HD12	1.87	0.56
2:Id:76:ALA:O	2:Id:80:GLN:NE2	2.38	0.56
2:JD:105:ARG:HB3	2:JD:153:VAL:HG12	1.88	0.56
4:JH:225:ASN:HD21	4:KH:176:VAL:H	1.53	0.56
4:JH:273:PRO:O	11:EC:127:ARG:NH1	2.36	0.56
1:Kg:801:MET:HG3	4:YH:122:LEU:HG	1.88	0.56
5:KK:166:THR:HG22	5:KK:168:TYR:H	1.70	0.56
2:Md:105:ARG:HB3	2:Md:153:VAL:HG23	1.88	0.56
4:XH:205:GLN:HB2	4:XH:214:MET:HB3	1.87	0.56
4:ZH:182:LEU:HB2	4:ZH:255:ARG:HG3	1.87	0.56
8:BN:88:HIS:ND1	8:BN:105:ASP:OD2	2.37	0.56
1:Cg:804:ALA:O	1:Cg:807:GLN:NE2	2.39	0.56
1:PG:972:PHE:HB3	1:PG:1005:VAL:HG22	1.87	0.56
6:DL:165:VAL:HG12	6:DL:231:ILE:HG12	1.88	0.56
2:FD:83:ALA:HA	5:FK:154:ILE:O	2.06	0.56
6:GL:171:ASN:OD1	6:GL:217:ASN:ND2	2.39	0.56
3:Gf:241:TYR:HB3	3:Gf:256:THR:HG21	1.87	0.56
6:IL:212:ASN:OD1	6:IL:212:ASN:N	2.38	0.56
7:IM:249:GLN:NE2	7:IM:267:ASN:OD1	2.39	0.56
4:LH:236:PRO:O	4:MH:251:ARG:NH1	2.38	0.56
7:LM:214:ILE:O	7:LM:215:ARG:NH1	2.35	0.56
1:EG:1017:GLN:OE1	1:FG:1020:GLN:NE2	2.37	0.56
4:MH:207:ASP:N	4:MH:207:ASP:OD1	2.38	0.56
5:MK:60:LEU:HD22	5:MK:65:ILE:HD11	1.87	0.56
7:CM:257:ASP:OD1	7:CM:257:ASP:N	2.37	0.56
11:CC:263:ARG:NH1	2:HD:62:ILE:O	2.39	0.56
11:GC:55:ARG:HH12	1:HG:874:ASP:HA	1.70	0.56
2:MD:140:GLY:O	2:Md:60:LYS:NZ	2.39	0.56
2:Ad:68:ASP:OD1	2:Ad:68:ASP:N	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:EC:148:TRP:O	11:EC:152:LEU:HB2	2.06	0.56
1:Cg:807:GLN:O	1:Cg:810:GLN:NE2	2.38	0.56
1:OG:904:ASN:N	1:OG:904:ASN:OD1	2.38	0.56
2:Dd:110:GLY:HA3	2:Dd:158:TYR:HB2	1.88	0.56
2:ED:162:TYR:HB3	11:MC:247:LEU:HD21	1.87	0.56
4:EH:275:SER:O	11:MC:118:ASN:ND2	2.39	0.56
2:Ed:36:ASP:N	2:Ed:36:ASP:OD1	2.38	0.56
3:AF:233:ARG:NH1	3:BF:269:SER:OG	2.39	0.56
2:GD:76:ALA:H	2:GD:79:LEU:HD12	1.71	0.56
1:Gg:821:THR:OG1	1:Gg:822:GLU:N	2.39	0.56
4:GH:324:TRP:HB3	4:GH:339:MET:HE2	1.88	0.56
2:HD:75:ASN:ND2	7:HM:306:GLN:O	2.39	0.56
7:IM:177:LEU:HD13	7:IM:181:PRO:HG2	1.87	0.56
7:JM:308:ASP:OD1	7:JM:308:ASP:N	2.39	0.56
4:KH:296:VAL:HB	4:KH:359:GLU:HB3	1.88	0.56
7:KM:168:VAL:H	7:KM:187:GLY:HA3	1.71	0.56
6:LL:44:HIS:HB2	6:LL:48:ASN:HA	1.87	0.56
1:Mg:791:GLN:N	1:Mg:793:GLU:OE1	2.39	0.56
7:MM:191:LEU:HD21	7:MM:194:LEU:HB2	1.87	0.56
6:AL:169:THR:OG1	6:AL:170:ASP:N	2.39	0.56
1:ZG:818:GLN:HG3	4:ZH:205:GLN:HE21	1.71	0.56
6:BL:115:GLN:HB3	6:BL:126:ILE:HB	1.87	0.56
3:CF:213:GLN:O	4:CH:245:GLN:NE2	2.39	0.56
1:AG:912:MET:HB3	1:AG:944:LEU:HB2	1.88	0.55
3:FF:233:ARG:NH1	3:WF:266:GLN:O	2.38	0.55
5:FK:87:GLN:HB3	5:FK:128:ARG:HH12	1.70	0.55
7:FM:157:ALA:O	7:FM:178:LYS:NZ	2.37	0.55
1:Hg:818:GLN:O	4:HH:205:GLN:NE2	2.39	0.55
2:ID:47:SER:OG	11:DC:203:LYS:NZ	2.39	0.55
5:IK:117:THR:HA	5:IK:157:GLN:O	2.06	0.55
4:KH:208:LYS:NZ	1:YG:822:GLU:O	2.39	0.55
2:MD:29:PRO:HG2	6:ML:225:GLN:HA	1.86	0.55
1:YG:791:GLN:O	1:YG:795:GLN:NE2	2.39	0.55
1:Cg:811:ASP:N	1:Cg:811:ASP:OD1	2.39	0.55
7:FM:308:ASP:OD1	3:Ff:253:ARG:NH2	2.39	0.55
4:JH:328:MET:HE1	11:EC:117:THR:HG22	1.87	0.55
5:AK:117:THR:HA	5:AK:157:GLN:O	2.05	0.55
4:VH:249:ASP:OD1	4:VH:249:ASP:N	2.38	0.55
4:ZH:158:VAL:HG22	4:ZH:256:VAL:HA	1.88	0.55
1:AG:865:THR:O	1:PG:898:LYS:NZ	2.38	0.55
6:EL:113:ASP:N	6:EL:113:ASP:OD1	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:FF:233:ARG:NH1	3:WF:269:SER:OG	2.40	0.55
11:GC:154:ASP:OD1	11:GC:154:ASP:N	2.39	0.55
3:IF:219:ARG:NH1	3:JF:269:SER:O	2.39	0.55
1:Ig:807:GLN:O	1:Ig:810:GLN:NE2	2.38	0.55
5:LK:117:THR:HA	5:LK:157:GLN:O	2.06	0.55
1:WG:794:ILE:O	1:WG:797:ARG:NH2	2.39	0.55
1:ZG:794:ILE:HD12	4:BH:110:LYS:HD2	1.89	0.55
11:FC:101:LEU:HB2	11:FC:105:ILE:HG23	1.88	0.55
2:CD:23:MET:N	2:CD:23:MET:SD	2.79	0.55
6:CL:127:ILE:HB	6:CL:229:ILE:HB	1.89	0.55
1:JG:919:MET:HG3	1:JG:930:ILE:HG23	1.88	0.55
7:DM:199:LYS:HA	7:DM:219:ALA:HB3	1.88	0.55
4:EH:207:ASP:OD1	4:EH:207:ASP:N	2.37	0.55
2:FD:23:MET:N	2:FD:23:MET:SD	2.79	0.55
4:FH:225:ASN:HD21	4:WH:176:VAL:HB	1.71	0.55
2:GD:73:ILE:O	2:GD:133:ARG:NH2	2.40	0.55
4:GH:284:LEU:O	4:GH:314:ARG:NH2	2.39	0.55
4:HH:225:ASN:HD21	4:XH:176:VAL:H	1.55	0.55
2:ID:36:ASP:N	2:ID:36:ASP:OD1	2.37	0.55
4:WH:324:TRP:HA	4:WH:339:MET:HG2	1.88	0.55
4:YH:249:ASP:OD1	4:YH:249:ASP:N	2.40	0.55
11:DC:230:ASP:OD1	11:DC:230:ASP:N	2.40	0.55
7:AM:288:ARG:NH2	7:AM:316:ASN:O	2.39	0.55
1:LG:899:LEU:HD13	1:LG:919:MET:HG2	1.88	0.55
4:EH:150:LYS:HE3	3:DF:231:THR:HG23	1.87	0.55
7:EM:214:ILE:O	7:EM:215:ARG:NH1	2.39	0.55
4:FH:182:LEU:HB2	4:FH:255:ARG:HE	1.72	0.55
6:GL:210:ASP:OD1	6:GL:210:ASP:N	2.39	0.55
7:GM:124:VAL:HB	7:GM:144:THR:HG23	1.88	0.55
2:KD:91:ILE:HD11	2:KD:156:LEU:HD11	1.88	0.55
3:Mf:264:PHE:O	3:Mf:266:GLN:NE2	2.40	0.55
2:BD:118:LEU:O	11:JC:98:ASN:ND2	2.40	0.55
4:BH:278:ASP:OD1	4:BH:278:ASP:N	2.38	0.55
6:BL:190:MET:HB2	6:BL:203:LEU:HD11	1.89	0.55
2:Bd:150:ASN:OD1	2:Bd:150:ASN:N	2.40	0.55
11:AC:176:ILE:HA	11:AC:179:ILE:HG12	1.89	0.55
1:AG:899:LEU:HD13	1:AG:919:MET:HG2	1.89	0.55
7:EM:290:ASP:N	7:EM:290:ASP:OD1	2.39	0.55
4:GH:296:VAL:HB	4:GH:359:GLU:HB2	1.87	0.55
4:KH:155:SER:OG	4:KH:255:ARG:NH1	2.39	0.55
5:KK:72:GLN:HB2	6:LL:215:SER:HA	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:MH:205:GLN:HB2	4:MH:214:MET:HB3	1.88	0.55
6:ML:136:SER:O	7:MM:314:ARG:NH1	2.39	0.55
4:VH:296:VAL:HG23	4:VH:359:GLU:HB2	1.89	0.55
6:AL:226:ASN:O	6:AL:228:ARG:NH1	2.39	0.55
6:CL:121:ASP:OD1	6:CL:121:ASP:N	2.38	0.55
5:EK:177:ASN:O	5:EK:179:ARG:NH1	2.39	0.55
3:Ff:211:TYR:O	3:Ff:213:GLN:NE2	2.40	0.55
7:HM:153:GLN:HE22	7:HM:174:GLN:HB2	1.72	0.55
2:Id:55:MET:SD	11:DC:213:ARG:NH1	2.80	0.55
4:LH:301:ASP:N	4:LH:301:ASP:OD1	2.39	0.55
4:VH:295:LEU:HD23	4:VH:360:GLY:HA3	1.87	0.55
4:BH:301:ASP:OD1	4:BH:301:ASP:N	2.36	0.55
5:BK:162:ASP:N	5:BK:162:ASP:OD1	2.38	0.55
4:CH:308:ASN:O	4:CH:310:LYS:NZ	2.40	0.55
8:CN:82:MET:N	8:CN:82:MET:SD	2.80	0.55
2:Cd:76:ALA:HB3	2:Cd:79:LEU:HD13	1.88	0.55
4:DH:114:ASP:HA	4:DH:117:ARG:HD3	1.89	0.55
1:KG:955:ARG:NH1	1:KG:1023:PHE:O	2.38	0.55
5:EK:38:VAL:HA	5:EK:41:LEU:HB2	1.89	0.55
3:FF:219:ARG:NH1	3:WF:269:SER:O	2.40	0.55
4:GH:278:ASP:OD1	4:GH:278:ASP:N	2.38	0.55
7:GM:174:GLN:NE2	7:GM:193:GLN:O	2.40	0.55
4:JH:108:ASP:OD1	4:JH:108:ASP:N	2.39	0.55
4:JH:147:THR:O	4:JH:246:LYS:NZ	2.38	0.55
7:JM:120:GLY:H	7:JM:140:ASN:HB2	1.71	0.55
4:KH:189:TRP:HE1	4:KH:232:GLY:H	1.54	0.55
6:KL:230:GLU:OE2	6:KL:232:GLN:NE2	2.36	0.55
7:KM:119:GLU:HG3	7:KM:139:ALA:HB3	1.88	0.55
6:ML:230:GLU:OE2	6:ML:232:GLN:NE2	2.39	0.55
8:MN:56:GLY:HA3	8:MN:74:ALA:HB2	1.88	0.55
1:GG:899:LEU:HD13	1:GG:919:MET:HG2	1.87	0.55
11:FC:230:ASP:OD1	11:FC:230:ASP:N	2.40	0.55
3:Cf:209:ILE:HG13	3:Cf:225:SER:HB3	1.88	0.55
5:GK:86:ASP:N	5:GK:86:ASP:OD1	2.38	0.55
6:GL:230:GLU:OE2	6:GL:232:GLN:NE2	2.39	0.55
3:Gf:244:VAL:HA	3:Gf:256:THR:HA	1.89	0.55
1:DG:951:HIS:H	1:DG:1027:THR:HG22	1.70	0.55
6:KL:130:ASP:OD1	6:KL:130:ASP:N	2.39	0.55
4:LH:147:THR:O	4:LH:246:LYS:NZ	2.40	0.55
4:LH:187:ALA:HB3	4:LH:260:GLY:HA3	1.89	0.55
7:LM:138:LEU:HD11	7:LM:142:GLY:HA3	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:LM:257:ASP:N	7:LM:257:ASP:OD1	2.38	0.55
2:Md:148:TYR:HB2	2:Md:153:VAL:HG12	1.88	0.55
8:AN:52:ASP:O	8:AN:56:GLY:N	2.40	0.55
11:IC:243:ASP:OD1	11:IC:243:ASP:N	2.40	0.55
6:CL:165:VAL:HG12	6:CL:231:ILE:HG12	1.89	0.55
4:FH:316:ASN:HB3	4:FH:334:THR:HG22	1.88	0.55
7:GM:156:GLU:OE1	7:GM:178:LYS:NZ	2.39	0.55
6:IL:165:VAL:HG12	6:IL:231:ILE:HG12	1.88	0.55
6:JL:44:HIS:HB2	6:JL:48:ASN:HA	1.89	0.55
6:LL:130:ASP:N	6:LL:130:ASP:OD1	2.38	0.55
6:ML:113:ASP:OD1	6:ML:113:ASP:N	2.40	0.55
1:FG:867:ASP:OD1	1:FG:867:ASP:N	2.40	0.55
3:ZF:233:ARG:NH1	3:ZF:235:GLY:O	2.40	0.55
4:ZH:182:LEU:O	4:ZH:255:ARG:HA	2.07	0.55
4:ZH:253:ASP:OD1	4:ZH:253:ASP:N	2.37	0.55
1:GG:1003:ASN:HA	1:GG:1006:ILE:HD12	1.89	0.55
4:DH:108:ASP:OD1	4:DH:108:ASP:N	2.40	0.55
1:PG:891:THR:OG1	1:PG:892:GLY:N	2.40	0.55
2:ED:150:ASN:N	2:ED:150:ASN:OD1	2.40	0.54
4:FH:278:ASP:N	4:FH:278:ASP:OD1	2.39	0.54
2:GD:36:ASP:N	2:GD:36:ASP:OD1	2.40	0.54
3:GF:247:ILE:HG12	3:GF:254:ILE:HG23	1.88	0.54
7:GM:146:LEU:HD23	7:GM:165:ILE:HG12	1.88	0.54
4:AH:230:LEU:HB2	4:AH:233:LEU:HB2	1.89	0.54
2:MD:150:ASN:OD1	2:MD:150:ASN:N	2.39	0.54
11:IC:215:LEU:HG	11:IC:220:MET:HB2	1.88	0.54
1:Cg:810:GLN:HA	1:Cg:813:LYS:HB2	1.88	0.54
5:CK:165:ILE:HD11	6:DL:120:GLY:HA3	1.88	0.54
4:DH:278:ASP:OD1	4:DH:278:ASP:N	2.38	0.54
1:KG:899:LEU:HD13	1:KG:919:MET:HG2	1.88	0.54
1:LG:1003:ASN:HA	1:LG:1006:ILE:HD12	1.88	0.54
7:EM:308:ASP:OD1	7:EM:308:ASP:N	2.37	0.54
1:BG:900:ILE:HG13	1:BG:918:THR:HB	1.87	0.54
11:GC:102:GLU:OE2	11:GC:103:HIS:ND1	2.39	0.54
1:Ig:801:MET:HB3	4:KH:115:MET:HG3	1.90	0.54
8:JN:110:GLU:HA	8:JN:113:SER:HB3	1.89	0.54
6:KL:127:ILE:HB	6:KL:229:ILE:HB	1.89	0.54
3:YF:245:LYS:HE3	3:YF:257:SER:HA	1.89	0.54
7:AM:257:ASP:N	7:AM:257:ASP:OD1	2.40	0.54
7:BM:199:LYS:HA	7:BM:219:ALA:HB3	1.89	0.54
3:CF:230:LEU:HA	4:CH:165:THR:HG21	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CL:44:HIS:HB2	6:CL:48:ASN:HA	1.88	0.54
9:EU:127:UNK:O	6:FL:232:GLN:NE2	2.39	0.54
7:FM:242:LYS:HA	7:FM:262:GLU:HB2	1.90	0.54
2:GD:130:GLU:OE2	2:GD:133:ARG:NH1	2.40	0.54
6:HL:165:VAL:HG12	6:HL:231:ILE:HG12	1.88	0.54
6:IL:168:PHE:HB2	6:IL:228:ARG:HG2	1.90	0.54
7:IM:308:ASP:N	7:IM:308:ASP:OD1	2.38	0.54
8:LN:72:ARG:NH2	4:MH:298:SER:OG	2.40	0.54
5:AK:148:GLY:H	2:Ad:30:ILE:HD13	1.72	0.54
3:ZF:219:ARG:NH2	3:ZF:231:THR:OG1	2.39	0.54
2:BD:162:TYR:HB3	11:JC:248:LEU:HD21	1.90	0.54
2:CD:31:ASN:OD1	2:CD:31:ASN:N	2.40	0.54
4:FH:181:PHE:O	4:FH:211:ASN:ND2	2.38	0.54
5:FK:113:ALA:HA	5:FK:153:ILE:O	2.08	0.54
6:GL:187:GLU:OE2	7:GM:250:ARG:NH2	2.40	0.54
11:GC:230:ASP:N	11:GC:230:ASP:OD1	2.40	0.54
4:IH:345:LEU:HB2	4:IH:356:LEU:HB2	1.90	0.54
6:IL:44:HIS:HB2	6:IL:48:ASN:HA	1.89	0.54
7:IM:269:GLN:NE2	7:IM:290:ASP:OD1	2.41	0.54
2:JD:150:ASN:N	2:JD:150:ASN:OD1	2.40	0.54
4:AH:159:ASN:ND2	4:AH:257:GLN:OE1	2.39	0.54
2:LD:124:LYS:O	7:LM:317:LYS:NZ	2.40	0.54
4:LH:315:THR:OG1	4:LH:316:ASN:N	2.40	0.54
6:ML:212:ASN:N	6:ML:212:ASN:OD1	2.40	0.54
1:FG:949:ASN:OD1	1:FG:949:ASN:N	2.41	0.54
11:DC:81:GLU:O	11:DC:84:ASN:ND2	2.40	0.54
2:Ad:87:TRP:O	2:Ad:120:SER:HA	2.08	0.54
6:BL:226:ASN:O	6:BL:228:ARG:NH1	2.40	0.54
4:CH:278:ASP:N	4:CH:278:ASP:OD1	2.36	0.54
1:Ag:791:GLN:N	1:Ag:793:GLU:OE2	2.40	0.54
11:BC:215:LEU:HD12	11:BC:220:MET:HB2	1.89	0.54
2:Gd:139:ALA:HB1	2:Gd:143:ALA:HB3	1.90	0.54
11:GC:213:ARG:NH1	2:Ld:55:MET:SD	2.81	0.54
4:HH:278:ASP:N	4:HH:278:ASP:OD1	2.37	0.54
2:ID:76:ALA:H	2:ID:79:LEU:HD12	1.73	0.54
1:Lg:818:GLN:NE2	4:LH:203:ASN:OD1	2.39	0.54
9:MU:127:UNK:O	6:AL:232:GLN:NE2	2.40	0.54
3:Mf:241:TYR:HB3	3:Mf:256:THR:HG21	1.89	0.54
4:VH:189:TRP:HE1	4:VH:232:GLY:H	1.56	0.54
11:DC:243:ASP:OD1	11:DC:243:ASP:N	2.39	0.54
11:MC:146:THR:OG1	11:MC:147:TRP:N	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:DH:179:LEU:HG	4:DH:252:VAL:HB	1.88	0.54
3:Df:247:ILE:HG22	3:Df:254:ILE:HG23	1.90	0.54
2:Ed:84:SER:H	11:AC:268:ALA:HB3	1.72	0.54
2:Ed:97:ARG:NH1	11:AC:265:ALA:O	2.40	0.54
1:DG:900:ILE:HG13	1:DG:918:THR:HB	1.90	0.54
1:Kg:800:ASP:N	1:Kg:800:ASP:OD1	2.40	0.54
4:LH:234:ASN:ND2	4:MH:211:ASN:OD1	2.40	0.54
6:LL:42:CYS:SG	6:LL:43:PHE:N	2.77	0.54
3:MF:256:THR:OG1	3:MF:257:SER:N	2.41	0.54
7:MM:136:LEU:HD23	7:MM:155:LEU:HD12	1.89	0.54
4:VH:176:VAL:H	4:CH:225:ASN:HD21	1.54	0.54
11:EC:231:ASP:N	11:EC:231:ASP:OD1	2.39	0.54
6:CL:212:ASN:OD1	6:CL:212:ASN:N	2.40	0.54
7:CM:306:GLN:HB3	7:CM:309:LEU:HB2	1.90	0.54
4:DH:179:LEU:HA	4:DH:252:VAL:O	2.08	0.54
2:Dd:105:ARG:HH21	2:Dd:153:VAL:HB	1.71	0.54
7:GM:119:GLU:HG3	7:GM:139:ALA:HB3	1.90	0.54
7:HM:312:PHE:HB2	7:HM:317:LYS:HG3	1.90	0.54
2:Hd:68:ASP:N	2:Hd:68:ASP:OD1	2.39	0.54
1:Bg:792:GLN:O	1:Bg:795:GLN:NE2	2.40	0.54
1:Bg:804:ALA:O	1:Bg:807:GLN:NE2	2.40	0.54
4:IH:228:VAL:HG13	4:IH:237:VAL:HB	1.89	0.54
5:IK:76:ILE:HD12	5:IK:102:ILE:HD11	1.88	0.54
6:IL:120:GLY:O	6:IL:123:ARG:NH2	2.40	0.54
7:IM:254:LYS:HE2	7:IM:272:LEU:HD23	1.90	0.54
2:JD:158:TYR:O	2:Jd:137:TYR:OH	2.26	0.54
4:JH:196:LEU:HD21	4:JH:202:PHE:HB2	1.89	0.54
7:JM:257:ASP:N	7:JM:257:ASP:OD1	2.40	0.54
2:MD:149:PRO:O	2:MD:152:GLN:NE2	2.41	0.54
7:BM:190:ASN:OD1	7:BM:192:ARG:NH2	2.37	0.54
11:HC:147:TRP:O	11:HC:151:LEU:HB2	2.07	0.54
1:KG:972:PHE:HB3	1:KG:1005:VAL:HG22	1.89	0.54
11:CC:44:ARG:O	11:CC:47:LYS:NZ	2.41	0.54
11:BC:151:LEU:HD21	11:BC:202:ILE:HG21	1.90	0.54
7:GM:306:GLN:HE22	3:Gf:253:ARG:HH22	1.56	0.54
2:HD:105:ARG:HB3	2:HD:153:VAL:HG12	1.90	0.54
11:KC:240:ILE:HG13	11:LC:132:TYR:HB2	1.90	0.54
7:JM:288:ARG:NH2	7:JM:316:ASN:O	2.41	0.54
2:Jd:76:ALA:O	2:Jd:80:GLN:NE2	2.41	0.54
3:Jf:209:ILE:HB	3:Jf:225:SER:HB3	1.88	0.54
5:KK:93:TRP:NE1	2:Kd:24:LYS:O	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:KL:130:ASP:OD2	6:KL:227:ARG:NH1	2.40	0.54
6:LL:230:GLU:OE2	6:LL:232:GLN:NE2	2.41	0.54
5:AK:44:ARG:NH2	5:AK:48:ALA:O	2.41	0.54
4:MH:172:SER:HB2	4:MH:248:VAL:HG11	1.90	0.54
5:MK:78:ILE:HB	5:MK:180:VAL:HG23	1.88	0.54
7:MM:203:SER:HB3	7:MM:223:GLN:HB3	1.89	0.54
6:AL:115:GLN:HB3	6:AL:126:ILE:HB	1.89	0.54
8:AN:94:GLN:NE2	8:AN:95:LEU:O	2.40	0.54
5:CK:166:THR:HG22	5:CK:168:TYR:H	1.72	0.54
7:CM:163:THR:HB	7:CM:183:VAL:HG12	1.89	0.54
2:ED:27:LYS:NZ	5:DK:71:GLY:O	2.41	0.54
11:BC:102:GLU:OE2	11:BC:103:HIS:ND1	2.40	0.54
7:GM:306:GLN:NE2	3:Gf:251:GLN:OE1	2.41	0.54
4:JH:172:SER:HB3	4:JH:248:VAL:HG11	1.90	0.54
7:LM:249:GLN:OE1	7:LM:267:ASN:ND2	2.41	0.54
2:MD:60:LYS:O	2:MD:60:LYS:NZ	2.40	0.54
7:MM:288:ARG:NH2	7:MM:316:ASN:O	2.39	0.54
3:YF:220:ALA:O	3:YF:231:THR:HA	2.08	0.54
6:AL:128:PRO:O	6:AL:132:TYR:HB2	2.08	0.54
4:YH:315:THR:OG1	4:YH:316:ASN:N	2.41	0.54
2:BD:83:ALA:HA	5:BK:154:ILE:O	2.08	0.54
2:Bd:60:LYS:NZ	2:Bd:61:VAL:O	2.41	0.54
1:GG:1032:TYR:HD1	1:HG:941:ARG:HH22	1.54	0.54
11:FC:194:ILE:O	11:FC:198:ASN:ND2	2.41	0.54
11:HC:215:LEU:HG	11:HC:220:MET:HB2	1.90	0.54
2:Dd:105:ARG:HB2	2:Dd:153:VAL:HG23	1.89	0.54
2:FD:130:GLU:OE2	2:FD:133:ARG:NH1	2.41	0.54
6:FL:212:ASN:OD1	6:FL:212:ASN:N	2.41	0.54
4:GH:152:THR:O	4:GH:250:TYR:N	2.41	0.54
7:GM:288:ARG:NH2	7:GM:318:GLN:O	2.40	0.54
11:GC:255:LEU:HD13	11:FC:240:ILE:HG12	1.90	0.54
6:HL:127:ILE:HB	6:HL:229:ILE:HB	1.89	0.54
1:Bg:793:GLU:O	1:Bg:796:GLN:NE2	2.41	0.54
2:Id:107:ARG:HE	2:Id:109:LEU:HD11	1.73	0.54
2:JD:107:ARG:HB3	2:JD:155:GLU:HG2	1.90	0.54
7:JM:119:GLU:HG3	7:JM:139:ALA:HB3	1.89	0.54
7:JM:249:GLN:NE2	7:JM:267:ASN:OD1	2.40	0.54
2:KD:23:MET:N	2:KD:23:MET:SD	2.81	0.54
5:AK:177:ASN:O	5:AK:179:ARG:NH1	2.40	0.54
7:MM:249:GLN:NE2	7:MM:267:ASN:OD1	2.41	0.54
2:Md:71:LEU:O	2:Md:133:ARG:NH1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AL:212:ASN:N	6:AL:212:ASN:OD1	2.40	0.54
4:BH:190:PRO:HB2	4:BH:231:ARG:HD3	1.89	0.54
11:HC:167:PRO:O	11:HC:173:LYS:NZ	2.40	0.54
7:EM:171:ARG:HD2	7:EM:172:ASN:HB2	1.88	0.53
5:FK:50:ASP:N	5:FK:50:ASP:OD1	2.41	0.53
2:HD:132:LEU:HD12	2:HD:145:ILE:HG21	1.90	0.53
1:Ig:811:ASP:OD1	1:Ig:814:GLN:NE2	2.40	0.53
7:IM:273:ALA:HB1	7:IM:277:SER:HB2	1.89	0.53
4:WH:183:ASP:OD1	4:WH:187:ALA:N	2.40	0.53
6:AL:113:ASP:OD1	6:AL:113:ASP:N	2.41	0.53
7:AM:186:SER:HA	7:AM:205:TYR:HB2	1.89	0.53
8:AN:113:SER:OG	8:AN:114:LEU:N	2.41	0.53
11:JC:115:ARG:HG2	11:JC:131:ARG:HG2	1.89	0.53
11:MC:240:ILE:HB	11:AC:256:LEU:HD13	1.90	0.53
4:CH:345:LEU:HB2	4:CH:356:LEU:HB2	1.90	0.53
7:CM:279:ILE:HB	7:CM:298:VAL:HG22	1.90	0.53
1:OG:891:THR:OG1	1:OG:892:GLY:N	2.41	0.53
6:EL:163:ILE:HG23	6:EL:233:TRP:HB3	1.90	0.53
2:Ed:76:ALA:O	2:Ed:80:GLN:NE2	2.37	0.53
1:BG:951:HIS:H	1:BG:1027:THR:HG22	1.72	0.53
4:KH:315:THR:OG1	4:KH:316:ASN:N	2.41	0.53
5:LK:71:GLY:O	2:MD:27:LYS:NZ	2.42	0.53
8:LN:82:MET:N	8:LN:82:MET:SD	2.81	0.53
2:Md:76:ALA:O	2:Md:80:GLN:NE2	2.38	0.53
11:IC:101:LEU:HB2	11:IC:105:ILE:HG23	1.90	0.53
11:MC:110:LEU:HD23	11:MC:212:TYR:HB2	1.89	0.53
5:DK:90:ARG:NH1	5:DK:91:LEU:O	2.41	0.53
1:OG:958:SER:O	1:OG:962:SER:OG	2.25	0.53
11:AC:231:ASP:OD1	11:AC:231:ASP:N	2.42	0.53
2:AD:32:ASN:OD1	2:AD:32:ASN:N	2.41	0.53
2:AD:76:ALA:O	2:AD:80:GLN:NE2	2.41	0.53
5:EK:150:ASP:HB2	5:EK:152:ARG:HH22	1.74	0.53
4:FH:177:SER:HB2	4:FH:215:ILE:HB	1.89	0.53
4:GH:108:ASP:OD1	4:GH:108:ASP:N	2.40	0.53
4:GH:131:LYS:NZ	4:WH:141:LYS:O	2.40	0.53
6:GL:169:THR:OG1	6:GL:170:ASP:N	2.39	0.53
4:HH:229:ARG:NH2	1:XG:822:GLU:OE2	2.42	0.53
6:IL:226:ASN:O	6:IL:228:ARG:NH1	2.41	0.53
4:LH:138:GLU:HB3	4:YH:221:TYR:HE2	1.73	0.53
3:Lf:218:GLY:H	3:Lf:247:ILE:HD11	1.73	0.53
6:BL:127:ILE:HB	6:BL:229:ILE:HB	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:BM:273:ALA:HB1	7:BM:277:SER:HB2	1.90	0.53
8:BN:113:SER:OG	8:BN:114:LEU:N	2.41	0.53
3:Bf:245:LYS:NZ	3:Bf:256:THR:O	2.41	0.53
11:AC:226:TYR:HB3	11:AC:252:ALA:HB3	1.89	0.53
2:ED:77:TYR:OH	5:EK:130:ARG:NH1	2.40	0.53
2:ED:86:ASP:N	2:ED:86:ASP:OD1	2.41	0.53
6:EL:118:GLU:O	5:DK:66:LYS:NZ	2.36	0.53
2:FD:140:GLY:O	2:Fd:60:LYS:NZ	2.42	0.53
3:Ff:254:ILE:HD11	3:Ff:262:ILE:HB	1.90	0.53
1:CG:873:LEU:H	1:CG:1036:GLY:HA2	1.73	0.53
2:ID:85:VAL:HG12	5:IK:153:ILE:HA	1.90	0.53
5:IK:127:LYS:NZ	7:IM:301:MET:SD	2.76	0.53
6:KL:115:GLN:HB3	6:KL:126:ILE:HB	1.90	0.53
2:LD:36:ASP:N	2:LD:36:ASP:OD1	2.41	0.53
4:MH:315:THR:OG1	4:MH:316:ASN:N	2.39	0.53
4:YH:190:PRO:HB2	4:YH:231:ARG:HE	1.74	0.53
11:MC:230:ASP:N	11:MC:230:ASP:OD1	2.40	0.53
4:CH:255:ARG:NH1	4:CH:256:VAL:O	2.42	0.53
5:CK:115:THR:HG22	5:CK:155:PHE:HB2	1.89	0.53
5:DK:87:GLN:HB3	5:DK:128:ARG:HH12	1.73	0.53
1:AG:878:ASN:ND2	1:AG:1030:GLU:OE1	2.41	0.53
6:FL:124:THR:HA	6:FL:231:ILE:O	2.09	0.53
11:BC:230:ASP:OD1	11:BC:230:ASP:N	2.39	0.53
4:GH:266:MET:SD	4:GH:266:MET:N	2.74	0.53
7:GM:269:GLN:NE2	7:GM:290:ASP:OD1	2.41	0.53
11:GC:75:ARG:HB2	11:GC:188:ILE:HG12	1.91	0.53
3:HF:231:THR:HG23	4:XH:150:LYS:HZ2	1.72	0.53
6:HL:212:ASN:OD1	6:HL:212:ASN:N	2.41	0.53
7:LM:306:GLN:HB3	7:LM:309:LEU:HB2	1.91	0.53
4:VH:183:ASP:O	4:VH:255:ARG:NH1	2.41	0.53
8:BN:76:MET:SD	8:BN:76:MET:N	2.81	0.53
6:CL:123:ARG:NH1	6:CL:235:THR:OG1	2.41	0.53
1:KG:874:ASP:N	1:KG:874:ASP:OD1	2.40	0.53
6:DL:169:THR:OG1	6:DL:170:ASP:N	2.42	0.53
1:AG:946:SER:OG	1:AG:1030:GLU:O	2.24	0.53
6:FL:168:PHE:HB2	6:FL:228:ARG:HG2	1.91	0.53
11:GC:215:LEU:HG	11:GC:220:MET:HB2	1.91	0.53
3:HF:207:ARG:NH1	3:HF:240:GLY:O	2.41	0.53
2:Md:29:PRO:HB2	2:Md:32:ASN:HB2	1.91	0.53
3:XF:245:LYS:NZ	3:XF:256:THR:O	2.37	0.53
8:BN:103:CYS:N	8:BN:107:TYR:O	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IG:899:LEU:HD13	1:IG:919:MET:HG2	1.90	0.53
1:Eg:797:ARG:NH1	1:Eg:797:ARG:O	2.42	0.53
2:FD:55:MET:HG2	11:AC:211:ILE:HD11	1.90	0.53
8:FN:49:ASN:HB3	8:FN:59:VAL:HG23	1.91	0.53
2:JD:147:VAL:HG22	2:JD:154:VAL:HG22	1.91	0.53
4:LH:114:ASP:OD1	4:LH:117:ARG:NH1	2.40	0.53
3:MF:233:ARG:NH1	3:ZF:266:GLN:OE1	2.41	0.53
11:DC:86:GLN:OE1	11:DC:89:ASN:ND2	2.41	0.53
4:ZH:106:VAL:HA	4:ZH:109:LYS:HE2	1.91	0.53
7:AM:168:VAL:H	7:AM:187:GLY:HA3	1.73	0.53
7:BM:177:LEU:HD22	7:BM:181:PRO:HG2	1.91	0.53
7:CM:316:ASN:OD1	7:CM:316:ASN:N	2.40	0.53
2:DD:88:SER:HA	2:DD:120:SER:HA	1.91	0.53
6:EL:216:ASP:OD1	5:DK:185:ARG:NH1	2.41	0.53
11:BC:142:THR:HG22	11:BC:143:THR:HG23	1.91	0.53
2:GD:158:TYR:O	2:Gd:137:TYR:OH	2.27	0.53
4:GH:230:LEU:HD12	4:GH:233:LEU:HD12	1.90	0.53
8:GN:57:ARG:NH1	8:GN:66:SER:O	2.42	0.53
11:GC:114:ARG:NH2	2:Kd:86:ASP:OD2	2.42	0.53
2:ID:158:TYR:O	2:Id:137:TYR:OH	2.27	0.53
4:IH:203:ASN:HB3	4:IH:216:GLN:HB3	1.90	0.53
1:Lg:791:GLN:NE2	1:Lg:793:GLU:OE2	2.42	0.53
4:VH:297:VAL:HA	4:VH:358:VAL:HA	1.90	0.53
7:BM:115:ARG:HG3	7:BM:135:ASP:HB3	1.90	0.53
1:Cg:791:GLN:N	1:Cg:793:GLU:OE1	2.42	0.53
1:KG:919:MET:HG3	1:KG:930:ILE:HG23	1.89	0.53
7:DM:254:LYS:HE2	7:DM:272:LEU:HD23	1.91	0.53
8:EN:57:ARG:NH1	8:EN:66:SER:O	2.41	0.53
3:FF:263:LYS:NZ	3:FF:264:PHE:O	2.42	0.53
11:CC:166:LEU:H	1:DG:938:ASN:HD21	1.57	0.53
5:GK:111:LYS:NZ	5:GK:150:ASP:OD1	2.42	0.53
4:HH:188:PRO:O	4:HH:262:ASN:ND2	2.41	0.53
7:HM:137:TYR:HA	7:HM:156:GLU:O	2.09	0.53
4:AH:354:MET:HE1	8:MN:78:LEU:H	1.72	0.53
1:Kg:818:GLN:HE22	4:KH:176:VAL:HG13	1.74	0.53
1:EG:898:LYS:NZ	1:FG:865:THR:O	2.37	0.53
4:VH:322:PRO:HG2	4:VH:345:LEU:HD12	1.91	0.53
6:AL:124:THR:HA	6:AL:231:ILE:O	2.09	0.53
2:CD:29:PRO:HG2	6:CL:225:GLN:HA	1.91	0.53
1:HG:900:ILE:HG13	1:HG:918:THR:HB	1.91	0.53
4:EH:230:LEU:HB2	4:EH:233:LEU:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:EH:311:MET:HE3	4:EH:341:LYS:HA	1.90	0.53
4:FH:191:ILE:HA	4:FH:230:LEU:HA	1.91	0.53
7:FM:214:ILE:O	7:FM:215:ARG:NH1	2.39	0.53
7:FM:265:ALA:O	7:FM:283:ASN:ND2	2.40	0.53
8:GN:39:ASP:OD1	8:GN:39:ASP:N	2.41	0.53
3:Gf:235:GLY:HA2	3:Gf:243:MET:HE1	1.90	0.53
2:HD:23:MET:N	2:HD:23:MET:SD	2.82	0.53
11:KC:154:ASP:N	11:KC:154:ASP:OD1	2.41	0.53
2:JD:77:TYR:OH	5:JK:130:ARG:NH1	2.41	0.53
7:JM:156:GLU:OE1	7:JM:178:LYS:NZ	2.42	0.53
7:JM:279:ILE:HB	7:JM:298:VAL:HG22	1.91	0.53
2:KD:148:TYR:O	2:KD:152:GLN:N	2.41	0.53
5:KK:50:ASP:OD1	5:KK:50:ASP:N	2.41	0.53
4:LH:278:ASP:N	4:LH:278:ASP:OD1	2.41	0.53
3:Lf:254:ILE:HB	3:Lf:262:ILE:HG23	1.91	0.53
6:AL:42:CYS:SG	6:AL:43:PHE:N	2.82	0.53
3:Af:219:ARG:HA	3:Af:232:VAL:O	2.08	0.53
4:DH:183:ASP:OD1	4:DH:187:ALA:N	2.38	0.53
1:HG:871:ALA:HB2	1:HG:889:ILE:HD13	1.91	0.53
1:JG:900:ILE:HG13	1:JG:918:THR:HB	1.91	0.53
1:KG:935:ILE:HG22	1:KG:942:THR:HG22	1.89	0.53
1:PG:871:ALA:HB2	1:PG:889:ILE:HD13	1.92	0.53
1:Ag:793:GLU:O	1:Ag:796:GLN:NE2	2.41	0.53
6:EL:165:VAL:HG12	6:EL:231:ILE:HG12	1.90	0.52
2:Ed:71:LEU:O	2:Ed:133:ARG:NH1	2.42	0.52
11:CC:126:ARG:NH1	4:HH:273:PRO:O	2.38	0.52
5:GK:92:ASN:OD1	5:GK:92:ASN:N	2.42	0.52
6:JL:169:THR:OG1	6:JL:170:ASP:N	2.42	0.52
7:JM:229:ASN:N	7:JM:229:ASN:OD1	2.43	0.52
1:DG:958:SER:O	1:DG:962:SER:OG	2.26	0.52
3:LF:241:TYR:HB3	3:LF:256:THR:HG21	1.91	0.52
3:Mf:212:ILE:HD11	3:Mf:215:VAL:HB	1.91	0.52
4:ZH:108:ASP:OD1	4:ZH:108:ASP:N	2.41	0.52
1:NG:958:SER:O	1:NG:962:SER:OG	2.28	0.52
2:Gd:123:THR:HG21	2:Gd:131:ILE:HD11	1.91	0.52
3:Hf:245:LYS:H	3:Hf:256:THR:HA	1.75	0.52
2:ID:73:ILE:O	2:ID:133:ARG:NH2	2.41	0.52
2:ID:160:LYS:NZ	2:ID:162:TYR:O	2.42	0.52
4:IH:177:SER:HB2	4:IH:215:ILE:HB	1.89	0.52
9:IU:127:UNK:O	6:JL:232:GLN:NE2	2.42	0.52
4:JH:317:LEU:HD11	4:JH:349:TRP:HD1	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:JN:115:GLN:NE2	11:EC:70:GLN:OE1	2.42	0.52
2:KD:118:LEU:O	11:FC:97:ASN:ND2	2.42	0.52
7:KM:257:ASP:OD1	7:KM:257:ASP:N	2.41	0.52
6:LL:169:THR:OG1	6:LL:170:ASP:N	2.42	0.52
3:XF:207:ARG:NH2	3:XF:208:ILE:O	2.42	0.52
2:Ad:60:LYS:NZ	2:AD:140:GLY:O	2.42	0.52
1:IG:958:SER:O	1:IG:962:SER:OG	2.27	0.52
1:KG:958:SER:O	1:KG:962:SER:OG	2.27	0.52
1:OG:931:SER:O	1:OG:1042:THR:OG1	2.27	0.52
6:DL:212:ASN:O	6:DL:228:ARG:NH2	2.41	0.52
6:EL:177:HIS:HD1	7:EM:315:TYR:HH	1.56	0.52
7:FM:211:THR:HA	7:FM:230:ARG:O	2.09	0.52
1:BG:931:SER:O	1:BG:1042:THR:OG1	2.27	0.52
4:GH:181:PHE:O	4:GH:211:ASN:ND2	2.41	0.52
6:GL:127:ILE:HB	6:GL:229:ILE:HB	1.92	0.52
1:DG:876:SER:N	1:EG:940:ALA:O	2.42	0.52
8:LN:39:ASP:OD1	8:LN:39:ASP:N	2.42	0.52
6:AL:220:ILE:HG13	2:AD:39:ILE:HD12	1.91	0.52
4:YH:352:LYS:NZ	4:YH:354:MET:SD	2.75	0.52
4:ZH:229:ARG:HG2	4:ZH:236:PRO:HB3	1.91	0.52
2:Ad:29:PRO:O	2:Ad:32:ASN:ND2	2.42	0.52
1:MG:958:SER:O	1:MG:962:SER:OG	2.28	0.52
1:NG:885:ILE:O	1:NG:900:ILE:HA	2.08	0.52
2:Ed:55:MET:HE2	11:MC:213:ARG:HH11	1.75	0.52
6:FL:123:ARG:NH1	6:FL:235:THR:OG1	2.43	0.52
11:BC:192:ASN:ND2	2:GD:36:ASP:OD2	2.42	0.52
4:GH:231:ARG:NH2	1:Hg:824:THR:O	2.42	0.52
11:GC:30:SER:HB3	11:FC:184:TRP:HZ3	1.75	0.52
1:Bg:806:THR:O	1:Bg:810:GLN:NE2	2.43	0.52
6:JL:226:ASN:O	6:JL:228:ARG:NH1	2.41	0.52
2:LD:75:ASN:N	2:LD:75:ASN:OD1	2.39	0.52
8:MN:89:GLY:O	8:MN:104:ASN:ND2	2.42	0.52
4:WH:155:SER:OG	4:WH:255:ARG:NH1	2.43	0.52
11:DC:215:LEU:HB3	11:DC:220:MET:HB2	1.92	0.52
8:AN:57:ARG:NH1	8:AN:66:SER:O	2.42	0.52
3:BF:254:ILE:O	3:BF:261:VAL:HA	2.10	0.52
6:CL:200:ALA:O	7:CM:230:ARG:NH2	2.42	0.52
1:NG:917:ASN:HA	1:NG:931:SER:HA	1.92	0.52
3:Ff:245:LYS:HB3	3:Ff:255:LEU:HB3	1.92	0.52
3:HF:253:ARG:HH22	3:HF:255:LEU:HB2	1.74	0.52
7:HM:242:LYS:HA	7:HM:262:GLU:HB2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AH:315:THR:OG1	4:AH:316:ASN:N	2.42	0.52
2:KD:130:GLU:OE2	2:KD:133:ARG:NH1	2.41	0.52
2:KD:150:ASN:N	2:KD:150:ASN:OD1	2.39	0.52
5:LK:46:ASP:OD1	5:LK:46:ASP:N	2.38	0.52
10:VX:20:UNK:HA	10:VX:79:UNK:HA	1.90	0.52
3:WF:254:ILE:O	3:WF:261:VAL:HA	2.09	0.52
11:DC:218:MET:HB3	11:DC:220:MET:HG2	1.91	0.52
3:ZF:248:ASP:OD2	3:ZF:253:ARG:NH1	2.42	0.52
4:ZH:354:MET:N	4:ZH:354:MET:SD	2.83	0.52
3:Af:222:LEU:HB3	3:Af:230:LEU:HB2	1.91	0.52
1:OG:951:HIS:H	1:OG:1027:THR:HG22	1.75	0.52
6:DL:121:ASP:OD1	6:DL:121:ASP:N	2.40	0.52
5:EK:92:ASN:OD1	5:EK:92:ASN:N	2.41	0.52
5:FK:87:GLN:NE2	5:FK:173:ASP:OD1	2.43	0.52
2:Fd:71:LEU:O	2:Fd:133:ARG:NH1	2.42	0.52
4:HH:284:LEU:HD22	4:HH:328:MET:HB3	1.92	0.52
7:IM:261:ALA:HB3	7:IM:279:ILE:HG23	1.91	0.52
4:JH:321:SER:OG	11:DC:148:ARG:NH1	2.42	0.52
5:JK:177:ASN:O	5:JK:179:ARG:NH1	2.40	0.52
7:JM:306:GLN:OE1	3:Jf:253:ARG:NH1	2.42	0.52
1:DG:871:ALA:HB2	1:DG:889:ILE:HD13	1.91	0.52
8:KN:78:LEU:H	4:LH:354:MET:HE1	1.74	0.52
2:Kd:107:ARG:O	2:Kd:155:GLU:HA	2.10	0.52
4:LH:155:SER:OG	4:LH:255:ARG:NH1	2.43	0.52
7:MM:131:THR:OG1	7:MM:132:SER:N	2.43	0.52
7:AM:275:ASP:HA	7:AM:295:ASN:H	1.75	0.52
11:EC:103:GLU:OE2	11:EC:104:HIS:ND1	2.42	0.52
7:CM:162:VAL:HG12	7:CM:182:LYS:HB2	1.91	0.52
5:DK:177:ASN:O	5:DK:179:ARG:NH1	2.39	0.52
1:MG:912:MET:HB3	1:MG:944:LEU:HB2	1.92	0.52
6:EL:226:ASN:O	6:EL:228:ARG:NH1	2.38	0.52
2:FD:148:TYR:HB2	2:FD:153:VAL:HG22	1.91	0.52
11:CC:154:ASP:N	11:CC:154:ASP:OD1	2.40	0.52
11:BC:69:GLN:NE2	8:GN:115:GLN:OE1	2.43	0.52
8:GN:52:ASP:O	8:GN:56:GLY:N	2.43	0.52
5:HK:71:GLY:O	2:ID:27:LYS:NZ	2.42	0.52
1:CG:900:ILE:HG13	1:CG:918:THR:HB	1.91	0.52
2:ID:161:ILE:HD11	11:DC:103:HIS:HE2	1.75	0.52
4:JH:207:ASP:N	4:JH:207:ASP:OD1	2.43	0.52
6:ML:216:ASP:OD1	6:ML:216:ASP:N	2.41	0.52
3:Bf:219:ARG:HG2	3:Bf:233:ARG:HA	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:IC:105:ILE:HA	11:IC:140:PHE:HA	1.92	0.52
2:CD:160:LYS:NZ	2:CD:162:TYR:O	2.42	0.52
5:DK:78:ILE:HB	5:DK:180:VAL:HG23	1.92	0.52
1:IG:1003:ASN:HA	1:IG:1006:ILE:HD12	1.92	0.52
1:NG:935:ILE:HG23	1:NG:1040:LEU:HD22	1.91	0.52
1:OG:937:PRO:HD3	1:OG:1037:LEU:HA	1.92	0.52
11:AC:169:LYS:O	11:AC:174:LYS:NZ	2.42	0.52
6:EL:232:GLN:HE22	9:DU:128:UNK:HA	1.75	0.52
9:FU:128:UNK:HA	6:GL:232:GLN:HE22	1.75	0.52
3:GF:247:ILE:HG23	3:GF:254:ILE:HG12	1.90	0.52
6:GL:63:ASP:O	6:GL:88:GLY:N	2.43	0.52
11:GC:245:ARG:HB2	11:HC:127:ILE:HG23	1.92	0.52
11:GC:248:ARG:NH1	4:MH:270:GLU:OE2	2.42	0.52
7:HM:254:LYS:HE2	7:HM:272:LEU:HD23	1.92	0.52
7:HM:312:PHE:HB3	7:HM:316:ASN:HB2	1.92	0.52
5:IK:66:LYS:HB3	5:IK:77:SER:HB3	1.90	0.52
7:IM:257:ASP:N	7:IM:257:ASP:OD1	2.40	0.52
3:VF:208:ILE:HG13	3:VF:225:SER:H	1.74	0.52
1:FG:900:ILE:HD11	1:GG:865:THR:HG22	1.91	0.52
8:AN:56:GLY:HA3	8:AN:74:ALA:HB2	1.92	0.52
5:BK:76:ILE:HD13	5:BK:102:ILE:HD11	1.92	0.52
11:IC:110:LEU:HD23	11:IC:212:TYR:HB2	1.91	0.52
11:LC:166:LEU:HG	1:OG:938:ASN:HD21	1.74	0.52
11:MC:104:ASN:ND2	11:MC:141:ILE:O	2.42	0.52
5:DK:104:ALA:HA	5:DK:107:LYS:HE2	1.91	0.52
1:NG:912:MET:HB3	1:NG:944:LEU:HB2	1.92	0.52
1:PG:958:SER:O	1:PG:962:SER:OG	2.26	0.52
6:DL:130:ASP:N	6:DL:130:ASP:OD1	2.42	0.52
3:Df:217:PRO:O	3:Df:219:ARG:NH2	2.42	0.52
4:EH:249:ASP:N	4:EH:249:ASP:OD1	2.41	0.52
11:CC:54:ILE:HG23	1:CG:872:VAL:HG13	1.91	0.52
6:GL:226:ASN:O	6:GL:228:ARG:NH1	2.43	0.52
2:ID:111:LYS:NZ	2:ID:112:SER:O	2.43	0.52
2:ID:149:PRO:O	2:ID:152:GLN:NE2	2.43	0.52
1:Ig:818:GLN:NE2	4:IH:203:ASN:OD1	2.43	0.52
5:JK:162:ASP:N	5:JK:162:ASP:OD1	2.42	0.52
4:AH:155:SER:OG	4:AH:255:ARG:NH2	2.43	0.52
6:KL:212:ASN:OD1	6:KL:212:ASN:N	2.41	0.52
7:KM:273:ALA:HB1	7:KM:277:SER:HB2	1.92	0.52
4:LH:354:MET:HE3	4:LH:355:GLN:H	1.75	0.52
7:MM:257:ASP:N	7:MM:257:ASP:OD1	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:BL:212:ASN:N	6:BL:212:ASN:OD1	2.43	0.52
2:Bd:71:LEU:O	2:Bd:133:ARG:NH1	2.43	0.52
1:JG:875:THR:HA	1:KG:940:ALA:HB1	1.92	0.52
1:OG:1017:GLN:OE1	1:PG:1020:GLN:NE2	2.43	0.52
7:DM:214:ILE:O	7:DM:215:ARG:NH1	2.38	0.52
3:EF:207:ARG:NH1	3:EF:239:PRO:O	2.43	0.52
4:FH:188:PRO:O	4:FH:262:ASN:ND2	2.42	0.52
4:FH:344:VAL:HA	4:FH:356:LEU:O	2.10	0.52
5:FK:116:VAL:HG22	5:FK:182:ILE:HG22	1.92	0.52
3:IF:210:TYR:HA	3:IF:224:GLY:HA2	1.91	0.52
5:IK:90:ARG:NH2	5:IK:92:ASN:OD1	2.42	0.52
7:LM:286:LYS:O	7:LM:316:ASN:ND2	2.42	0.52
5:MK:72:GLN:HB3	5:MK:185:ARG:HG3	1.91	0.52
4:VH:149:PRO:HA	4:VH:246:LYS:O	2.10	0.52
11:DC:89:ASN:OD1	11:DC:89:ASN:N	2.43	0.52
7:CM:210:ASP:HA	7:CM:229:ASN:H	1.74	0.52
2:DD:136:ASP:O	2:Dd:60:LYS:NZ	2.41	0.52
1:MG:939:THR:HG22	1:MG:941:ARG:HG3	1.92	0.52
6:EL:145:TYR:HA	6:EL:148:LEU:HB2	1.91	0.51
5:GK:44:ARG:HA	8:GN:68:CYS:HA	1.91	0.51
2:Gd:148:TYR:HB2	2:Gd:153:VAL:HG12	1.92	0.51
11:KC:175:ILE:HA	11:KC:178:ILE:HG12	1.92	0.51
10:JX:22:UNK:HA	10:JX:77:UNK:HA	1.91	0.51
3:XF:265:SER:HB3	3:XF:268:ASP:HB3	1.91	0.51
7:AM:300:ASP:OD2	7:AM:302:ARG:NE	2.43	0.51
7:BM:183:VAL:O	7:BM:202:LEU:HA	2.10	0.51
7:BM:279:ILE:O	7:BM:298:VAL:HA	2.09	0.51
11:HC:245:ARG:HB3	11:IC:127:ILE:HG23	1.92	0.51
11:IC:109:VAL:HG13	11:IC:208:GLY:HA3	1.92	0.51
11:LC:88:ARG:NH1	2:DD:86:ASP:OD1	2.43	0.51
2:CD:150:ASN:N	2:CD:150:ASN:OD1	2.43	0.51
3:Cf:247:ILE:HA	3:Cf:254:ILE:HG22	1.91	0.51
4:DH:332:ASP:OD1	4:DH:332:ASP:N	2.43	0.51
6:DL:125:LEU:HB2	6:DL:231:ILE:HB	1.91	0.51
2:ED:147:VAL:HG22	2:ED:154:VAL:HG12	1.92	0.51
6:EL:212:ASN:N	6:EL:212:ASN:OD1	2.41	0.51
2:Ed:29:PRO:O	2:Ed:32:ASN:ND2	2.42	0.51
11:CC:61:GLU:O	8:HN:116:LYS:NZ	2.43	0.51
11:GC:176:TRP:O	11:GC:180:THR:OG1	2.28	0.51
4:HH:292:SER:HB2	4:HH:307:SER:HB3	1.93	0.51
4:HH:315:THR:OG1	4:HH:316:ASN:N	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:JX:21:UNK:N	10:JX:78:UNK:O	2.42	0.51
3:KF:265:SER:HB3	3:KF:268:ASP:HB3	1.92	0.51
6:KL:168:PHE:HB2	6:KL:228:ARG:HG2	1.92	0.51
5:MK:90:ARG:NH1	5:MK:91:LEU:O	2.42	0.51
3:WF:241:TYR:HB3	3:WF:256:THR:HG21	1.92	0.51
4:WH:317:LEU:O	4:WH:335:HIS:ND1	2.39	0.51
2:Dd:148:TYR:HB2	2:Dd:153:VAL:HG12	1.91	0.51
5:FK:72:GLN:HB2	5:FK:186:ARG:HB3	1.92	0.51
3:IF:219:ARG:HG2	4:JH:148:PRO:HD2	1.91	0.51
6:JL:212:ASN:N	6:JL:212:ASN:OD1	2.44	0.51
7:KM:306:GLN:HB3	7:KM:309:LEU:HB2	1.92	0.51
1:FG:958:SER:O	1:FG:962:SER:OG	2.28	0.51
4:ZH:230:LEU:HB2	4:ZH:233:LEU:HB2	1.91	0.51
11:MC:117:LEU:HD11	11:MC:125:ILE:HB	1.92	0.51
11:MC:221:VAL:HG12	11:MC:255:LEU:HD23	1.90	0.51
4:CH:112:PHE:HA	4:CH:115:MET:HE2	1.91	0.51
1:NG:1003:ASN:HA	1:NG:1006:ILE:HD12	1.92	0.51
2:ED:29:PRO:HG2	6:EL:225:GLN:HA	1.92	0.51
2:FD:105:ARG:NH2	2:Fd:130:GLU:OE2	2.44	0.51
1:Fg:794:ILE:HD13	4:GH:107:ILE:HG23	1.93	0.51
2:Fd:150:ASN:N	2:Fd:150:ASN:OD1	2.43	0.51
6:GL:136:SER:OG	7:GM:314:ARG:NH2	2.40	0.51
1:CG:931:SER:O	1:CG:1042:THR:OG1	2.29	0.51
6:KL:94:VAL:HA	6:KL:97:ILE:HG12	1.93	0.51
8:KN:39:ASP:N	8:KN:39:ASP:OD1	2.43	0.51
3:Lf:256:THR:OG1	3:Lf:257:SER:N	2.43	0.51
5:BK:86:ASP:OD1	5:BK:86:ASP:N	2.39	0.51
5:BK:110:ARG:NH1	8:BN:75:VAL:O	2.43	0.51
11:EC:241:ILE:HG12	11:FC:255:LEU:HD13	1.91	0.51
6:CL:120:GLY:O	6:CL:123:ARG:NH2	2.44	0.51
1:JG:874:ASP:OD1	1:JG:874:ASP:N	2.43	0.51
1:KG:867:ASP:OD1	1:KG:867:ASP:N	2.38	0.51
5:FK:92:ASN:OD1	5:FK:92:ASN:N	2.44	0.51
1:BG:921:ILE:HD12	1:BG:926:LYS:HD2	1.93	0.51
3:AF:266:GLN:NE2	3:ZF:235:GLY:O	2.43	0.51
4:HH:189:TRP:HE1	4:HH:232:GLY:H	1.57	0.51
6:HL:226:ASN:O	6:HL:228:ARG:NH1	2.42	0.51
7:IM:199:LYS:HA	7:IM:219:ALA:HB3	1.92	0.51
1:Jg:793:GLU:O	1:Jg:796:GLN:NE2	2.44	0.51
4:KH:273:PRO:O	11:FC:126:ARG:NH1	2.43	0.51
2:LD:114:SER:HA	11:HC:115:ASN:HD21	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AM:249:GLN:OE1	7:AM:267:ASN:ND2	2.42	0.51
4:BH:315:THR:OG1	4:BH:316:ASN:N	2.43	0.51
2:Cd:110:GLY:HA3	2:Cd:158:TYR:HB2	1.92	0.51
2:DD:130:GLU:HA	2:DD:133:ARG:HD2	1.93	0.51
1:HG:931:SER:O	1:HG:1042:THR:OG1	2.28	0.51
1:AG:958:SER:O	1:AG:962:SER:OG	2.27	0.51
7:FM:129:LEU:HB2	7:FM:150:ILE:HD11	1.93	0.51
1:BG:958:SER:O	1:BG:962:SER:OG	2.28	0.51
7:GM:273:ALA:HB1	7:GM:277:SER:HB2	1.92	0.51
4:HH:183:ASP:HA	4:HH:256:VAL:HB	1.93	0.51
7:HM:211:THR:HA	7:HM:230:ARG:O	2.10	0.51
1:Ig:802:LEU:HA	4:KH:115:MET:HE3	1.92	0.51
7:JM:313:ASP:N	7:JM:313:ASP:OD1	2.44	0.51
8:KN:77:ASP:OD1	8:KN:79:GLN:NE2	2.44	0.51
2:Kd:110:GLY:HA3	2:Kd:158:TYR:HB2	1.92	0.51
2:LD:47:SER:O	2:LD:51:SER:OG	2.29	0.51
3:LF:269:SER:OG	3:YF:233:ARG:NH1	2.44	0.51
2:MD:32:ASN:N	2:MD:32:ASN:OD1	2.40	0.51
5:MK:113:ALA:HA	5:MK:153:ILE:O	2.11	0.51
7:MM:158:VAL:HA	7:MM:178:LYS:HE2	1.93	0.51
2:Md:87:TRP:NE1	2:Md:90:PRO:O	2.43	0.51
11:FC:109:VAL:HG13	11:FC:208:GLY:HA3	1.92	0.51
11:IC:108:PRO:HD3	11:IC:138:ALA:HB2	1.92	0.51
11:LC:146:THR:HG23	11:LC:148:ARG:HB3	1.92	0.51
11:MC:243:ASP:N	11:MC:243:ASP:OD1	2.41	0.51
5:CK:162:ASP:OD1	5:CK:162:ASP:N	2.44	0.51
7:CM:117:ARG:HG2	7:CM:137:TYR:HB3	1.91	0.51
5:DK:110:ARG:NH1	8:DN:75:VAL:O	2.41	0.51
6:DL:113:ASP:OD1	6:DL:113:ASP:N	2.42	0.51
6:FL:51:GLN:NE2	6:FL:52:PRO:O	2.43	0.51
7:FM:257:ASP:OD1	7:FM:257:ASP:N	2.43	0.51
11:BC:97:ASN:ND2	2:GD:118:LEU:O	2.44	0.51
11:BC:146:THR:OG1	11:BC:147:TRP:N	2.44	0.51
2:GD:32:ASN:ND2	2:Gd:34:SER:OG	2.43	0.51
2:GD:88:SER:HA	2:GD:120:SER:HA	1.93	0.51
5:GK:117:THR:HG22	5:GK:157:GLN:HB2	1.93	0.51
11:GC:172:GLU:HA	11:GC:175:ILE:HG12	1.92	0.51
4:IH:253:ASP:OD1	4:IH:253:ASP:N	2.44	0.51
3:If:237:LYS:NZ	3:If:238:ILE:O	2.44	0.51
4:KH:150:LYS:H	4:KH:247:ALA:HA	1.75	0.51
7:KM:275:ASP:HA	7:KM:295:ASN:H	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LD:31:ASN:ND2	2:Ld:34:SER:O	2.43	0.51
4:LH:207:ASP:HB2	4:LH:210:SER:HB3	1.93	0.51
4:VH:324:TRP:NE1	4:CH:270:GLU:OE2	2.43	0.51
7:BM:165:ILE:HB	7:BM:185:ILE:HG12	1.92	0.51
7:BM:174:GLN:NE2	7:BM:193:GLN:O	2.43	0.51
6:CL:168:PHE:HB2	6:CL:228:ARG:HG2	1.93	0.51
1:HG:867:ASP:OD1	1:HG:867:ASP:N	2.44	0.51
1:Eg:811:ASP:O	1:Eg:814:GLN:NE2	2.40	0.51
11:CC:154:ASP:HB3	8:HN:84:CYS:HA	1.93	0.51
2:HD:36:ASP:OD1	2:HD:36:ASP:N	2.43	0.51
5:HK:150:ASP:O	5:HK:152:ARG:NH1	2.43	0.51
6:HL:168:PHE:HB2	6:HL:228:ARG:HG2	1.93	0.51
2:Hd:29:PRO:HB2	2:Hd:32:ASN:HB2	1.93	0.51
11:KC:240:ILE:HD11	11:LC:255:LEU:HD22	1.92	0.51
4:JH:301:ASP:OD1	4:JH:301:ASP:N	2.41	0.51
6:JL:177:HIS:HD1	7:JM:315:TYR:HH	1.53	0.51
6:KL:171:ASN:OD1	6:KL:217:ASN:ND2	2.44	0.51
5:LK:143:TYR:HE1	2:Ld:26:LYS:HE3	1.76	0.51
1:EG:958:SER:O	1:EG:962:SER:OG	2.29	0.51
2:Ad:148:TYR:HB2	2:Ad:153:VAL:HG12	1.92	0.51
3:BF:231:THR:HG23	4:CH:150:LYS:HE3	1.93	0.51
11:LC:266:VAL:HG12	2:Cd:97:ARG:HE	1.76	0.51
3:CF:213:GLN:HG3	4:CH:170:ARG:HH21	1.74	0.51
5:CK:45:VAL:HG12	5:CK:48:ALA:HB2	1.93	0.51
5:CK:72:GLN:HB2	5:CK:185:ARG:HG3	1.92	0.51
4:DH:315:THR:OG1	4:DH:316:ASN:N	2.43	0.51
11:AC:235:THR:OG1	11:AC:236:GLY:N	2.44	0.51
6:DL:124:THR:HA	6:DL:231:ILE:O	2.10	0.51
7:FM:201:THR:HG22	7:FM:221:LYS:HB2	1.92	0.51
11:BC:126:ARG:NH1	4:GH:273:PRO:O	2.40	0.51
4:IH:249:ASP:OD1	4:IH:249:ASP:N	2.44	0.51
1:Jg:807:GLN:O	1:Jg:810:GLN:NE2	2.44	0.51
2:LD:158:TYR:O	2:Ld:137:TYR:OH	2.29	0.51
6:LL:212:ASN:N	6:LL:212:ASN:OD1	2.41	0.51
5:AK:71:GLY:O	2:BD:27:LYS:NZ	2.44	0.51
2:Md:55:MET:SD	11:HC:213:ARG:NH1	2.84	0.51
7:AM:154:LYS:NZ	7:AM:156:GLU:OE2	2.43	0.51
6:BL:113:ASP:OD1	6:BL:113:ASP:N	2.40	0.51
11:HC:157:LYS:HD2	11:HC:159:GLU:HG3	1.93	0.51
3:Cf:212:ILE:HA	3:Cf:222:LEU:HG	1.93	0.51
1:PG:931:SER:O	1:PG:1042:THR:OG1	2.28	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Eg:810:GLN:HA	1:Eg:813:LYS:HB2	1.93	0.51
5:EK:54:ILE:HA	5:EK:57:MET:HG2	1.93	0.51
1:Fg:800:ASP:N	1:Fg:800:ASP:OD1	2.44	0.51
7:IM:193:GLN:HG3	7:IM:213:THR:HB	1.93	0.51
4:AH:170:ARG:HA	4:AH:242:ILE:O	2.10	0.51
5:MK:122:LYS:NZ	5:MK:129:GLU:OE2	2.39	0.51
7:AM:163:THR:HB	7:AM:183:VAL:HG12	1.93	0.51
11:IC:86:GLN:OE1	11:IC:89:ASN:ND2	2.44	0.51
1:NG:869:MET:HB2	1:NG:1041:PHE:HE1	1.75	0.51
2:AD:132:LEU:HD12	2:AD:145:ILE:HG21	1.93	0.51
7:EM:313:ASP:H	7:EM:316:ASN:HB2	1.75	0.50
4:FH:238:MET:N	4:FH:238:MET:SD	2.84	0.50
7:FM:302:ARG:HH11	7:FM:309:LEU:HD11	1.77	0.50
2:Fd:148:TYR:HB2	2:Fd:153:VAL:HG12	1.93	0.50
1:Gg:811:ASP:O	1:Gg:814:GLN:NE2	2.45	0.50
4:GH:304:ALA:HA	4:GH:312:TYR:O	2.11	0.50
7:GM:228:VAL:HG11	7:GM:231:LEU:HB2	1.93	0.50
2:HD:140:GLY:O	2:Hd:60:LYS:NZ	2.42	0.50
5:HK:142:GLU:OE2	6:HL:139:ARG:NH1	2.43	0.50
1:CG:869:MET:HB2	1:CG:1041:PHE:HE1	1.75	0.50
1:CG:958:SER:O	1:CG:962:SER:OG	2.28	0.50
2:Ld:97:ARG:HE	11:HC:263:ARG:HH12	1.60	0.50
5:AK:45:VAL:HG22	8:AN:67:THR:HB	1.93	0.50
8:MN:84:CYS:SG	8:MN:85:CYS:N	2.84	0.50
3:Mf:222:LEU:HD23	3:Mf:230:LEU:HD12	1.92	0.50
10:VX:21:UNK:O	10:VX:78:UNK:N	2.45	0.50
11:DC:175:ILE:HA	11:DC:178:ILE:HG12	1.93	0.50
5:BK:90:ARG:NH1	5:BK:91:LEU:O	2.43	0.50
4:CH:191:ILE:HA	4:CH:230:LEU:HA	1.92	0.50
1:LG:966:GLN:O	1:LG:970:ASN:ND2	2.44	0.50
1:MG:886:LEU:HA	1:MG:899:LEU:O	2.11	0.50
1:MG:1003:ASN:HA	1:MG:1006:ILE:HD12	1.93	0.50
11:AC:122:ASP:N	11:AC:122:ASP:OD1	2.44	0.50
6:DL:230:GLU:OE2	6:DL:232:GLN:NE2	2.43	0.50
2:Dd:29:PRO:HB2	2:Dd:32:ASN:HB2	1.92	0.50
6:EL:169:THR:O	6:EL:226:ASN:ND2	2.45	0.50
11:CC:54:ILE:HG12	1:CG:872:VAL:HG22	1.92	0.50
8:FN:39:ASP:N	8:FN:39:ASP:OD1	2.43	0.50
6:HL:63:ASP:O	6:HL:88:GLY:N	2.44	0.50
7:HM:119:GLU:HG3	7:HM:139:ALA:HB3	1.93	0.50
1:Bg:824:THR:HA	4:AH:231:ARG:HH12	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:IM:127:ASN:HB3	7:IM:147:ALA:HB3	1.93	0.50
2:JD:87:TRP:CD1	2:JD:89:GLY:H	2.29	0.50
5:JK:110:ARG:NH1	8:JN:75:VAL:O	2.43	0.50
2:Kd:81:ALA:HB3	2:Kd:128:LEU:HD11	1.93	0.50
7:AM:201:THR:HG22	7:AM:221:LYS:HB2	1.92	0.50
2:BD:77:TYR:OH	5:BK:130:ARG:NH1	2.44	0.50
4:BH:126:GLN:NE2	4:CH:108:ASP:OD2	2.42	0.50
4:BH:221:TYR:HB3	4:BH:244:GLY:HA3	1.93	0.50
6:BL:130:ASP:N	6:BL:130:ASP:OD1	2.43	0.50
11:FC:231:LEU:HB2	11:FC:244:ASP:HB3	1.94	0.50
11:JC:107:LEU:HD12	11:JC:108:PRO:HD2	1.92	0.50
2:Cd:139:ALA:HB1	2:Cd:143:ALA:HB3	1.92	0.50
2:Fd:97:ARG:HH22	11:BC:263:ARG:HD2	1.76	0.50
2:HD:24:LYS:O	6:HL:110:GLN:NE2	2.44	0.50
4:HH:155:SER:OG	4:HH:255:ARG:NH1	2.44	0.50
7:HM:173:LEU:O	7:HM:174:GLN:NE2	2.43	0.50
7:HM:189:VAL:HB	7:HM:207:ILE:HG22	1.93	0.50
1:Bg:818:GLN:O	4:BH:205:GLN:NE2	2.45	0.50
5:JK:142:GLU:OE2	6:JL:139:ARG:NH1	2.45	0.50
7:KM:308:ASP:OD2	3:Kf:263:LYS:NZ	2.44	0.50
2:LD:125:ASP:OD2	5:LK:138:ARG:NH2	2.41	0.50
3:LF:250:LEU:HG	3:LF:251:GLN:HG3	1.92	0.50
2:Ld:78:ASN:N	2:Ld:78:ASN:OD1	2.43	0.50
5:BK:116:VAL:HG22	5:BK:182:ILE:HG13	1.94	0.50
6:BL:169:THR:OG1	6:BL:170:ASP:N	2.41	0.50
1:GG:958:SER:O	1:GG:962:SER:OG	2.29	0.50
1:Cg:816:GLU:O	4:CH:216:GLN:NE2	2.43	0.50
1:HG:919:MET:HG3	1:HG:930:ILE:HG23	1.91	0.50
1:NG:931:SER:O	1:NG:1042:THR:OG1	2.28	0.50
1:OG:876:SER:OG	1:OG:1031:VAL:O	2.27	0.50
7:DM:191:LEU:HD21	7:DM:194:LEU:HD23	1.92	0.50
5:EK:87:GLN:NE2	5:EK:173:ASP:OD1	2.45	0.50
6:FL:138:PRO:HD3	7:FM:314:ARG:HH22	1.76	0.50
5:GK:68:ALA:HB3	5:GK:75:LEU:HG	1.94	0.50
6:GL:165:VAL:HG12	6:GL:231:ILE:HG12	1.93	0.50
5:HK:76:ILE:HB	5:HK:182:ILE:HG12	1.92	0.50
5:JK:72:GLN:HB3	5:JK:185:ARG:HG3	1.93	0.50
5:LK:72:GLN:HB2	5:LK:186:ARG:HB3	1.93	0.50
3:YF:223:ILE:HA	3:YF:228:SER:O	2.12	0.50
11:DC:230:ASP:HB3	11:DC:245:ARG:HG3	1.93	0.50
7:BM:257:ASP:N	7:BM:257:ASP:OD1	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:LG:1024:ASN:OD1	1:LG:1024:ASN:N	2.45	0.50
1:Ag:804:ALA:O	1:Ag:807:GLN:NE2	2.44	0.50
2:AD:23:MET:N	2:AD:23:MET:SD	2.85	0.50
1:AG:931:SER:O	1:AG:1042:THR:OG1	2.30	0.50
4:GH:169:ILE:HD12	4:GH:252:VAL:HG21	1.93	0.50
4:GH:173:GLN:HA	4:GH:217:ALA:HB3	1.94	0.50
7:GM:163:THR:HB	7:GM:183:VAL:HG12	1.92	0.50
11:GC:101:LEU:HB2	11:GC:105:ILE:HG23	1.93	0.50
11:KC:44:ARG:O	11:KC:47:LYS:NZ	2.42	0.50
2:LD:130:GLU:HA	2:LD:133:ARG:HD2	1.93	0.50
6:BL:127:ILE:HG23	6:BL:132:TYR:HD2	1.77	0.50
3:CF:208:ILE:HG13	3:CF:225:SER:H	1.77	0.50
6:EL:168:PHE:HB2	6:EL:228:ARG:HG2	1.93	0.50
9:GU:127:UNK:O	6:HL:232:GLN:NE2	2.44	0.50
3:Gf:245:LYS:NZ	3:Gf:256:THR:O	2.40	0.50
11:GC:127:ILE:HG12	11:FC:245:ARG:HB2	1.93	0.50
4:IH:106:VAL:HA	4:IH:109:LYS:HE2	1.93	0.50
7:IM:211:THR:HA	7:IM:230:ARG:O	2.12	0.50
1:Kg:811:ASP:O	1:Kg:814:GLN:NE2	2.39	0.50
4:LH:117:ARG:HB2	1:YG:797:ARG:HH22	1.75	0.50
5:MK:50:ASP:OD1	5:MK:50:ASP:N	2.44	0.50
7:MM:193:GLN:NE2	7:MM:195:ASP:OD2	2.45	0.50
4:YH:289:PRO:HG2	4:YH:292:SER:HB3	1.92	0.50
4:YH:343:PRO:HA	4:YH:358:VAL:HG12	1.93	0.50
11:DC:172:GLU:HA	11:DC:175:ILE:HG12	1.94	0.50
7:BM:141:GLU:OE2	7:BM:143:THR:OG1	2.29	0.50
11:EC:229:HIS:HB3	11:EC:248:LEU:HG	1.94	0.50
11:HC:263:ARG:HH11	11:HC:264:ALA:H	1.60	0.50
2:CD:98:ILE:HG21	2:CD:132:LEU:HD21	1.94	0.50
4:CH:173:GLN:NE2	4:CH:218:THR:O	2.42	0.50
1:IG:871:ALA:HB2	1:IG:889:ILE:HD13	1.92	0.50
1:IG:929:SER:O	1:IG:1043:GLN:NE2	2.44	0.50
11:AC:115:ARG:HG2	11:AC:131:ARG:HG2	1.92	0.50
8:DN:102:VAL:HA	8:DN:108:VAL:HA	1.92	0.50
7:FM:199:LYS:HA	7:FM:219:ALA:HB3	1.94	0.50
8:FN:63:GLY:HA3	2:GD:27:LYS:HB2	1.93	0.50
4:HH:256:VAL:HG12	4:HH:258:GLY:H	1.77	0.50
7:HM:173:LEU:HD22	7:HM:175:ILE:HD11	1.94	0.50
5:IK:86:ASP:N	5:IK:86:ASP:OD1	2.39	0.50
7:IM:290:ASP:HB3	7:IM:298:VAL:HG21	1.93	0.50
2:Jd:110:GLY:HA3	2:Jd:158:TYR:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AH:229:ARG:HG2	4:AH:236:PRO:HB3	1.92	0.50
4:AH:250:TYR:HE1	4:ZH:225:ASN:HD22	1.58	0.50
2:Ld:36:ASP:OD1	2:Ld:36:ASP:N	2.45	0.50
4:MH:114:ASP:OD1	4:MH:117:ARG:NH1	2.45	0.50
4:VH:304:ALA:HA	4:VH:312:TYR:O	2.12	0.50
4:XH:190:PRO:HA	4:XH:211:ASN:HB3	1.94	0.50
3:YF:247:ILE:HG12	3:YF:254:ILE:HG23	1.92	0.50
11:DC:189:ASP:O	11:DC:193:THR:OG1	2.30	0.50
3:ZF:246:LEU:HB3	3:ZF:255:LEU:HD12	1.92	0.50
4:ZH:330:SER:OG	4:ZH:334:THR:OG1	2.29	0.50
11:HC:243:ASP:N	11:HC:243:ASP:OD1	2.41	0.50
7:CM:306:GLN:HG2	7:CM:308:ASP:H	1.77	0.50
1:PG:1042:THR:OG1	1:PG:1043:GLN:OE1	2.29	0.50
1:Fg:802:LEU:HA	4:GH:115:MET:HE3	1.93	0.50
4:FH:115:MET:HG3	1:Dg:801:MET:HG3	1.92	0.50
3:GF:207:ARG:NH1	3:GF:239:PRO:O	2.45	0.50
7:GM:162:VAL:HG12	7:GM:182:LYS:HB2	1.93	0.50
11:GC:267:ALA:HB3	2:Kd:84:SER:H	1.76	0.50
6:HL:102:LYS:HA	6:HL:105:ILE:HD12	1.94	0.50
1:CG:885:ILE:O	1:CG:900:ILE:HA	2.12	0.50
5:IK:50:ASP:N	5:IK:50:ASP:OD1	2.44	0.50
7:IM:210:ASP:OD1	7:IM:210:ASP:N	2.45	0.50
8:IN:46:GLY:O	8:IN:61:ASN:ND2	2.44	0.50
6:KL:125:LEU:HB2	6:KL:231:ILE:HB	1.94	0.50
2:Ld:29:PRO:O	2:Ld:32:ASN:ND2	2.45	0.50
1:WG:797:ARG:NH1	1:WG:801:MET:SD	2.85	0.50
7:AM:227:ILE:HG13	3:Af:213:GLN:HE21	1.76	0.50
6:BL:230:GLU:OE2	6:BL:232:GLN:NE2	2.45	0.50
1:GG:938:ASN:HB2	11:FC:51:MET:HB3	1.93	0.50
11:HC:140:PHE:HE2	11:IC:123:GLN:HA	1.76	0.50
4:CH:170:ARG:HG3	4:CH:249:ASP:H	1.76	0.50
5:CK:66:LYS:NZ	6:DL:118:GLU:O	2.42	0.50
6:CL:169:THR:OG1	6:CL:170:ASP:N	2.44	0.50
1:IG:919:MET:HG3	1:IG:930:ILE:HG23	1.93	0.50
11:AC:110:VAL:HG13	11:AC:209:GLY:HA3	1.93	0.50
1:AG:874:ASP:OD1	1:AG:874:ASP:N	2.43	0.50
7:EM:199:LYS:HA	7:EM:219:ALA:HB3	1.94	0.50
2:Gd:149:PRO:O	2:Gd:152:GLN:NE2	2.44	0.50
2:HD:29:PRO:HG2	6:HL:225:GLN:HA	1.93	0.50
5:IK:46:ASP:OD1	5:IK:46:ASP:N	2.41	0.50
2:KD:76:ALA:O	2:KD:80:GLN:NE2	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:LM:165:ILE:HB	7:LM:185:ILE:HG12	1.93	0.50
1:EG:904:ASN:OD1	1:EG:904:ASN:N	2.45	0.50
8:MN:56:GLY:HA2	8:MN:71:THR:HG22	1.93	0.50
2:Md:36:ASP:N	2:Md:36:ASP:OD1	2.44	0.50
11:DC:109:VAL:HG13	11:DC:208:GLY:HA3	1.94	0.50
5:CK:92:ASN:OD1	5:CK:92:ASN:N	2.44	0.50
6:CL:113:ASP:OD1	6:CL:113:ASP:N	2.38	0.50
7:DM:308:ASP:OD2	3:Df:253:ARG:NH2	2.45	0.50
4:GH:132:GLN:HG3	4:WH:145:PRO:HB3	1.94	0.49
6:GL:91:VAL:HA	6:GL:94:VAL:HG22	1.93	0.49
4:IH:150:LYS:HZ2	3:XF:219:ARG:HH22	1.60	0.49
2:LD:88:SER:HA	2:LD:120:SER:HA	1.94	0.49
5:LK:78:ILE:HB	5:LK:180:VAL:HG23	1.93	0.49
7:LM:146:LEU:HD23	7:LM:165:ILE:HG12	1.94	0.49
1:FG:1015:TRP:NE1	1:GG:956:TYR:OH	2.46	0.49
7:AM:210:ASP:O	7:AM:230:ARG:N	2.41	0.49
10:AX:20:UNK:HA	10:AX:79:UNK:HA	1.92	0.49
5:BK:177:ASN:O	5:BK:179:ARG:NH1	2.44	0.49
4:DH:171:LEU:HD11	4:DH:241:LEU:HB3	1.94	0.49
1:IG:880:ASP:OD1	1:IG:880:ASP:N	2.44	0.49
7:DM:275:ASP:OD1	7:DM:275:ASP:N	2.44	0.49
5:EK:185:ARG:NH2	6:FL:213:ALA:O	2.44	0.49
7:EM:288:ARG:NH2	7:EM:316:ASN:O	2.45	0.49
8:EN:102:VAL:HG12	8:EN:108:VAL:HB	1.95	0.49
2:Ed:66:SER:OG	2:Ed:67:LYS:NZ	2.44	0.49
11:CC:151:LEU:HD21	11:CC:202:ILE:HG21	1.94	0.49
4:FH:170:ARG:NH1	4:FH:249:ASP:OD1	2.45	0.49
9:FU:127:UNK:O	6:GL:232:GLN:NE2	2.45	0.49
5:HK:115:THR:HG22	5:HK:155:PHE:HB2	1.94	0.49
6:HL:193:LEU:HA	6:HL:196:ASN:HD22	1.76	0.49
5:IK:76:ILE:HG13	5:IK:182:ILE:HB	1.93	0.49
7:JM:199:LYS:HA	7:JM:219:ALA:HB3	1.94	0.49
3:Jf:251:GLN:HB3	3:Jf:253:ARG:HH11	1.76	0.49
1:DG:1003:ASN:HA	1:DG:1006:ILE:HD12	1.93	0.49
5:KK:87:GLN:OE1	5:KK:128:ARG:NH1	2.46	0.49
4:LH:199:PRO:HG2	1:Mg:819:VAL:HG13	1.93	0.49
4:LH:320:LEU:HD11	4:LH:348:SER:HB3	1.94	0.49
7:LM:157:ALA:O	7:LM:178:LYS:NZ	2.45	0.49
5:AK:76:ILE:HG13	5:AK:182:ILE:HB	1.94	0.49
5:AK:92:ASN:OD1	5:AK:92:ASN:N	2.45	0.49
6:ML:226:ASN:O	6:ML:228:ARG:NH1	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:VH:354:MET:SD	4:VH:354:MET:N	2.84	0.49
3:WF:251:GLN:HB2	3:WF:253:ARG:HE	1.77	0.49
4:XH:182:LEU:HB2	4:XH:255:ARG:HD2	1.94	0.49
11:DC:219:ASN:ND2	11:DC:261:GLU:O	2.44	0.49
7:AM:128:ASN:HB3	7:AM:130:ARG:HH12	1.77	0.49
11:EC:176:ILE:HA	11:EC:179:ILE:HG12	1.94	0.49
3:DF:251:GLN:OE1	3:DF:253:ARG:NH1	2.42	0.49
1:OG:893:LYS:HD2	8:DN:98:SER:HA	1.94	0.49
2:AD:68:ASP:OD2	2:AD:70:THR:OG1	2.29	0.49
7:EM:288:ARG:NH1	7:EM:318:GLN:O	2.39	0.49
3:FF:208:ILE:HG13	3:FF:225:SER:H	1.77	0.49
1:BG:1003:ASN:HA	1:BG:1006:ILE:HD12	1.93	0.49
2:GD:32:ASN:OD1	2:GD:32:ASN:N	2.45	0.49
4:GH:170:ARG:NH1	4:GH:249:ASP:OD1	2.44	0.49
2:Gd:36:ASP:OD1	2:Gd:36:ASP:N	2.44	0.49
11:GC:154:ASP:HB3	8:LN:84:CYS:HA	1.93	0.49
7:HM:256:HIS:O	7:HM:259:SER:OG	2.30	0.49
7:IM:271:SER:OG	7:IM:290:ASP:OD1	2.31	0.49
2:JD:62:ILE:HD13	11:EC:266:ALA:HB2	1.94	0.49
1:DG:1017:GLN:OE1	1:EG:1020:GLN:NE2	2.45	0.49
1:DG:1017:GLN:NE2	1:DG:1018:GLN:OE1	2.42	0.49
4:LH:173:GLN:HA	4:LH:217:ALA:HB3	1.93	0.49
2:Ld:36:ASP:HA	2:Ld:39:ILE:HD12	1.94	0.49
7:MM:254:LYS:HE2	7:MM:272:LEU:HD23	1.94	0.49
10:YX:21:UNK:N	10:YX:78:UNK:O	2.46	0.49
7:AM:171:ARG:O	7:AM:190:ASN:ND2	2.46	0.49
4:BH:284:LEU:HD11	4:BH:330:SER:HB3	1.94	0.49
8:BN:41:CYS:HB2	8:BN:48:ILE:HD11	1.94	0.49
1:GG:972:PHE:HB3	1:GG:1005:VAL:HG22	1.94	0.49
5:CK:76:ILE:HG13	5:CK:182:ILE:HB	1.93	0.49
4:DH:152:THR:O	4:DH:250:TYR:N	2.42	0.49
5:DK:50:ASP:OD1	5:DK:50:ASP:N	2.44	0.49
1:HG:886:LEU:HD11	1:IG:868:ILE:HD11	1.94	0.49
1:JG:886:LEU:HD11	1:KG:868:ILE:HD11	1.93	0.49
6:FL:210:ASP:OD1	6:FL:210:ASP:N	2.43	0.49
7:FM:207:ILE:HG13	7:FM:226:GLY:HA3	1.94	0.49
7:GM:279:ILE:O	7:GM:298:VAL:HA	2.12	0.49
3:HF:248:ASP:HB3	3:HF:253:ARG:HB3	1.94	0.49
7:IM:206:TRP:HZ2	3:If:219:ARG:HD2	1.76	0.49
7:IM:273:ALA:HB2	7:IM:279:ILE:HD11	1.94	0.49
2:JD:92:GLU:OE1	2:JD:158:TYR:OH	2.29	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DG:912:MET:HB3	1:DG:944:LEU:HB2	1.93	0.49
2:MD:73:ILE:O	2:MD:133:ARG:NH2	2.37	0.49
3:MF:263:LYS:NZ	3:MF:264:PHE:O	2.43	0.49
7:AM:128:ASN:O	7:AM:130:ARG:NH1	2.45	0.49
2:Ad:81:ALA:HB3	2:Ad:128:LEU:HD11	1.93	0.49
2:Bd:48:VAL:HG11	11:JC:94:ILE:HG13	1.94	0.49
11:IC:258:ASN:OD1	11:IC:258:ASN:N	2.44	0.49
4:CH:279:LEU:HD11	4:CH:289:PRO:HB3	1.93	0.49
5:CK:116:VAL:HG12	5:CK:182:ILE:HG12	1.95	0.49
1:MG:871:ALA:HB2	1:MG:889:ILE:HD13	1.95	0.49
6:DL:212:ASN:N	6:DL:212:ASN:OD1	2.44	0.49
5:EK:68:ALA:HB3	5:EK:75:LEU:HB2	1.94	0.49
5:GK:177:ASN:N	5:GK:177:ASN:OD1	2.45	0.49
7:GM:145:ARG:HH22	7:GM:162:VAL:HG23	1.77	0.49
11:GC:145:PRO:HB3	11:GC:149:GLN:HE22	1.77	0.49
10:HX:25:UNK:N	10:HX:71:UNK:O	2.45	0.49
2:Hd:72:THR:OG1	2:Hd:73:ILE:N	2.45	0.49
6:JL:113:ASP:OD1	6:JL:113:ASP:N	2.45	0.49
6:KL:210:ASP:OD1	6:KL:210:ASP:N	2.46	0.49
2:MD:67:LYS:HE3	2:Md:62:ILE:HD11	1.94	0.49
3:VF:208:ILE:HD11	3:VF:224:GLY:HA3	1.95	0.49
4:VH:192:ALA:HB2	4:VH:231:ARG:HA	1.93	0.49
2:Ad:36:ASP:OD1	2:Ad:36:ASP:N	2.44	0.49
4:BH:173:GLN:HA	4:BH:217:ALA:HB3	1.95	0.49
7:BM:249:GLN:OE1	7:BM:267:ASN:ND2	2.45	0.49
7:CM:214:ILE:O	7:CM:215:ARG:NH1	2.41	0.49
1:JG:1003:ASN:HA	1:JG:1006:ILE:HD12	1.93	0.49
1:NG:969:GLY:HA3	1:NG:1009:ALA:HB2	1.94	0.49
6:DL:159:PRO:O	6:DL:202:ARG:NH1	2.46	0.49
2:ED:27:LYS:HB2	8:DN:63:GLY:HA3	1.95	0.49
5:EK:76:ILE:HG21	5:EK:102:ILE:HD11	1.95	0.49
4:FH:282:HIS:HB3	4:FH:287:VAL:HB	1.95	0.49
2:Fd:82:ARG:NH2	2:Fd:126:GLU:O	2.41	0.49
3:GF:246:LEU:HD23	3:GF:255:LEU:HD12	1.94	0.49
6:GL:124:THR:HA	6:GL:231:ILE:O	2.12	0.49
7:HM:210:ASP:OD1	7:HM:229:ASN:ND2	2.45	0.49
2:ID:123:THR:O	2:ID:124:LYS:NZ	2.44	0.49
11:KC:263:ARG:NH1	2:CD:62:ILE:O	2.45	0.49
4:JH:183:ASP:OD1	4:JH:187:ALA:N	2.45	0.49
4:AH:176:VAL:HG22	1:Ag:818:GLN:HE22	1.77	0.49
3:KF:231:THR:HG23	4:YH:150:LYS:HE3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:KH:206:TRP:NE1	4:KH:210:SER:O	2.45	0.49
5:KK:162:ASP:N	5:KK:162:ASP:OD1	2.45	0.49
7:KM:256:HIS:O	7:KM:259:SER:OG	2.29	0.49
6:LL:183:GLN:NE2	6:LL:206:GLU:OE2	2.44	0.49
6:LL:226:ASN:O	6:LL:228:ARG:NH1	2.45	0.49
7:LM:149:ASN:OD1	7:LM:149:ASN:N	2.43	0.49
3:Lf:221:TRP:HE1	3:Lf:229:THR:HB	1.76	0.49
7:MM:290:ASP:N	7:MM:290:ASP:OD1	2.45	0.49
4:WH:311:MET:HG3	4:WH:341:LYS:HA	1.94	0.49
4:XH:313:VAL:HG13	4:XH:337:TYR:HB2	1.93	0.49
4:YH:345:LEU:HB2	4:YH:356:LEU:HG	1.94	0.49
11:EC:199:ASN:OD1	11:EC:202:ARG:NH1	2.45	0.49
11:FC:151:LEU:HD21	11:FC:202:ILE:HG21	1.93	0.49
5:CK:109:PHE:O	5:CK:111:LYS:NZ	2.46	0.49
5:DK:46:ASP:OD1	5:DK:46:ASP:N	2.42	0.49
4:EH:207:ASP:O	4:EH:210:SER:OG	2.31	0.49
4:EH:277:ASN:HD21	4:EH:279:LEU:HG	1.77	0.49
8:EN:58:LEU:HB2	8:EN:66:SER:HB3	1.93	0.49
2:Fd:78:ASN:ND2	2:Fd:102:ALA:O	2.41	0.49
4:GH:221:TYR:HA	4:GH:243:PRO:HG2	1.94	0.49
7:GM:124:VAL:O	7:GM:144:THR:HA	2.12	0.49
2:Hd:79:LEU:O	2:Hd:127:SER:OG	2.30	0.49
1:CG:867:ASP:OD1	1:CG:867:ASP:N	2.46	0.49
6:JL:121:ASP:O	6:JL:123:ARG:NH1	2.45	0.49
2:Jd:105:ARG:HH22	2:Jd:151:SER:HB2	1.78	0.49
7:KM:271:SER:OG	7:KM:290:ASP:OD1	2.30	0.49
2:Kd:87:TRP:NE1	2:Kd:90:PRO:O	2.45	0.49
1:VG:823:GLY:HA3	4:CH:206:TRP:HH2	1.77	0.49
2:Ad:105:ARG:HH22	2:Ad:151:SER:HB2	1.78	0.49
2:Ad:119:ILE:HD12	2:Ad:138:GLN:HB3	1.94	0.49
11:HC:139:HIS:ND1	11:HC:140:PHE:O	2.42	0.49
2:CD:79:LEU:HA	2:CD:128:LEU:HD12	1.95	0.49
2:DD:87:TRP:CD1	2:DD:89:GLY:H	2.31	0.49
1:Dg:807:GLN:OE1	1:Dg:810:GLN:NE2	2.45	0.49
1:JG:867:ASP:OD1	1:JG:867:ASP:N	2.40	0.49
1:AG:900:ILE:HG13	1:AG:918:THR:HB	1.94	0.49
4:EH:196:LEU:HD22	4:EH:204:ILE:HD13	1.94	0.49
7:EM:193:GLN:HG3	7:EM:213:THR:HB	1.93	0.49
2:FD:36:ASP:OD1	2:FD:36:ASP:N	2.44	0.49
1:Hg:820:TYR:OH	1:Hg:822:GLU:OE1	2.29	0.49
7:IM:306:GLN:HB2	7:IM:309:LEU:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:JK:138:ARG:NH1	7:JM:318:GLN:O	2.45	0.49
4:AH:207:ASP:OD1	4:AH:207:ASP:N	2.46	0.49
5:LK:57:MET:HG3	5:LK:67:VAL:HG11	1.94	0.49
7:LM:134:LEU:HD13	7:LM:136:LEU:HD23	1.94	0.49
1:EG:891:THR:OG1	1:EG:892:GLY:N	2.46	0.49
1:EG:1003:ASN:HA	1:EG:1006:ILE:HD12	1.95	0.49
5:MK:86:ASP:OD1	5:MK:86:ASP:N	2.42	0.49
4:VH:279:LEU:HD21	4:VH:289:PRO:HB3	1.94	0.49
4:XH:315:THR:OG1	4:XH:316:ASN:N	2.46	0.49
8:BN:102:VAL:HA	8:BN:108:VAL:HA	1.94	0.49
2:Bd:76:ALA:O	2:Bd:80:GLN:NE2	2.40	0.49
11:MC:121:ASP:OD1	11:MC:124:SER:OG	2.30	0.49
2:CD:77:TYR:OH	5:CK:130:ARG:NH1	2.46	0.49
4:CH:203:ASN:HB3	4:CH:216:GLN:HB3	1.93	0.49
7:DM:157:ALA:O	7:DM:178:LYS:NZ	2.43	0.49
7:EM:271:SER:O	7:EM:290:ASP:HA	2.13	0.49
6:FL:94:VAL:HA	6:FL:97:ILE:HG12	1.95	0.49
1:BG:912:MET:HB3	1:BG:944:LEU:HB2	1.95	0.49
2:GD:70:THR:HG22	2:GD:133:ARG:HD3	1.94	0.49
6:IL:47:TYR:OH	6:IL:142:GLU:OE1	2.31	0.49
1:DG:946:SER:OG	1:DG:1030:GLU:O	2.27	0.49
4:KH:229:ARG:HG2	4:KH:236:PRO:HB3	1.95	0.49
2:Kd:79:LEU:O	2:Kd:127:SER:OG	2.31	0.49
4:LH:320:LEU:HB2	4:LH:346:LEU:HD23	1.95	0.49
6:LL:126:ILE:HA	6:LL:229:ILE:O	2.12	0.49
1:Mg:813:LYS:NZ	4:ZH:138:GLU:OE2	2.46	0.49
4:MH:316:ASN:N	4:MH:316:ASN:OD1	2.44	0.49
6:ML:49:ASN:ND2	7:MM:293:ALA:O	2.46	0.49
4:WH:204:ILE:HD11	4:WH:226:LEU:HD11	1.94	0.49
6:AL:108:ASP:HA	6:AL:111:LYS:HE2	1.95	0.49
1:FG:1019:ALA:O	1:FG:1023:PHE:HB2	2.13	0.49
1:JG:958:SER:O	1:JG:962:SER:OG	2.29	0.49
7:DM:149:ASN:N	7:DM:149:ASN:OD1	2.45	0.49
4:EH:296:VAL:HB	4:EH:359:GLU:HB2	1.95	0.49
8:EN:76:MET:HB2	8:EN:78:LEU:HD23	1.95	0.49
5:GK:146:SER:HB2	2:Gd:29:PRO:HG3	1.95	0.49
3:Gf:256:THR:HG23	3:Gf:258:SER:H	1.77	0.49
7:HM:249:GLN:OE1	7:HM:267:ASN:ND2	2.45	0.49
1:Ig:820:TYR:OH	1:Ig:822:GLU:OE2	2.31	0.49
2:Id:108:VAL:HG12	2:Id:156:LEU:HB2	1.95	0.49
8:JN:82:MET:N	8:JN:82:MET:SD	2.86	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:KH:203:ASN:HB2	4:KH:216:GLN:HB3	1.94	0.49
6:KL:63:ASP:O	6:KL:88:GLY:N	2.46	0.49
6:KL:114:ILE:HD12	6:KL:127:ILE:HG12	1.95	0.49
6:KL:169:THR:OG1	6:KL:170:ASP:N	2.45	0.49
7:KM:310:LYS:NZ	7:KM:311:ASP:O	2.45	0.49
7:LM:273:ALA:HB1	7:LM:277:SER:HB2	1.94	0.49
1:EG:886:LEU:HD11	1:FG:868:ILE:HD11	1.95	0.49
2:Md:68:ASP:OD1	2:Md:68:ASP:N	2.43	0.49
4:WH:203:ASN:OD1	4:WH:203:ASN:N	2.46	0.49
1:ZG:802:LEU:HB2	4:BH:115:MET:HG2	1.94	0.49
4:ZH:330:SER:OG	4:ZH:332:ASP:OD1	2.31	0.49
11:FC:233:VAL:HG12	11:FC:242:ILE:HA	1.95	0.49
6:CL:108:ASP:OD2	6:CL:150:ASN:ND2	2.45	0.49
2:AD:150:ASN:OD1	2:AD:150:ASN:N	2.46	0.49
4:EH:251:ARG:HB3	4:DH:238:MET:HE3	1.94	0.48
7:EM:275:ASP:HA	7:EM:295:ASN:H	1.77	0.48
3:FF:233:ARG:NH1	3:WF:266:GLN:OE1	2.46	0.48
7:FM:314:ARG:HA	7:FM:317:LYS:HE2	1.95	0.48
11:BC:199:ILE:HD12	2:GD:41:LEU:HD22	1.95	0.48
4:GH:179:LEU:O	4:GH:212:THR:HA	2.13	0.48
4:GH:183:ASP:HA	4:GH:256:VAL:HB	1.95	0.48
6:GL:223:SER:OG	6:GL:227:ARG:NH2	2.46	0.48
7:GM:180:ASP:O	7:GM:182:LYS:NZ	2.39	0.48
6:IL:169:THR:OG1	6:IL:170:ASP:N	2.46	0.48
3:If:219:ARG:HA	3:If:232:VAL:O	2.13	0.48
3:If:245:LYS:HE3	3:If:257:SER:HA	1.95	0.48
2:JD:44:ALA:O	11:EC:204:LYS:NZ	2.43	0.48
7:JM:275:ASP:HA	7:JM:295:ASN:H	1.78	0.48
7:KM:242:LYS:HA	7:KM:262:GLU:HB2	1.94	0.48
8:LN:63:GLY:HA3	2:MD:27:LYS:HB2	1.95	0.48
3:Mf:244:VAL:HA	3:Mf:256:THR:HA	1.95	0.48
4:YH:339:MET:N	4:YH:339:MET:SD	2.85	0.48
9:AU:128:UNK:HA	6:BL:232:GLN:HE22	1.78	0.48
8:BN:110:GLU:HA	8:BN:113:SER:HB3	1.95	0.48
11:FC:110:LEU:HD23	11:FC:212:TYR:HB2	1.95	0.48
3:DF:254:ILE:HB	3:DF:262:ILE:HB	1.94	0.48
1:IG:937:PRO:HD3	1:IG:1037:LEU:HA	1.95	0.48
1:PG:968:PHE:O	1:PG:972:PHE:HB2	2.12	0.48
2:AD:87:TRP:CD1	2:AD:89:GLY:H	2.30	0.48
4:EH:138:GLU:HG3	4:DH:221:TYR:HE2	1.78	0.48
4:EH:238:MET:HB3	4:FH:250:TYR:HD2	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:FF:207:ARG:NH2	3:FF:208:ILE:O	2.45	0.48
11:CC:198:ASN:OD1	11:CC:201:ARG:NH1	2.43	0.48
6:FL:186:ALA:HB1	6:FL:205:ALA:HB1	1.95	0.48
1:BG:951:HIS:O	1:BG:955:ARG:NE	2.45	0.48
4:HH:204:ILE:HB	4:HH:215:ILE:HG23	1.95	0.48
6:HL:94:VAL:HA	6:HL:97:ILE:HG12	1.94	0.48
3:IF:265:SER:HB3	3:IF:268:ASP:HB3	1.95	0.48
6:IL:63:ASP:O	6:IL:88:GLY:N	2.46	0.48
5:JK:73:ASN:OD1	5:JK:185:ARG:NE	2.44	0.48
6:KL:150:ASN:OD1	6:KL:153:ARG:NH2	2.38	0.48
3:LF:246:LEU:HB3	3:LF:255:LEU:HD12	1.94	0.48
4:LH:183:ASP:OD1	4:LH:187:ALA:N	2.46	0.48
2:Ld:74:PRO:HG3	2:Ld:147:VAL:HG11	1.95	0.48
5:AK:119:TYR:HB2	5:AK:179:ARG:HG2	1.95	0.48
1:XG:807:GLN:NE2	1:XG:811:ASP:OD2	2.46	0.48
4:BH:229:ARG:HG2	4:BH:236:PRO:HB3	1.94	0.48
9:BU:128:UNK:HA	6:CL:232:GLN:HE22	1.78	0.48
2:Bd:36:ASP:OD1	2:Bd:36:ASP:N	2.45	0.48
11:EC:226:TYR:HB3	11:EC:252:ALA:HB3	1.94	0.48
3:DF:213:GLN:HB2	3:DF:223:ILE:HG22	1.95	0.48
1:JG:917:ASN:HA	1:JG:931:SER:HA	1.95	0.48
2:ED:92:GLU:OE2	2:ED:158:TYR:OH	2.31	0.48
11:CC:230:ASP:OD1	11:CC:230:ASP:N	2.46	0.48
11:BC:189:ASP:O	11:BC:193:THR:OG1	2.31	0.48
5:GK:92:ASN:O	5:GK:95:SER:OG	2.31	0.48
3:Hf:235:GLY:HA2	3:Hf:243:MET:HE1	1.94	0.48
4:IH:273:PRO:O	11:DC:126:ARG:NH1	2.42	0.48
11:KC:151:LEU:HD21	11:KC:202:ILE:HG21	1.95	0.48
2:JD:36:ASP:HA	2:JD:39:ILE:HD12	1.96	0.48
2:JD:70:THR:HA	2:JD:133:ARG:HE	1.79	0.48
4:AH:200:SER:O	4:AH:218:THR:OG1	2.31	0.48
2:Kd:105:ARG:HG3	2:Kd:153:VAL:HG23	1.94	0.48
3:LF:240:GLY:O	3:LF:260:GLN:NE2	2.47	0.48
4:LH:198:ASP:OD1	4:LH:200:SER:OG	2.31	0.48
2:Ld:76:ALA:O	2:Ld:80:GLN:NE2	2.38	0.48
5:AK:46:ASP:OD1	5:AK:46:ASP:N	2.40	0.48
2:MD:87:TRP:CD1	2:MD:89:GLY:H	2.31	0.48
3:VF:246:LEU:HB3	3:VF:255:LEU:HD12	1.96	0.48
3:WF:265:SER:HB3	3:WF:268:ASP:HB3	1.95	0.48
6:AL:108:ASP:OD2	6:AL:150:ASN:ND2	2.46	0.48
4:ZH:160:LEU:HD22	4:ZH:257:GLN:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BD:73:ILE:O	2:BD:133:ARG:NH2	2.39	0.48
6:BL:136:SER:OG	7:BM:314:ARG:NH1	2.46	0.48
11:EC:257:ASN:ND2	11:EC:262:GLU:OE2	2.46	0.48
11:MC:97:ASN:OD1	11:MC:97:ASN:N	2.38	0.48
5:CK:76:ILE:HD12	5:CK:102:ILE:HD11	1.94	0.48
7:CM:225:ALA:HA	7:CM:246:LEU:HB2	1.95	0.48
1:JG:876:SER:HB3	1:KG:941:ARG:HG2	1.94	0.48
1:JG:880:ASP:OD1	1:JG:880:ASP:N	2.45	0.48
1:AG:871:ALA:HB2	1:AG:889:ILE:HD13	1.95	0.48
5:EK:115:THR:HB	5:EK:183:THR:HG23	1.95	0.48
1:BG:946:SER:OG	1:BG:1030:GLU:O	2.24	0.48
6:GL:168:PHE:HB2	6:GL:228:ARG:HG2	1.96	0.48
11:GC:128:SER:HA	11:FC:243:ASP:HB3	1.95	0.48
7:HM:146:LEU:HD23	7:HM:165:ILE:HG12	1.95	0.48
7:IM:155:LEU:HB3	7:IM:175:ILE:HD12	1.95	0.48
6:LL:115:GLN:HB3	6:LL:126:ILE:HB	1.95	0.48
6:LL:129:THR:O	6:LL:133:PHE:HB2	2.13	0.48
1:EG:900:ILE:HG13	1:EG:918:THR:HB	1.93	0.48
4:WH:278:ASP:OD1	4:WH:278:ASP:N	2.47	0.48
2:BD:36:ASP:OD1	11:JC:76:ARG:NH2	2.47	0.48
4:CH:192:ALA:HB2	4:CH:231:ARG:HA	1.96	0.48
5:DK:76:ILE:HB	5:DK:182:ILE:HG12	1.95	0.48
1:OG:1006:ILE:O	1:OG:1010:THR:OG1	2.31	0.48
4:EH:322:PRO:HG2	4:EH:339:MET:HE1	1.96	0.48
5:HK:117:THR:HG22	5:HK:157:GLN:HG3	1.95	0.48
7:IM:165:ILE:HB	7:IM:185:ILE:HG23	1.94	0.48
7:JM:211:THR:HA	7:JM:230:ARG:O	2.13	0.48
4:KH:259:TYR:HB3	4:KH:263:ALA:HB2	1.96	0.48
3:MF:212:ILE:HG13	3:MF:262:ILE:HG22	1.96	0.48
4:VH:191:ILE:HA	4:VH:230:LEU:HA	1.95	0.48
7:AM:288:ARG:HH22	7:AM:318:GLN:H	1.61	0.48
8:BN:89:GLY:HA3	8:BN:104:ASN:HB2	1.94	0.48
1:GG:921:ILE:HB	1:GG:926:LYS:HZ3	1.78	0.48
11:HC:167:PRO:HB2	11:HC:173:LYS:HG3	1.96	0.48
7:CM:215:ARG:HG3	7:CM:234:GLU:HB3	1.94	0.48
1:HG:958:SER:O	1:HG:962:SER:OG	2.29	0.48
1:MG:876:SER:OG	1:MG:1031:VAL:O	2.32	0.48
2:Dd:92:GLU:OE2	2:Dd:158:TYR:OH	2.31	0.48
4:EH:313:VAL:HG22	4:EH:337:TYR:HB2	1.94	0.48
11:BC:175:ILE:HA	11:BC:178:ILE:HG12	1.94	0.48
6:GL:52:PRO:HB2	6:GL:54:ARG:HH22	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:HL:44:HIS:HB2	6:HL:48:ASN:HA	1.95	0.48
6:HL:109:LEU:HD12	6:HL:114:ILE:HB	1.93	0.48
6:HL:187:GLU:OE1	7:HM:268:HIS:ND1	2.46	0.48
3:Hf:241:TYR:HB3	3:Hf:256:THR:HG21	1.95	0.48
1:CG:1042:THR:OG1	1:CG:1043:GLN:OE1	2.30	0.48
2:JD:149:PRO:O	2:JD:152:GLN:NE2	2.46	0.48
2:JD:162:TYR:OH	11:EC:103:GLU:O	2.31	0.48
6:JL:213:ALA:HA	6:JL:228:ARG:HH22	1.78	0.48
6:KL:136:SER:OG	7:KM:314:ARG:NH1	2.47	0.48
2:Ld:76:ALA:HB3	2:Ld:79:LEU:HD13	1.95	0.48
1:EG:874:ASP:OD1	1:EG:874:ASP:N	2.46	0.48
4:MH:273:PRO:O	11:HC:126:ARG:NH1	2.38	0.48
5:MK:76:ILE:HG13	5:MK:182:ILE:HB	1.95	0.48
6:ML:125:LEU:HB2	6:ML:231:ILE:HB	1.96	0.48
8:MN:46:GLY:HA3	8:MN:61:ASN:HB2	1.94	0.48
4:VH:315:THR:OG1	4:VH:316:ASN:N	2.44	0.48
3:XF:219:ARG:NH2	3:XF:231:THR:OG1	2.47	0.48
4:XH:176:VAL:HG13	4:XH:214:MET:HG3	1.95	0.48
7:AM:181:PRO:HD2	7:AM:200:GLY:HA2	1.96	0.48
11:MC:175:ILE:HA	11:MC:178:ILE:HG12	1.96	0.48
1:MG:921:ILE:HB	1:MG:926:LYS:HD2	1.96	0.48
1:AG:1003:ASN:HA	1:AG:1006:ILE:HD12	1.96	0.48
2:ED:82:ARG:HB2	5:EK:156:THR:HG23	1.95	0.48
4:EH:191:ILE:HG13	4:EH:211:ASN:HA	1.96	0.48
4:EH:203:ASN:HB3	4:EH:216:GLN:HB3	1.96	0.48
2:Fd:72:THR:OG1	2:Fd:73:ILE:N	2.47	0.48
7:GM:257:ASP:OD1	7:GM:257:ASP:N	2.44	0.48
11:GC:91:ASP:OD1	11:GC:147:TRP:NE1	2.37	0.48
6:HL:124:THR:HA	6:HL:231:ILE:O	2.13	0.48
4:AH:170:ARG:NH1	4:AH:249:ASP:OD1	2.42	0.48
4:AH:189:TRP:HE1	4:AH:232:GLY:H	1.60	0.48
2:KD:155:GLU:OE2	2:KD:157:ARG:NE	2.44	0.48
5:KK:87:GLN:NE2	5:KK:173:ASP:OD1	2.45	0.48
5:KK:185:ARG:NH2	6:LL:214:ILE:O	2.46	0.48
2:LD:71:LEU:H	2:LD:71:LEU:HG	1.45	0.48
3:MF:230:LEU:HA	4:MH:165:THR:HG21	1.96	0.48
3:Mf:256:THR:OG1	3:Mf:257:SER:N	2.46	0.48
4:VH:225:ASN:HD21	4:DH:176:VAL:HB	1.79	0.48
6:AL:230:GLU:OE2	6:AL:232:GLN:NE2	2.47	0.48
1:FG:900:ILE:HG13	1:FG:918:THR:HB	1.96	0.48
2:BD:92:GLU:OE2	2:BD:158:TYR:OH	2.32	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CK:90:ARG:NH1	5:CK:91:LEU:O	2.47	0.48
2:Cd:36:ASP:N	2:Cd:36:ASP:OD1	2.44	0.48
3:DF:248:ASP:HB3	3:DF:253:ARG:HG3	1.96	0.48
3:EF:246:LEU:HB3	3:EF:255:LEU:HD12	1.94	0.48
4:EH:157:PHE:HE1	4:EH:257:GLN:HG2	1.79	0.48
7:EM:254:LYS:HE2	7:EM:272:LEU:HD23	1.96	0.48
2:FD:87:TRP:CD1	2:FD:89:GLY:H	2.32	0.48
11:CC:176:TRP:O	11:CC:180:THR:OG1	2.28	0.48
7:FM:275:ASP:HA	7:FM:295:ASN:H	1.78	0.48
3:GF:207:ARG:NH2	3:GF:208:ILE:O	2.47	0.48
6:GL:121:ASP:OD1	6:GL:121:ASP:N	2.42	0.48
7:GM:254:LYS:HE2	7:GM:272:LEU:HD23	1.95	0.48
2:HD:47:SER:O	2:HD:51:SER:OG	2.30	0.48
5:HK:72:GLN:NE2	6:IL:216:ASP:OD1	2.47	0.48
1:Bg:791:GLN:N	1:Bg:793:GLU:OE1	2.47	0.48
1:EG:886:LEU:HA	1:EG:899:LEU:O	2.14	0.48
3:Mf:245:LYS:NZ	3:Mf:256:THR:O	2.38	0.48
2:BD:87:TRP:CD1	2:BD:89:GLY:H	2.31	0.48
11:IC:151:LEU:HD21	11:IC:202:ILE:HG21	1.95	0.48
2:CD:72:THR:HG23	2:CD:73:ILE:HG12	1.96	0.48
1:MG:876:SER:HB3	1:NG:941:ARG:HG2	1.95	0.48
11:CC:172:GLU:HA	11:CC:175:ILE:HG12	1.95	0.48
5:FK:146:SER:OG	5:FK:147:GLN:NE2	2.47	0.48
6:FL:169:THR:OG1	6:FL:170:ASP:N	2.47	0.48
6:FL:177:HIS:ND1	7:FM:315:TYR:OH	2.35	0.48
7:FM:229:ASN:OD1	7:FM:229:ASN:N	2.46	0.48
1:BG:919:MET:HG3	1:BG:930:ILE:HG23	1.95	0.48
2:HD:83:ALA:HA	5:HK:154:ILE:O	2.14	0.48
7:HM:168:VAL:HB	7:HM:187:GLY:HA3	1.96	0.48
8:IN:52:ASP:O	8:IN:56:GLY:N	2.47	0.48
8:JN:102:VAL:HA	8:JN:108:VAL:HA	1.95	0.48
3:KF:216:ILE:HD11	3:KF:219:ARG:HB2	1.95	0.48
1:Kg:818:GLN:O	4:KH:205:GLN:NE2	2.47	0.48
5:KK:71:GLY:O	2:LD:27:LYS:NZ	2.47	0.48
6:LL:170:ASP:N	6:LL:170:ASP:OD1	2.46	0.48
5:AK:49:CYS:O	5:AK:52:THR:OG1	2.31	0.48
3:MF:246:LEU:N	3:MF:255:LEU:O	2.45	0.48
4:MH:278:ASP:OD1	4:MH:278:ASP:N	2.40	0.48
6:ML:115:GLN:HB3	6:ML:126:ILE:HB	1.96	0.48
1:FG:886:LEU:HD23	1:GG:1040:LEU:HD12	1.96	0.48
2:Ad:84:SER:H	11:JC:268:ALA:HB3	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Ad:97:ARG:NH1	11:JC:265:ALA:O	2.47	0.48
4:BH:161:SER:HB2	4:BH:164:SER:HB3	1.95	0.48
4:BH:208:LYS:HE3	1:Cg:824:THR:H	1.77	0.48
1:GG:873:LEU:HD23	1:GG:1037:LEU:HB3	1.96	0.48
11:IC:219:ASN:ND2	11:IC:261:GLU:O	2.46	0.48
11:IC:225:TYR:HB2	11:IC:251:ALA:HB3	1.94	0.48
2:CD:147:VAL:HG22	2:CD:154:VAL:HG12	1.96	0.48
4:CH:280:LEU:HD23	4:CH:328:MET:HG2	1.96	0.48
7:CM:308:ASP:N	7:CM:308:ASP:OD1	2.47	0.48
4:DH:262:ASN:OD1	4:DH:262:ASN:N	2.42	0.48
5:EK:116:VAL:HG22	5:EK:182:ILE:HG22	1.96	0.48
4:FH:315:THR:OG1	4:FH:316:ASN:N	2.45	0.48
11:KC:79:ILE:HD11	11:KC:195:LEU:HD13	1.96	0.48
7:JM:210:ASP:O	7:JM:230:ARG:N	2.46	0.48
2:KD:36:ASP:HA	2:KD:39:ILE:HD12	1.96	0.48
7:KM:303:GLU:OE2	3:Kf:251:GLN:NE2	2.46	0.48
1:Lg:795:GLN:HA	1:Lg:798:THR:HB	1.96	0.48
1:EG:878:ASN:HD21	1:EG:1028:THR:HG21	1.79	0.48
3:Mf:254:ILE:HB	3:Mf:262:ILE:HB	1.96	0.48
3:WF:248:ASP:HB3	3:WF:253:ARG:HG3	1.96	0.48
4:ZH:198:ASP:OD1	4:ZH:200:SER:OG	2.31	0.48
4:ZH:302:ALA:HB2	4:ZH:315:THR:HG23	1.95	0.48
2:BD:125:ASP:OD1	7:BM:317:LYS:NZ	2.41	0.48
11:LC:181:GLU:OE1	11:LC:185:LYS:NZ	2.46	0.48
4:CH:206:TRP:NE1	4:CH:210:SER:O	2.42	0.48
2:Cd:35:ASP:O	2:Cd:38:THR:OG1	2.29	0.48
1:MG:1006:ILE:O	1:MG:1010:THR:OG1	2.32	0.48
3:FF:216:ILE:HD11	3:FF:219:ARG:HB2	1.96	0.47
11:CC:141:ILE:HD11	11:CC:145:PRO:HD3	1.96	0.47
11:CC:145:PRO:HB3	11:CC:149:GLN:HE22	1.79	0.47
4:FH:115:MET:HE3	1:Dg:802:LEU:HA	1.96	0.47
2:Hd:150:ASN:OD1	2:Hd:150:ASN:N	2.46	0.47
2:ID:140:GLY:O	2:Id:60:LYS:NZ	2.43	0.47
5:AK:114:ILE:HB	5:AK:154:ILE:HG12	1.95	0.47
6:ML:136:SER:OG	7:MM:314:ARG:NH1	2.47	0.47
10:AX:21:UNK:O	10:AX:78:UNK:N	2.47	0.47
1:GG:1031:VAL:O	1:HG:941:ARG:NH2	2.47	0.47
11:HC:166:LEU:HD13	11:HC:167:PRO:HD2	1.96	0.47
7:CM:119:GLU:HG3	7:CM:139:ALA:HB3	1.96	0.47
7:CM:275:ASP:HA	7:CM:295:ASN:H	1.78	0.47
1:JG:951:HIS:H	1:JG:1027:THR:HG22	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MG:876:SER:N	1:NG:940:ALA:O	2.43	0.47
6:DL:49:ASN:HB3	7:DM:293:ALA:HB1	1.96	0.47
8:DN:46:GLY:O	8:DN:61:ASN:ND2	2.46	0.47
2:ED:36:ASP:OD1	2:ED:36:ASP:N	2.45	0.47
4:EH:106:VAL:HA	4:EH:109:LYS:HE2	1.96	0.47
5:EK:54:ILE:HD11	8:EN:44:LYS:HB3	1.96	0.47
11:GC:116:THR:OG1	11:GC:128:SER:OG	2.31	0.47
11:GC:175:ILE:HA	11:GC:178:ILE:HG12	1.95	0.47
4:HH:270:GLU:OE2	4:XH:327:SER:N	2.46	0.47
7:IM:117:ARG:HG2	7:IM:137:TYR:HB3	1.96	0.47
3:If:256:THR:OG1	3:If:257:SER:N	2.46	0.47
2:JD:60:LYS:O	2:JD:60:LYS:NZ	2.42	0.47
4:JH:279:LEU:HD21	4:JH:289:PRO:HB3	1.95	0.47
6:JL:124:THR:HA	6:JL:231:ILE:O	2.13	0.47
4:AH:282:HIS:HB3	4:AH:287:VAL:HB	1.94	0.47
5:KK:114:ILE:HB	5:KK:154:ILE:HG12	1.96	0.47
2:LD:149:PRO:O	2:LD:152:GLN:NE2	2.47	0.47
4:XH:289:PRO:HG3	4:XH:312:TYR:HD2	1.79	0.47
8:AN:71:THR:HG22	8:AN:73:HIS:H	1.79	0.47
2:Ad:36:ASP:OD1	2:AD:34:SER:OG	2.32	0.47
6:BL:177:HIS:HD1	7:BM:315:TYR:HH	1.59	0.47
8:BN:46:GLY:O	8:BN:61:ASN:ND2	2.47	0.47
1:GG:931:SER:O	1:GG:1042:THR:OG1	2.31	0.47
11:LC:175:ILE:HA	11:LC:178:ILE:HG12	1.95	0.47
5:CK:78:ILE:HB	5:CK:180:VAL:HG13	1.96	0.47
2:DD:132:LEU:HD12	2:DD:145:ILE:HG21	1.96	0.47
5:DK:65:ILE:HD12	5:DK:78:ILE:HG12	1.96	0.47
4:EH:154:THR:O	4:EH:252:VAL:HA	2.13	0.47
3:Ff:219:ARG:HD3	3:Ff:233:ARG:HH11	1.80	0.47
4:GH:313:VAL:HG13	4:GH:337:TYR:HB2	1.95	0.47
8:GN:111:GLU:OE1	8:GN:112:CYS:N	2.47	0.47
11:GC:95:ASP:O	11:GC:98:SER:OG	2.32	0.47
4:HH:180:VAL:HG11	4:HH:251:ARG:HH11	1.79	0.47
7:HM:143:THR:HG22	7:HM:145:ARG:HH12	1.79	0.47
1:CG:999:SER:HB2	1:DG:972:PHE:HZ	1.79	0.47
5:IK:116:VAL:HG22	5:IK:182:ILE:HG23	1.95	0.47
2:JD:82:ARG:NH2	2:JD:125:ASP:OD2	2.47	0.47
4:JH:292:SER:OG	4:JH:293:ARG:N	2.47	0.47
7:KM:245:TYR:HB3	3:Kf:215:VAL:HB	1.94	0.47
4:LH:231:ARG:NH2	1:Mg:824:THR:O	2.47	0.47
1:EG:917:ASN:HA	1:EG:931:SER:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:AL:219:ILE:HD12	6:AL:219:ILE:HA	1.82	0.47
11:DC:69:GLN:HB3	11:DC:158:PRO:HG2	1.96	0.47
8:BN:89:GLY:O	8:BN:104:ASN:ND2	2.47	0.47
8:BN:102:VAL:HB	8:BN:108:VAL:HG12	1.95	0.47
2:CD:36:ASP:HA	2:CD:39:ILE:HD12	1.95	0.47
2:DD:150:ASN:OD1	2:DD:150:ASN:N	2.45	0.47
2:DD:158:TYR:O	2:Dd:137:TYR:OH	2.28	0.47
1:HG:947:ARG:HE	1:HG:947:ARG:H	1.59	0.47
2:AD:47:SER:O	2:AD:51:SER:OG	2.31	0.47
5:FK:54:ILE:HD13	8:FN:45:MET:HE2	1.95	0.47
7:FM:279:ILE:HB	7:FM:298:VAL:HG22	1.97	0.47
8:GN:63:GLY:HA3	2:HD:27:LYS:HB2	1.96	0.47
2:ID:26:LYS:O	6:IL:115:GLN:NE2	2.39	0.47
2:ID:87:TRP:CD1	2:ID:89:GLY:H	2.32	0.47
2:JD:73:ILE:O	2:JD:133:ARG:NH2	2.48	0.47
7:LM:201:THR:HG22	7:LM:221:LYS:HB2	1.95	0.47
5:AK:88:SER:O	5:AK:136:ARG:NH2	2.45	0.47
4:WH:196:LEU:HD22	4:WH:204:ILE:HG13	1.96	0.47
3:XF:235:GLY:HA2	3:XF:243:MET:HE1	1.96	0.47
1:FG:875:THR:HA	1:GG:940:ALA:HB1	1.96	0.47
7:BM:284:LEU:HD23	7:BM:310:LYS:HD2	1.96	0.47
5:CK:44:ARG:HD2	5:CK:48:ALA:HB3	1.97	0.47
2:CD:68:ASP:N	2:CD:68:ASP:OD1	2.47	0.47
2:DD:36:ASP:N	2:DD:36:ASP:OD1	2.46	0.47
2:DD:82:ARG:NH2	2:DD:125:ASP:O	2.46	0.47
4:DH:170:ARG:HH21	4:DH:245:GLN:HB3	1.79	0.47
1:JG:886:LEU:HD23	1:KG:1040:LEU:HD12	1.96	0.47
1:JG:928:ILE:HD12	1:JG:1045:VAL:HG11	1.96	0.47
1:MG:1017:GLN:NE2	1:MG:1018:GLN:OE1	2.44	0.47
2:Dd:136:ASP:HB2	2:Dd:145:ILE:HD11	1.97	0.47
5:EK:76:ILE:HB	5:EK:182:ILE:HG13	1.96	0.47
7:EM:282:TYR:HE1	7:EM:301:MET:HB3	1.78	0.47
5:GK:128:ARG:HA	7:GM:301:MET:HE1	1.97	0.47
11:GC:54:ILE:HG12	1:HG:872:VAL:HG22	1.95	0.47
2:JD:83:ALA:HA	5:JK:154:ILE:O	2.15	0.47
4:JH:344:VAL:HA	4:JH:356:LEU:O	2.14	0.47
4:AH:320:LEU:N	4:AH:346:LEU:O	2.42	0.47
6:LL:174:SER:HB3	6:LL:177:HIS:HB3	1.95	0.47
8:MN:52:ASP:O	8:MN:56:GLY:N	2.47	0.47
6:AL:47:TYR:OH	6:AL:142:GLU:OE1	2.33	0.47
4:ZH:320:LEU:HD22	4:ZH:348:SER:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:AM:171:ARG:O	7:AM:192:ARG:NH2	2.47	0.47
1:GG:876:SER:OG	1:GG:1031:VAL:O	2.32	0.47
2:FD:160:LYS:HB2	2:FD:160:LYS:HE2	1.68	0.47
7:GM:201:THR:HG22	7:GM:221:LYS:HB2	1.96	0.47
1:Hg:798:THR:HA	1:Hg:801:MET:HE3	1.96	0.47
5:HK:78:ILE:HB	5:HK:180:VAL:HG23	1.97	0.47
7:HM:257:ASP:OD1	7:HM:257:ASP:N	2.45	0.47
4:IH:198:ASP:OD2	4:IH:201:SER:OG	2.32	0.47
6:IL:116:TYR:OH	6:IL:118:GLU:OE1	2.29	0.47
11:KC:147:TRP:HB2	11:KC:151:LEU:HD23	1.97	0.47
4:KH:223:TYR:HB3	4:KH:242:ILE:HG13	1.95	0.47
8:KN:46:GLY:O	8:KN:61:ASN:ND2	2.48	0.47
8:KN:58:LEU:HB2	8:KN:66:SER:HB3	1.95	0.47
5:LK:75:LEU:HA	5:LK:182:ILE:O	2.14	0.47
1:EG:876:SER:HB3	1:FG:941:ARG:HG2	1.96	0.47
4:VH:150:LYS:NZ	3:CF:231:THR:O	2.47	0.47
4:VH:183:ASP:OD1	4:VH:187:ALA:N	2.48	0.47
4:WH:160:LEU:HG	4:WH:257:GLN:HB3	1.95	0.47
1:FG:885:ILE:O	1:FG:900:ILE:HA	2.14	0.47
7:AM:157:ALA:O	7:AM:178:LYS:NZ	2.47	0.47
4:BH:179:LEU:O	4:BH:212:THR:HA	2.15	0.47
5:BK:81:SER:OG	5:BK:173:ASP:O	2.31	0.47
6:BL:179:ARG:O	6:BL:183:GLN:NE2	2.47	0.47
6:BL:210:ASP:OD1	6:BL:210:ASP:N	2.46	0.47
11:FC:102:GLU:OE2	11:FC:103:HIS:ND1	2.46	0.47
7:CM:124:VAL:HG23	7:CM:144:THR:HG23	1.97	0.47
10:CX:24:UNK:O	10:CX:32:UNK:N	2.47	0.47
1:KG:966:GLN:O	1:KG:970:ASN:ND2	2.47	0.47
11:AC:152:LEU:HD21	11:AC:203:ILE:HG21	1.94	0.47
6:EL:139:ARG:HD2	7:EM:319:PHE:HD2	1.80	0.47
7:FM:254:LYS:HE2	7:FM:272:LEU:HD23	1.96	0.47
2:HD:34:SER:OG	2:Hd:36:ASP:OD1	2.32	0.47
11:GC:248:ARG:NE	11:HC:123:GLN:O	2.48	0.47
2:Hd:79:LEU:HA	2:Hd:128:LEU:HD12	1.97	0.47
1:Bg:794:ILE:HD13	4:VH:107:ILE:HG23	1.97	0.47
2:Id:76:ALA:HB3	2:Id:79:LEU:HD23	1.96	0.47
11:KC:210:ILE:HD11	2:CD:55:MET:HG2	1.96	0.47
3:If:210:TYR:HD2	3:If:222:LEU:HB3	1.80	0.47
4:JH:226:LEU:HB2	4:JH:241:LEU:HD21	1.96	0.47
2:Jd:55:MET:O	2:Jd:59:GLU:HB2	2.14	0.47
1:DG:876:SER:OG	1:DG:1031:VAL:O	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AH:182:LEU:O	4:AH:255:ARG:HA	2.15	0.47
5:LK:44:ARG:HH21	5:LK:48:ALA:H	1.63	0.47
5:LK:115:THR:HB	5:LK:183:THR:HG23	1.96	0.47
6:LL:170:ASP:HB3	6:LL:227:ARG:HH21	1.79	0.47
7:LM:163:THR:HB	7:LM:183:VAL:HG12	1.97	0.47
7:LM:177:LEU:HD13	7:LM:181:PRO:HG2	1.95	0.47
7:LM:199:LYS:HA	7:LM:219:ALA:HB3	1.96	0.47
3:MF:246:LEU:HD23	3:MF:255:LEU:HD23	1.97	0.47
3:MF:250:LEU:HD12	3:MF:251:GLN:HG3	1.96	0.47
7:MM:230:ARG:HA	7:MM:250:ARG:HB2	1.97	0.47
6:AL:168:PHE:HB2	6:AL:228:ARG:HG2	1.97	0.47
7:BM:162:VAL:HG12	7:BM:182:LYS:HB2	1.97	0.47
11:EC:158:LYS:HD2	11:EC:158:LYS:HA	1.72	0.47
11:JC:80:ILE:HD11	11:JC:196:LEU:HD13	1.96	0.47
11:JC:148:TRP:HB2	11:JC:152:LEU:HD23	1.96	0.47
7:CM:115:ARG:NH1	7:CM:135:ASP:OD2	2.48	0.47
2:Cd:136:ASP:HB2	2:Cd:145:ILE:HD11	1.97	0.47
1:HG:1032:TYR:HD1	1:IG:941:ARG:HH22	1.62	0.47
1:NG:966:GLN:O	1:NG:970:ASN:ND2	2.48	0.47
2:ED:47:SER:OG	11:MC:203:LYS:NZ	2.39	0.47
6:FL:165:VAL:HG12	6:FL:231:ILE:HG12	1.96	0.47
7:FM:275:ASP:HB3	7:FM:294:PHE:HB2	1.97	0.47
4:GH:315:THR:OG1	4:GH:316:ASN:N	2.47	0.47
2:ID:55:MET:HE3	2:ID:59:GLU:HB2	1.96	0.47
7:IM:137:TYR:HA	7:IM:156:GLU:O	2.15	0.47
1:Jg:801:MET:HB2	4:YH:115:MET:HG3	1.96	0.47
5:KK:172:GLY:O	5:KK:175:SER:OG	2.32	0.47
11:DC:61:GLU:HA	11:DC:64:LEU:HD12	1.96	0.47
2:Ad:150:ASN:OD1	2:Ad:150:ASN:N	2.46	0.47
7:BM:191:LEU:H	7:BM:209:SER:HB2	1.80	0.47
1:GG:921:ILE:HD12	1:GG:926:LYS:HD2	1.97	0.47
11:CC:128:SER:HA	11:BC:243:ASP:O	2.15	0.47
5:FK:70:VAL:O	5:FK:73:ASN:ND2	2.46	0.47
7:FM:168:VAL:HB	7:FM:187:GLY:HA3	1.96	0.47
11:BC:123:GLN:O	11:AC:249:ARG:NE	2.38	0.47
5:GK:87:GLN:N	5:GK:173:ASP:OD2	2.47	0.47
6:GL:212:ASN:O	6:GL:228:ARG:NH2	2.46	0.47
2:HD:32:ASN:N	2:HD:32:ASN:OD1	2.45	0.47
11:GC:147:TRP:HB2	11:GC:151:LEU:HD23	1.97	0.47
4:IH:225:ASN:ND2	4:JH:176:VAL:O	2.48	0.47
7:IM:278:ASP:OD1	7:IM:297:SER:OG	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:JK:68:ALA:HB3	5:JK:75:LEU:HB3	1.96	0.47
4:MH:238:MET:HE3	4:MH:238:MET:HB2	1.78	0.47
4:XH:253:ASP:N	4:XH:253:ASP:OD1	2.48	0.47
11:DC:101:LEU:HB2	11:DC:105:ILE:HG13	1.95	0.47
3:ZF:212:ILE:HG13	3:ZF:262:ILE:HG22	1.96	0.47
11:MC:233:VAL:HG11	11:AC:263:TRP:HH2	1.79	0.47
6:CL:178:LYS:O	6:CL:182:SER:OG	2.31	0.47
4:DH:126:GLN:HA	4:DH:129:LYS:HE3	1.97	0.47
1:HG:966:GLN:O	1:HG:970:ASN:ND2	2.47	0.47
2:Dd:87:TRP:O	2:Dd:120:SER:HA	2.14	0.47
1:Eg:794:ILE:O	1:Eg:797:ARG:NE	2.47	0.47
11:CC:61:GLU:O	11:CC:65:SER:OG	2.30	0.47
11:BC:147:TRP:HB2	11:BC:151:LEU:HD23	1.97	0.47
6:GL:52:PRO:O	6:GL:54:ARG:NH1	2.48	0.47
3:Hf:212:ILE:HD11	3:Hf:262:ILE:HG23	1.97	0.47
2:JD:119:ILE:HD12	2:JD:138:GLN:HG2	1.96	0.47
3:JF:243:MET:O	3:JF:257:SER:N	2.48	0.47
4:KH:207:ASP:O	4:KH:210:SER:OG	2.31	0.47
8:KN:86:LEU:HB3	8:KN:87:TRP:HE3	1.80	0.47
3:Lf:243:MET:O	3:Lf:257:SER:N	2.46	0.47
1:EG:912:MET:HB3	1:EG:944:LEU:HB2	1.97	0.47
5:MK:92:ASN:O	5:MK:95:SER:OG	2.33	0.47
3:VF:221:TRP:HZ3	4:VH:165:THR:HB	1.80	0.47
7:AM:199:LYS:HA	7:AM:219:ALA:HB3	1.97	0.47
5:BK:54:ILE:O	5:BK:58:THR:OG1	2.32	0.47
6:BL:121:ASP:N	6:BL:121:ASP:OD1	2.48	0.47
11:MC:168:LYS:N	11:MC:172:GLU:OE1	2.48	0.47
1:MG:900:ILE:HG13	1:MG:918:THR:HB	1.96	0.47
1:NG:1017:GLN:NE2	1:NG:1018:GLN:OE1	2.47	0.47
2:ED:47:SER:O	2:ED:51:SER:OG	2.31	0.46
4:EH:251:ARG:NH1	4:EH:253:ASP:OD2	2.47	0.46
3:GF:207:ARG:HD2	3:GF:240:GLY:HA3	1.96	0.46
4:GH:170:ARG:HA	4:GH:242:ILE:O	2.15	0.46
4:GH:183:ASP:OD1	4:GH:187:ALA:N	2.48	0.46
4:HH:183:ASP:OD1	4:HH:187:ALA:N	2.47	0.46
7:HM:174:GLN:HE22	7:HM:192:ARG:HB2	1.80	0.46
7:IM:168:VAL:HB	7:IM:187:GLY:HA3	1.97	0.46
2:JD:76:ALA:H	2:JD:79:LEU:HD12	1.80	0.46
4:JH:229:ARG:HG2	4:JH:236:PRO:HB3	1.96	0.46
6:KL:191:THR:HG21	7:KM:289:ALA:HB3	1.97	0.46
2:LD:87:TRP:CD1	2:LD:89:GLY:H	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:LM:206:TRP:HZ3	3:Lf:214:ALA:HB3	1.80	0.46
4:MH:324:TRP:HA	4:MH:339:MET:HB3	1.98	0.46
1:FG:1003:ASN:HA	1:FG:1006:ILE:HD12	1.97	0.46
4:YH:223:TYR:HB2	4:YH:242:ILE:HG13	1.96	0.46
11:DC:168:LYS:O	11:DC:173:LYS:NZ	2.48	0.46
5:BK:52:THR:HA	5:BK:55:LYS:HG2	1.97	0.46
11:JC:122:ASP:OD1	11:JC:125:SER:OG	2.29	0.46
11:LC:69:GLN:OE1	8:DN:115:GLN:NE2	2.44	0.46
6:CL:191:THR:HG21	7:CM:289:ALA:HB3	1.96	0.46
3:Cf:246:LEU:HB3	3:Cf:255:LEU:HB2	1.97	0.46
5:DK:129:GLU:OE1	5:DK:129:GLU:N	2.47	0.46
2:Fd:119:ILE:HD12	2:Fd:135:ILE:HD12	1.96	0.46
3:AF:216:ILE:HD11	3:AF:219:ARG:HB2	1.97	0.46
7:GM:308:ASP:OD1	7:GM:308:ASP:N	2.48	0.46
4:HH:292:SER:OG	4:HH:293:ARG:N	2.48	0.46
7:HM:124:VAL:HB	7:HM:144:THR:HG23	1.97	0.46
7:HM:199:LYS:HA	7:HM:219:ALA:HB3	1.98	0.46
2:Id:36:ASP:OD1	2:Id:36:ASP:N	2.47	0.46
11:KC:172:GLU:HA	11:KC:175:ILE:HG12	1.97	0.46
4:JH:327:SER:HA	4:JH:336:ALA:O	2.15	0.46
7:JM:284:LEU:HB2	7:JM:302:ARG:HH12	1.81	0.46
4:AH:172:SER:OG	4:AH:173:GLN:N	2.44	0.46
3:LF:235:GLY:HA2	3:LF:243:MET:HE1	1.96	0.46
1:EG:884:PRO:HG2	1:FG:1040:LEU:HD21	1.96	0.46
5:MK:114:ILE:HB	5:MK:154:ILE:HG22	1.98	0.46
6:AL:94:VAL:HA	6:AL:97:ILE:HG12	1.97	0.46
1:FG:966:GLN:O	1:FG:970:ASN:ND2	2.48	0.46
5:BK:51:ALA:O	8:BN:44:LYS:NZ	2.46	0.46
11:JC:173:GLU:HA	11:JC:176:ILE:HG12	1.96	0.46
4:DH:302:ALA:O	4:DH:303:ARG:NH1	2.42	0.46
1:IG:869:MET:HB2	1:IG:1041:PHE:HE1	1.80	0.46
1:AG:963:SER:HB3	1:PG:1010:THR:HB	1.97	0.46
3:Ef:243:MET:O	3:Ef:257:SER:N	2.46	0.46
8:FN:89:GLY:O	8:FN:104:ASN:ND2	2.48	0.46
2:HD:36:ASP:HA	2:HD:39:ILE:HD12	1.97	0.46
11:GC:154:ASP:OD2	8:LN:85:CYS:N	2.44	0.46
2:Hd:84:SER:H	11:DC:267:ALA:HB3	1.80	0.46
6:IL:94:VAL:HA	6:IL:97:ILE:HG12	1.98	0.46
11:KC:101:LEU:HB2	11:KC:105:ILE:HG23	1.96	0.46
5:JK:59:ASP:HA	5:JK:62:LYS:HG2	1.97	0.46
4:KH:183:ASP:HB3	4:KH:259:TYR:HA	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:KM:186:SER:HA	7:KM:205:TYR:HB2	1.97	0.46
2:LD:140:GLY:HA2	2:Ld:60:LYS:HD2	1.97	0.46
5:LK:93:TRP:O	2:Ld:24:LYS:N	2.48	0.46
5:AK:121:SER:OG	5:AK:122:LYS:N	2.47	0.46
1:Mg:792:GLN:O	1:Mg:795:GLN:NE2	2.48	0.46
4:MH:316:ASN:HB3	4:MH:334:THR:HG22	1.97	0.46
4:MH:357:LYS:HZ2	4:MH:359:GLU:HG2	1.81	0.46
5:MK:87:GLN:HB3	5:MK:128:ARG:HH12	1.79	0.46
8:MN:63:GLY:HA3	2:AD:27:LYS:HB2	1.98	0.46
4:VH:174:GLY:HA2	4:VH:216:GLN:HE21	1.81	0.46
1:YG:791:GLN:N	1:YG:793:GLU:OE1	2.49	0.46
11:DC:167:PRO:HA	11:DC:172:GLU:HG3	1.98	0.46
2:BD:150:ASN:OD1	2:BD:150:ASN:N	2.46	0.46
4:BH:110:LYS:HA	4:BH:113:LYS:HG2	1.97	0.46
1:GG:881:GLU:HB2	1:HG:911:LYS:HD3	1.97	0.46
5:CK:75:LEU:HD21	5:CK:181:GLU:HB3	1.97	0.46
11:AC:155:ASP:OD1	11:AC:155:ASP:N	2.47	0.46
7:DM:261:ALA:HB1	7:DM:263:ILE:HD11	1.97	0.46
1:AG:891:THR:OG1	1:AG:892:GLY:N	2.48	0.46
1:AG:966:GLN:O	1:AG:970:ASN:ND2	2.49	0.46
6:EL:170:ASP:HA	6:EL:226:ASN:HD22	1.81	0.46
6:FL:113:ASP:OD1	6:FL:113:ASP:N	2.33	0.46
7:FM:215:ARG:NH2	7:FM:232:ASP:OD2	2.48	0.46
3:Ff:216:ILE:HD12	3:Ff:216:ILE:HA	1.82	0.46
1:BG:935:ILE:HG22	1:BG:942:THR:HG22	1.96	0.46
1:Gg:811:ASP:OD1	1:Gg:811:ASP:N	2.48	0.46
5:GK:115:THR:O	5:GK:182:ILE:HA	2.16	0.46
6:GL:129:THR:O	6:GL:133:PHE:HB2	2.15	0.46
2:Gd:64:PRO:HG2	2:Gd:67:LYS:HB2	1.97	0.46
1:CG:891:THR:OG1	1:CG:892:GLY:N	2.48	0.46
1:CG:1024:ASN:OD1	1:CG:1024:ASN:N	2.45	0.46
4:IH:230:LEU:HB2	4:IH:233:LEU:HB3	1.98	0.46
7:IM:222:ILE:HD13	7:IM:241:PHE:HD1	1.81	0.46
2:Jd:79:LEU:O	2:Jd:127:SER:OG	2.33	0.46
4:AH:203:ASN:OD1	4:AH:216:GLN:NE2	2.49	0.46
3:LF:266:GLN:OE1	3:YF:233:ARG:NH2	2.43	0.46
4:LH:213:LEU:HB3	4:LH:215:ILE:HD11	1.98	0.46
6:ML:190:MET:HE3	6:ML:190:MET:HB3	1.78	0.46
4:WH:185:THR:HG21	4:WH:263:ALA:HA	1.97	0.46
11:EC:122:ASP:OD1	11:EC:125:SER:OG	2.34	0.46
2:CD:75:ASN:ND2	7:CM:306:GLN:O	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IG:966:GLN:O	1:IG:970:ASN:ND2	2.48	0.46
1:NG:1017:GLN:OE1	1:OG:1020:GLN:NE2	2.42	0.46
5:FK:148:GLY:H	2:Fd:30:ILE:HD13	1.80	0.46
2:Fd:36:ASP:N	2:Fd:36:ASP:OD1	2.46	0.46
11:BC:109:VAL:HG13	11:BC:208:GLY:HA3	1.96	0.46
11:BC:176:TRP:O	11:BC:180:THR:OG1	2.30	0.46
1:BG:910:ASP:OD1	1:BG:910:ASP:N	2.49	0.46
2:GD:107:ARG:HB3	2:GD:155:GLU:HB2	1.98	0.46
1:CG:951:HIS:O	1:CG:955:ARG:NE	2.43	0.46
2:ID:39:ILE:HD12	6:IL:220:ILE:HG13	1.98	0.46
4:IH:206:TRP:NE1	4:IH:210:SER:O	2.47	0.46
6:IL:115:GLN:HB3	6:IL:126:ILE:HB	1.96	0.46
4:JH:230:LEU:H	4:JH:233:LEU:HD12	1.80	0.46
7:JM:159:GLY:HA2	7:JM:181:PRO:HG3	1.97	0.46
2:Jd:148:TYR:HB2	2:Jd:153:VAL:HG12	1.97	0.46
1:DG:1019:ALA:O	1:DG:1023:PHE:HB2	2.15	0.46
3:KF:233:ARG:NH1	3:YF:269:SER:OG	2.49	0.46
2:Kd:134:ASP:OD2	2:Kd:138:GLN:NE2	2.48	0.46
5:AK:106:LEU:HB3	5:AK:149:VAL:HG23	1.97	0.46
4:MH:170:ARG:HH12	4:MH:247:ALA:HB3	1.81	0.46
6:AL:225:GLN:HA	2:AD:29:PRO:HG2	1.96	0.46
7:AM:124:VAL:O	7:AM:144:THR:HA	2.15	0.46
2:CD:107:ARG:HE	2:CD:155:GLU:HG3	1.80	0.46
4:DH:207:ASP:O	4:DH:210:SER:OG	2.34	0.46
1:NG:900:ILE:HG13	1:NG:918:THR:HB	1.98	0.46
7:DM:215:ARG:HG3	7:DM:234:GLU:HB3	1.97	0.46
8:FN:77:ASP:OD1	8:FN:77:ASP:N	2.35	0.46
11:BC:57:MET:SD	11:BC:57:MET:N	2.85	0.46
2:GD:47:SER:O	2:GD:51:SER:OG	2.32	0.46
1:Gg:797:ARG:NH2	4:HH:121:PRO:O	2.48	0.46
1:Gg:819:VAL:HG12	4:WH:199:PRO:HG3	1.98	0.46
7:GM:241:PHE:O	7:GM:261:ALA:HA	2.15	0.46
2:Gd:72:THR:OG1	2:Gd:73:ILE:N	2.48	0.46
4:HH:285:GLU:O	4:HH:314:ARG:NH2	2.49	0.46
7:HM:191:LEU:HD21	7:HM:194:LEU:HD13	1.97	0.46
1:Bg:816:GLU:OE2	4:AH:200:SER:OG	2.34	0.46
7:IM:215:ARG:NH1	7:IM:232:ASP:OD2	2.48	0.46
11:KC:116:THR:HG22	4:CH:328:MET:HE1	1.97	0.46
6:JL:200:ALA:HA	6:JL:203:LEU:HD23	1.98	0.46
3:Jf:233:ARG:O	3:Jf:236:SER:OG	2.33	0.46
5:MK:163:LYS:HA	5:MK:163:LYS:HD2	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:MK:185:ARG:NH2	6:AL:214:ILE:O	2.49	0.46
7:MM:174:GLN:NE2	7:MM:193:GLN:OE1	2.49	0.46
3:Bf:246:LEU:HD23	3:Bf:255:LEU:HD13	1.97	0.46
1:GG:1017:GLN:NE2	1:GG:1018:GLN:OE1	2.46	0.46
11:HC:109:VAL:HG13	11:HC:208:GLY:HA3	1.97	0.46
11:IC:102:GLU:HG2	11:IC:103:HIS:CD2	2.51	0.46
2:ED:140:GLY:O	2:Ed:60:LYS:NZ	2.48	0.46
7:EM:274:THR:OG1	7:EM:275:ASP:N	2.49	0.46
2:FD:31:ASN:ND2	2:Fd:34:SER:O	2.48	0.46
2:Fd:82:ARG:NH2	2:Fd:83:ALA:O	2.44	0.46
5:HK:81:SER:OG	5:HK:173:ASP:O	2.34	0.46
3:IF:263:LYS:HE3	3:IF:263:LYS:HB3	1.82	0.46
6:IL:170:ASP:N	6:IL:170:ASP:OD1	2.36	0.46
2:JD:111:LYS:HE3	2:Jd:120:SER:H	1.81	0.46
7:KM:279:ILE:HB	7:KM:298:VAL:HG22	1.98	0.46
8:KN:63:GLY:HA3	2:LD:27:LYS:HB2	1.98	0.46
4:LH:130:LEU:HA	4:LH:133:ILE:HG12	1.98	0.46
4:LH:131:LYS:HE3	1:YG:812:TRP:HE1	1.81	0.46
6:ML:165:VAL:HG12	6:ML:231:ILE:HG12	1.98	0.46
6:ML:200:ALA:O	7:MM:230:ARG:NH2	2.49	0.46
7:MM:123:VAL:HG22	7:MM:143:THR:HB	1.97	0.46
4:WH:313:VAL:HG23	4:WH:337:TYR:HB2	1.98	0.46
1:FG:951:HIS:O	1:FG:955:ARG:NE	2.48	0.46
4:ZH:187:ALA:HB1	4:ZH:262:ASN:HB2	1.98	0.46
4:BH:285:GLU:HG2	11:JC:205:GLU:HB2	1.97	0.46
11:LC:121:ASP:OD1	11:LC:124:SER:OG	2.30	0.46
4:CH:295:LEU:HD21	4:CH:306:LEU:HB2	1.98	0.46
1:LG:958:SER:O	1:LG:962:SER:OG	2.34	0.46
2:FD:32:ASN:OD1	2:FD:32:ASN:N	2.49	0.46
4:FH:179:LEU:O	4:FH:212:THR:HA	2.16	0.46
1:BG:1019:ALA:O	1:BG:1023:PHE:HB2	2.16	0.46
6:HL:165:VAL:HG21	6:HL:190:MET:HB3	1.98	0.46
7:HM:229:ASN:OD1	7:HM:229:ASN:N	2.48	0.46
4:IH:180:VAL:HG13	4:IH:253:ASP:HA	1.98	0.46
4:AH:202:PHE:HA	4:AH:217:ALA:HA	1.98	0.46
7:MM:180:ASP:OD1	7:MM:199:LYS:N	2.49	0.46
7:AM:275:ASP:N	7:AM:275:ASP:OD1	2.49	0.46
7:BM:300:ASP:OD2	7:BM:302:ARG:NE	2.48	0.46
3:Bf:209:ILE:HG13	3:Bf:225:SER:HB3	1.97	0.46
11:HC:182:ARG:HA	11:HC:185:LYS:HE2	1.97	0.46
11:IC:163:VAL:HG12	11:IC:166:LEU:HD11	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IG:917:ASN:N	1:IG:917:ASN:OD1	2.48	0.46
1:OG:867:ASP:OD1	1:OG:867:ASP:N	2.47	0.46
1:PG:1003:ASN:HA	1:PG:1006:ILE:HD12	1.97	0.46
8:DN:58:LEU:HD12	8:DN:68:CYS:HB2	1.97	0.46
8:FN:102:VAL:HA	8:FN:108:VAL:HA	1.97	0.46
2:HD:85:VAL:HG12	5:HK:153:ILE:HG23	1.97	0.46
11:GC:204:GLU:HB2	4:LH:285:GLU:HG2	1.98	0.46
3:HF:245:LYS:HE3	3:HF:257:SER:HA	1.98	0.46
6:JL:121:ASP:OD1	6:JL:121:ASP:N	2.43	0.46
4:KH:221:TYR:OH	4:YH:138:GLU:OE1	2.34	0.46
4:KH:324:TRP:HA	4:KH:339:MET:HB3	1.98	0.46
4:LH:189:TRP:HE1	4:LH:230:LEU:HB3	1.81	0.46
4:LH:198:ASP:OD2	4:LH:201:SER:OG	2.32	0.46
2:Ld:89:GLY:HA2	2:Ld:118:LEU:HD23	1.98	0.46
1:EG:1017:GLN:NE2	1:EG:1018:GLN:OE1	2.48	0.46
4:VH:138:GLU:HB3	4:CH:221:TYR:HE2	1.81	0.46
4:YH:107:ILE:HG23	4:YH:110:LYS:HE2	1.98	0.46
5:BK:129:GLU:OE1	5:BK:129:GLU:N	2.49	0.46
11:FC:114:ARG:HG2	11:FC:130:ARG:HG2	1.96	0.46
11:MC:106:LEU:HD12	11:MC:107:PRO:HD2	1.97	0.46
11:MC:129:ASP:N	11:MC:129:ASP:OD1	2.47	0.46
2:CD:88:SER:HA	2:CD:120:SER:HA	1.97	0.46
7:CM:204:LEU:HB2	7:CM:207:ILE:HD11	1.98	0.46
1:HG:1003:ASN:HA	1:HG:1006:ILE:HD12	1.96	0.46
1:OG:951:HIS:O	1:OG:955:ARG:NE	2.40	0.46
11:AC:92:ASP:OD1	11:AC:148:TRP:NE1	2.35	0.46
7:DM:273:ALA:HB1	7:DM:277:SER:HB2	1.97	0.46
2:Dd:36:ASP:OD1	2:Dd:36:ASP:N	2.47	0.46
4:EH:311:MET:HG3	4:EH:339:MET:HG3	1.98	0.46
7:EM:201:THR:HG22	7:EM:221:LYS:HD2	1.98	0.46
7:EM:215:ARG:HG3	7:EM:234:GLU:HB3	1.97	0.46
3:FF:254:ILE:O	3:FF:261:VAL:HA	2.16	0.46
5:FK:166:THR:HG22	5:FK:168:TYR:H	1.80	0.46
7:FM:271:SER:OG	7:FM:290:ASP:OD1	2.34	0.46
7:HM:181:PRO:O	7:HM:201:THR:OG1	2.33	0.46
6:JL:131:LYS:O	6:JL:141:ASN:ND2	2.46	0.46
2:KD:158:TYR:O	2:Kd:137:TYR:OH	2.34	0.46
7:KM:117:ARG:HG2	7:KM:137:TYR:HB3	1.98	0.46
5:LK:92:ASN:O	5:LK:95:SER:OG	2.31	0.46
2:Ld:107:ARG:O	2:Ld:155:GLU:HA	2.16	0.46
7:MM:284:LEU:HD23	7:MM:310:LYS:HE2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:YF:247:ILE:HG23	3:YF:254:ILE:HG12	1.97	0.46
7:AM:256:HIS:O	7:AM:259:SER:OG	2.34	0.46
5:BK:73:ASN:OD1	5:BK:185:ARG:NE	2.48	0.46
2:CD:40:LYS:HA	2:CD:43:GLU:HG2	1.98	0.46
4:DH:343:PRO:HA	4:DH:358:VAL:HB	1.98	0.46
1:OG:1017:GLN:NE2	1:OG:1018:GLN:OE1	2.49	0.46
1:AG:865:THR:HB	1:PG:920:SER:HB2	1.98	0.45
1:AG:941:ARG:HH21	1:PG:1030:GLU:HG2	1.81	0.45
1:AG:1019:ALA:O	1:AG:1023:PHE:HB2	2.15	0.45
5:EK:93:TRP:CD1	6:EL:46:PRO:HD3	2.51	0.45
4:FH:309:GLU:O	4:FH:341:LYS:NZ	2.45	0.45
5:FK:38:VAL:HA	5:FK:41:LEU:HD23	1.97	0.45
3:Ff:243:MET:O	3:Ff:257:SER:N	2.49	0.45
2:GD:60:LYS:HB2	2:GD:60:LYS:HE3	1.84	0.45
7:HM:207:ILE:HD11	7:HM:224:LEU:HB3	1.99	0.45
8:HN:66:SER:OG	8:HN:67:THR:N	2.44	0.45
6:IL:129:THR:O	6:IL:133:PHE:HB2	2.16	0.45
7:IM:275:ASP:N	7:IM:275:ASP:OD1	2.47	0.45
4:JH:203:ASN:HB3	4:JH:216:GLN:HB3	1.98	0.45
3:KF:243:MET:O	3:KF:257:SER:N	2.49	0.45
6:KL:165:VAL:HG12	6:KL:231:ILE:HG12	1.97	0.45
8:KN:87:TRP:O	8:KN:88:HIS:ND1	2.48	0.45
5:LK:111:LYS:HD3	5:LK:114:ILE:HD11	1.98	0.45
3:MF:219:ARG:NH1	3:ZF:269:SER:O	2.48	0.45
5:MK:120:SER:HA	5:MK:178:ALA:HA	1.97	0.45
3:VF:214:ALA:HB3	3:VF:221:TRP:HB2	1.97	0.45
3:YF:265:SER:OG	3:YF:267:GLU:OE2	2.34	0.45
4:ZH:151:PRO:HA	4:ZH:248:VAL:HG13	1.98	0.45
7:AM:273:ALA:HB1	7:AM:277:SER:HB2	1.97	0.45
5:BK:85:ALA:HB3	5:BK:88:SER:HB2	1.98	0.45
3:Bf:256:THR:HG21	3:Bf:260:GLN:HE21	1.81	0.45
1:GG:1030:GLU:HG2	1:HG:941:ARG:HH21	1.81	0.45
11:LC:97:ASN:OD1	11:LC:97:ASN:N	2.38	0.45
2:CD:83:ALA:HA	5:CK:154:ILE:O	2.16	0.45
4:DH:207:ASP:OD1	4:DH:207:ASP:N	2.35	0.45
1:LG:1006:ILE:O	1:LG:1010:THR:OG1	2.34	0.45
1:NG:1006:ILE:O	1:NG:1010:THR:OG1	2.34	0.45
11:AC:90:ASN:N	11:AC:90:ASN:OD1	2.48	0.45
2:Dd:81:ALA:HB3	2:Dd:128:LEU:HD11	1.98	0.45
5:EK:73:ASN:HA	5:EK:185:ARG:HA	1.99	0.45
7:EM:279:ILE:HB	7:EM:298:VAL:HG22	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:FD:105:ARG:HB2	2:FD:153:VAL:HG12	1.97	0.45
5:FK:92:ASN:O	5:FK:95:SER:OG	2.33	0.45
3:Ff:245:LYS:N	3:Ff:255:LEU:O	2.47	0.45
4:GH:145:PRO:HG3	4:HH:131:LYS:HG2	1.98	0.45
2:Gd:150:ASN:OD1	2:Gd:150:ASN:N	2.43	0.45
5:HK:50:ASP:OD1	5:HK:50:ASP:N	2.48	0.45
1:CG:871:ALA:HB2	1:CG:889:ILE:HD13	1.98	0.45
4:IH:225:ASN:HD21	4:JH:176:VAL:H	1.65	0.45
6:IL:136:SER:HG	7:IM:314:ARG:HH22	1.60	0.45
6:IL:145:TYR:HA	6:IL:148:LEU:HD23	1.96	0.45
5:JK:92:ASN:O	5:JK:95:SER:OG	2.34	0.45
6:JL:114:ILE:HD12	6:JL:127:ILE:HG12	1.99	0.45
4:AH:316:ASN:N	4:AH:316:ASN:OD1	2.48	0.45
7:KM:214:ILE:O	7:KM:215:ARG:NH1	2.49	0.45
5:BK:111:LYS:HG3	5:BK:114:ILE:HD11	1.97	0.45
11:HC:170:LYS:HA	11:HC:173:LYS:HE2	1.97	0.45
3:DF:214:ALA:HB3	3:DF:221:TRP:HB2	1.98	0.45
1:PG:966:GLN:O	1:PG:970:ASN:ND2	2.49	0.45
8:DN:103:CYS:N	8:DN:107:TYR:O	2.41	0.45
5:EK:71:GLY:O	2:FD:27:LYS:NZ	2.49	0.45
7:FM:262:GLU:HA	7:FM:280:TYR:O	2.16	0.45
7:JM:271:SER:OG	7:JM:290:ASP:OD1	2.34	0.45
4:AH:238:MET:HE1	4:BH:251:ARG:HD3	1.99	0.45
5:KK:87:GLN:HB3	5:KK:128:ARG:HH12	1.82	0.45
2:Kd:148:TYR:HB2	2:Kd:153:VAL:HG12	1.98	0.45
2:MD:73:ILE:HG22	2:MD:147:VAL:HB	1.97	0.45
4:YH:191:ILE:HD12	4:YH:206:TRP:HE1	1.82	0.45
3:Af:253:ARG:HH21	3:Af:255:LEU:H	1.65	0.45
1:GG:966:GLN:O	1:GG:970:ASN:ND2	2.49	0.45
11:HC:105:ILE:HA	11:HC:140:PHE:HA	1.97	0.45
11:MC:150:TYR:O	11:MC:198:ASN:ND2	2.49	0.45
7:CM:303:GLU:OE2	3:Cf:251:GLN:NE2	2.50	0.45
4:EH:170:ARG:HG2	4:EH:245:GLN:HG3	1.98	0.45
5:EK:121:SER:OG	5:EK:122:LYS:N	2.49	0.45
2:GD:67:LYS:HE3	2:Gd:62:ILE:HG13	1.98	0.45
11:GC:55:ARG:NH1	1:HG:1033:SER:O	2.50	0.45
5:HK:129:GLU:OE1	5:HK:129:GLU:N	2.49	0.45
1:CG:884:PRO:HA	1:CG:901:GLY:O	2.16	0.45
2:Id:78:ASN:OD1	2:Id:78:ASN:N	2.50	0.45
2:Id:107:ARG:O	2:Id:155:GLU:HA	2.16	0.45
6:JL:170:ASP:N	6:JL:170:ASP:OD1	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AH:220:LEU:HD12	4:BH:138:GLU:HG3	1.98	0.45
2:Kd:60:LYS:NZ	2:Kd:61:VAL:O	2.49	0.45
3:LF:266:GLN:O	3:LF:269:SER:OG	2.33	0.45
1:Lg:808:LEU:HA	1:Lg:811:ASP:HB3	1.98	0.45
7:LM:124:VAL:O	7:LM:144:THR:HA	2.16	0.45
8:BN:84:CYS:SG	8:BN:85:CYS:N	2.89	0.45
1:Dg:800:ASP:OD1	1:Dg:800:ASP:N	2.47	0.45
1:JG:885:ILE:O	1:JG:900:ILE:HA	2.17	0.45
1:JG:920:SER:HB2	1:KG:865:THR:HB	1.99	0.45
1:JG:1017:GLN:NE2	1:KG:1020:GLN:OE1	2.50	0.45
1:KG:917:ASN:HA	1:KG:931:SER:HA	1.99	0.45
1:NG:968:PHE:O	1:NG:972:PHE:HB2	2.16	0.45
11:AC:102:LEU:HB2	11:AC:106:ILE:HG23	1.98	0.45
2:AD:148:TYR:O	2:AD:152:GLN:N	2.50	0.45
3:FF:222:LEU:HD21	3:FF:254:ILE:HD12	1.97	0.45
5:FK:71:GLY:O	2:GD:27:LYS:NZ	2.50	0.45
2:GD:36:ASP:HA	2:GD:39:ILE:HD12	1.98	0.45
8:GN:99:GLY:O	8:GN:113:SER:OG	2.33	0.45
11:GC:234:THR:HG23	11:GC:241:HIS:HD2	1.81	0.45
6:HL:97:ILE:O	6:HL:101:SER:HB3	2.17	0.45
11:KC:244:ASP:OD1	11:LC:126:ARG:NE	2.43	0.45
5:JK:81:SER:OG	5:JK:173:ASP:O	2.35	0.45
1:EG:871:ALA:HB2	1:EG:889:ILE:HD13	1.99	0.45
1:EG:920:SER:HB2	1:FG:865:THR:HB	1.99	0.45
1:EG:1006:ILE:O	1:EG:1010:THR:OG1	2.35	0.45
2:MD:158:TYR:O	2:Md:137:TYR:OH	2.31	0.45
10:ZX:24:UNK:O	10:ZX:32:UNK:N	2.49	0.45
7:AM:162:VAL:HG12	7:AM:182:LYS:HB2	1.98	0.45
11:HC:226:VAL:HB	11:HC:249:ILE:HG22	1.98	0.45
11:IC:176:TRP:O	11:IC:180:THR:OG1	2.29	0.45
11:MC:109:VAL:HG13	11:MC:136:LYS:H	1.82	0.45
11:MC:234:THR:HG21	11:MC:244:ASP:HB2	1.96	0.45
2:CD:116:PRO:HG2	2:CD:118:LEU:HD21	1.98	0.45
4:EH:278:ASP:OD1	4:EH:278:ASP:N	2.50	0.45
7:FM:235:LEU:HB2	7:FM:255:THR:HG22	1.98	0.45
4:GH:196:LEU:HD13	4:GH:204:ILE:HD11	1.99	0.45
4:GH:208:LYS:O	4:GH:231:ARG:NH2	2.48	0.45
11:GC:121:ASP:OD1	11:GC:124:SER:OG	2.33	0.45
7:KM:190:ASN:OD1	7:KM:192:ARG:NH2	2.40	0.45
3:MF:224:GLY:N	3:MF:228:SER:O	2.46	0.45
5:MK:45:VAL:HG12	5:MK:48:ALA:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:VH:339:MET:N	4:VH:339:MET:SD	2.90	0.45
7:AM:313:ASP:H	7:AM:316:ASN:HB2	1.82	0.45
8:AN:99:GLY:HA3	8:AN:114:LEU:HB3	1.98	0.45
10:AX:22:UNK:HA	10:AX:77:UNK:HA	1.99	0.45
2:BD:88:SER:HA	2:BD:120:SER:HA	1.98	0.45
2:BD:88:SER:N	4:CH:351:GLY:O	2.50	0.45
3:Cf:232:VAL:HG21	3:Cf:244:VAL:HG21	1.99	0.45
1:HG:876:SER:OG	1:HG:1031:VAL:O	2.30	0.45
1:OG:946:SER:OG	1:OG:1030:GLU:O	2.31	0.45
1:OG:966:GLN:O	1:OG:970:ASN:ND2	2.49	0.45
1:AG:1042:THR:OG1	1:AG:1043:GLN:OE1	2.35	0.45
1:CG:917:ASN:HA	1:CG:931:SER:HA	1.97	0.45
4:IH:282:HIS:HB3	4:IH:287:VAL:HB	1.98	0.45
11:KC:41:LYS:HA	11:KC:44:ARG:HE	1.82	0.45
2:JD:155:GLU:OE2	2:Jd:133:ARG:NE	2.50	0.45
7:JM:188:PHE:HB3	7:JM:208:LYS:HD3	1.98	0.45
2:KD:62:ILE:HD12	2:KD:62:ILE:HA	1.88	0.45
8:KN:62:ASN:OD1	8:KN:62:ASN:N	2.47	0.45
4:LH:114:ASP:HA	4:LH:117:ARG:HG2	1.98	0.45
5:LK:81:SER:OG	5:LK:173:ASP:O	2.35	0.45
2:Ld:72:THR:OG1	2:Ld:73:ILE:N	2.49	0.45
4:MH:298:SER:HB2	4:MH:357:LYS:HG2	1.98	0.45
3:Mf:218:GLY:H	3:Mf:247:ILE:HD11	1.81	0.45
4:VH:198:ASP:OD1	4:VH:200:SER:OG	2.33	0.45
3:YF:243:MET:N	3:YF:243:MET:SD	2.90	0.45
6:AL:91:VAL:HA	6:AL:94:VAL:HG22	1.99	0.45
6:AL:115:GLN:HE21	2:AD:28:PRO:HD3	1.82	0.45
11:LC:97:ASN:HB3	11:LC:144:PRO:HG3	1.97	0.45
11:LC:101:LEU:HB2	11:LC:105:ILE:HG23	1.99	0.45
6:CL:98:TYR:O	6:CL:101:SER:OG	2.34	0.45
1:HG:885:ILE:O	1:HG:900:ILE:HA	2.17	0.45
1:KG:876:SER:OG	1:KG:1031:VAL:O	2.29	0.45
2:AD:123:THR:OG1	2:AD:124:LYS:N	2.48	0.45
3:EF:216:ILE:HD11	3:EF:219:ARG:HB2	1.99	0.45
4:EH:131:LYS:HG2	4:DH:145:PRO:HG3	1.99	0.45
7:FM:306:GLN:HB3	7:FM:309:LEU:HB2	1.97	0.45
3:Gf:233:ARG:O	3:Gf:236:SER:OG	2.35	0.45
11:GC:132:TYR:O	11:FC:239:GLU:HA	2.17	0.45
4:HH:238:MET:H	4:HH:238:MET:HG2	1.67	0.45
7:HM:217:LYS:HA	7:HM:236:TRP:HB2	1.98	0.45
2:JD:85:VAL:HG12	5:JK:153:ILE:HG23	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AH:201:SER:HA	4:AH:219:LYS:HB2	1.99	0.45
2:KD:67:LYS:HE3	2:KD:67:LYS:HB3	1.72	0.45
2:MD:140:GLY:HA2	2:Md:60:LYS:HD2	1.99	0.45
5:MK:163:LYS:NZ	5:MK:164:PRO:O	2.50	0.45
4:ZH:115:MET:HA	4:ZH:118:ASN:HB3	1.99	0.45
7:AM:207:ILE:HD11	7:AM:224:LEU:HB3	1.98	0.45
6:BL:57:VAL:HA	6:BL:60:VAL:HG22	1.99	0.45
7:BM:166:ASN:HA	7:BM:186:SER:HB3	1.99	0.45
1:GG:874:ASP:OD1	1:GG:874:ASP:N	2.50	0.45
11:HC:168:LYS:O	11:HC:170:LYS:NZ	2.49	0.45
11:LC:71:GLY:HA3	11:LC:184:TRP:HA	1.98	0.45
11:LC:170:LYS:HA	11:LC:173:LYS:HE2	1.99	0.45
6:CL:91:VAL:HA	6:CL:94:VAL:HG12	1.98	0.45
1:KG:1005:VAL:O	1:KG:1009:ALA:HB2	2.16	0.45
1:MG:1024:ASN:OD1	1:MG:1024:ASN:N	2.48	0.45
1:NG:1005:VAL:O	1:NG:1009:ALA:CB	2.65	0.45
3:EF:247:ILE:HG23	3:EF:254:ILE:HG12	1.98	0.45
5:EK:113:ALA:HA	5:EK:153:ILE:O	2.17	0.45
7:EM:256:HIS:O	7:EM:259:SER:OG	2.34	0.45
1:BG:885:ILE:O	1:BG:900:ILE:HA	2.17	0.45
1:BG:920:SER:HB2	1:CG:865:THR:HB	1.98	0.45
5:GK:119:TYR:HE2	5:GK:163:LYS:HB2	1.80	0.45
6:GL:108:ASP:OD2	6:GL:150:ASN:ND2	2.50	0.45
7:GM:290:ASP:HB3	7:GM:298:VAL:HG21	1.98	0.45
5:JK:113:ALA:HA	5:JK:153:ILE:O	2.17	0.45
7:LM:133:TYR:HE1	7:LM:154:LYS:H	1.63	0.45
2:Md:86:ASP:HA	2:Md:121:ILE:O	2.17	0.45
4:BH:189:TRP:HE1	4:BH:232:GLY:H	1.64	0.45
6:BL:44:HIS:N	6:BL:48:ASN:OD1	2.49	0.45
3:Df:245:LYS:NZ	3:Df:256:THR:O	2.41	0.45
2:Ed:86:ASP:OD2	11:AC:115:ARG:NH2	2.43	0.45
11:CC:175:ILE:HA	11:CC:178:ILE:HG12	1.99	0.45
4:FH:123:ASN:OD1	4:FH:126:GLN:NE2	2.50	0.45
4:GH:229:ARG:NH2	4:HH:212:THR:OG1	2.50	0.45
3:JF:241:TYR:O	3:JF:256:THR:OG1	2.34	0.45
1:DG:931:SER:O	1:DG:1042:THR:OG1	2.34	0.45
7:KM:279:ILE:O	7:KM:298:VAL:HA	2.17	0.45
3:MF:219:ARG:HH12	3:MF:233:ARG:HE	1.65	0.45
4:MH:244:GLY:O	4:MH:245:GLN:NE2	2.50	0.45
10:VX:25:UNK:N	10:VX:71:UNK:O	2.50	0.45
3:XF:226:ASN:ND2	3:XF:228:SER:OG	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:XF:258:SER:OG	3:XF:260:GLN:NE2	2.43	0.45
2:BD:35:ASP:O	2:BD:38:THR:OG1	2.31	0.45
11:HC:116:THR:O	11:HC:116:THR:OG1	2.35	0.45
11:HC:150:TYR:HB2	11:HC:202:ILE:HD12	1.99	0.45
5:CK:129:GLU:N	5:CK:129:GLU:OE1	2.50	0.45
4:DH:226:LEU:HB2	4:DH:241:LEU:HD21	1.99	0.45
1:HG:944:LEU:HD11	1:HG:1031:VAL:HG12	1.98	0.45
11:CC:117:LEU:HB2	11:CC:127:ILE:HG22	1.98	0.44
11:GC:106:LEU:HD12	11:GC:107:PRO:HD2	1.99	0.44
4:HH:225:ASN:N	4:HH:225:ASN:OD1	2.50	0.44
5:IK:92:ASN:O	5:IK:95:SER:OG	2.31	0.44
1:DG:874:ASP:OD1	1:DG:874:ASP:N	2.50	0.44
4:KH:325:LEU:HG	4:KH:339:MET:HA	1.99	0.44
4:LH:178:SER:OG	4:LH:251:ARG:NH1	2.50	0.44
2:Ld:35:ASP:O	2:Ld:38:THR:OG1	2.30	0.44
5:AK:81:SER:OG	5:AK:173:ASP:O	2.34	0.44
2:MD:36:ASP:OD1	2:MD:36:ASP:N	2.49	0.44
6:ML:53:ASP:OD1	6:ML:53:ASP:N	2.50	0.44
7:MM:146:LEU:HB2	7:MM:165:ILE:HG12	1.99	0.44
1:FG:876:SER:HB3	1:GG:941:ARG:HG2	1.99	0.44
11:DC:215:LEU:HD22	11:DC:220:MET:HG3	1.99	0.44
2:Ad:107:ARG:O	2:Ad:155:GLU:HA	2.18	0.44
3:Af:223:ILE:HD12	3:Af:223:ILE:HA	1.91	0.44
2:BD:29:PRO:HG2	6:BL:225:GLN:HA	1.98	0.44
2:Bd:93:GLU:H	2:Bd:93:GLU:HG3	1.60	0.44
11:EC:107:LEU:HD12	11:EC:108:PRO:HD2	1.99	0.44
11:EC:147:THR:OG1	11:EC:148:TRP:N	2.49	0.44
6:CL:124:THR:HA	6:CL:231:ILE:O	2.16	0.44
7:CM:288:ARG:NH1	7:CM:290:ASP:OD2	2.44	0.44
1:IG:1006:ILE:O	1:IG:1010:THR:OG1	2.35	0.44
11:AC:117:THR:OG1	11:AC:129:SER:OG	2.33	0.44
7:DM:276:ALA:H	7:DM:295:ASN:HB2	1.81	0.44
7:DM:306:GLN:HG3	7:DM:308:ASP:H	1.82	0.44
1:Ag:811:ASP:OD1	1:Ag:811:ASP:N	2.50	0.44
4:EH:276:ALA:HA	11:MC:118:ASN:HD22	1.82	0.44
4:EH:295:LEU:HD11	4:EH:306:LEU:HB2	2.00	0.44
2:FD:32:ASN:ND2	2:Fd:34:SER:OG	2.50	0.44
2:FD:45:ALA:HA	2:FD:48:VAL:HG12	1.99	0.44
4:FH:161:SER:O	4:FH:164:SER:OG	2.35	0.44
6:FL:193:LEU:HD13	6:FL:193:LEU:HA	1.86	0.44
3:GF:265:SER:HB3	3:GF:268:ASP:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Gg:802:LEU:HD12	4:XH:115:MET:HG2	1.98	0.44
7:GM:158:VAL:HA	7:GM:178:LYS:HE2	1.99	0.44
6:HL:210:ASP:OD1	6:HL:210:ASP:N	2.38	0.44
6:IL:129:THR:HG22	6:IL:229:ILE:HG12	1.98	0.44
11:KC:95:ASP:O	11:KC:98:SER:OG	2.35	0.44
6:JL:108:ASP:OD2	6:JL:150:ASN:ND2	2.50	0.44
8:JN:109:SER:OG	11:EC:155:ASP:OD2	2.35	0.44
1:DG:925:GLU:H	1:DG:925:GLU:HG2	1.57	0.44
2:LD:83:ALA:HA	5:LK:154:ILE:O	2.17	0.44
2:LD:140:GLY:O	2:Ld:60:LYS:NZ	2.42	0.44
4:LH:148:PRO:HD2	3:YF:219:ARG:HG2	1.98	0.44
3:MF:248:ASP:HB3	3:MF:253:ARG:HG3	1.98	0.44
7:MM:197:TYR:HA	7:MM:217:LYS:HB3	1.98	0.44
4:VH:325:LEU:N	4:VH:338:GLU:O	2.50	0.44
2:BD:38:THR:HA	2:BD:41:LEU:HD12	1.98	0.44
5:CK:146:SER:OG	5:CK:147:GLN:NE2	2.48	0.44
11:AC:227:VAL:HB	11:AC:250:ILE:HG12	1.98	0.44
3:EF:254:ILE:O	3:EF:261:VAL:HA	2.18	0.44
1:Eg:797:ARG:H	1:Eg:797:ARG:HG3	1.68	0.44
11:CC:243:ASP:O	11:DC:128:SER:HA	2.17	0.44
7:FM:273:ALA:HB1	7:FM:277:SER:HB2	1.98	0.44
8:FN:66:SER:OG	8:FN:67:THR:N	2.50	0.44
11:GC:57:MET:N	11:GC:57:MET:SD	2.81	0.44
7:IM:273:ALA:O	7:IM:292:MET:HA	2.16	0.44
2:JD:67:LYS:HB3	2:Jd:62:ILE:HD11	1.99	0.44
7:KM:199:LYS:HA	7:KM:219:ALA:HB3	1.98	0.44
7:KM:308:ASP:OD1	3:Kf:253:ARG:NH2	2.50	0.44
3:LF:231:THR:HG23	4:MH:150:LYS:HE3	2.00	0.44
1:Lg:797:ARG:NH2	4:MH:121:PRO:O	2.51	0.44
3:Lf:245:LYS:NZ	3:Lf:256:THR:O	2.51	0.44
5:AK:61:ASN:HD21	5:AK:67:VAL:HB	1.82	0.44
3:MF:220:ALA:O	3:MF:231:THR:HA	2.16	0.44
6:ML:151:VAL:O	6:ML:155:LEU:HB2	2.17	0.44
2:Ad:110:GLY:HA3	2:Ad:158:TYR:HB2	1.99	0.44
11:HC:110:LEU:HD23	11:HC:212:TYR:HB2	1.98	0.44
11:MC:101:LEU:HB2	11:MC:105:ILE:HG23	1.99	0.44
5:CK:177:ASN:O	5:CK:179:ARG:NH1	2.48	0.44
3:Cf:223:ILE:HD12	3:Cf:223:ILE:HA	1.90	0.44
1:LG:931:SER:O	1:LG:1042:THR:OG1	2.36	0.44
2:Dd:71:LEU:O	2:Dd:133:ARG:NH1	2.44	0.44
3:EF:254:ILE:HB	3:EF:262:ILE:HB	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Eg:801:MET:H	1:Eg:801:MET:HG3	1.49	0.44
6:EL:190:MET:HE2	6:EL:190:MET:HB2	1.80	0.44
3:Ef:219:ARG:HA	3:Ef:232:VAL:O	2.17	0.44
2:FD:59:GLU:O	2:FD:63:THR:OG1	2.35	0.44
6:FL:177:HIS:HD1	7:FM:315:TYR:HH	1.61	0.44
8:FN:84:CYS:SG	8:FN:85:CYS:N	2.91	0.44
11:BC:225:TYR:HB3	11:BC:251:ALA:HB3	1.98	0.44
1:BG:898:LYS:HE2	1:BG:898:LYS:HB2	1.86	0.44
1:BG:966:GLN:O	1:BG:970:ASN:ND2	2.50	0.44
7:GM:168:VAL:H	7:GM:187:GLY:HA3	1.82	0.44
4:HH:158:VAL:HG13	4:HH:167:PRO:HG2	1.99	0.44
5:HK:162:ASP:OD1	5:HK:162:ASP:N	2.49	0.44
7:HM:303:GLU:OE1	7:HM:306:GLN:N	2.51	0.44
1:DG:966:GLN:O	1:DG:970:ASN:ND2	2.50	0.44
5:LK:60:LEU:HD13	5:LK:65:ILE:HG21	1.98	0.44
5:LK:109:PHE:O	5:LK:111:LYS:NZ	2.37	0.44
7:LM:194:LEU:HD22	7:LM:196:MET:HE1	1.98	0.44
4:XH:171:LEU:HD21	4:XH:241:LEU:HB3	2.00	0.44
6:AL:152:ILE:HD13	6:AL:152:ILE:HA	1.87	0.44
7:BM:118:TYR:CZ	7:BM:122:GLY:HA3	2.53	0.44
8:BN:51:CYS:HB2	8:BN:58:LEU:HD13	1.99	0.44
11:IC:111:LEU:O	11:IC:132:TYR:HA	2.16	0.44
11:JC:259:ASN:O	11:JC:263:TRP:NE1	2.50	0.44
11:MC:215:LEU:HD12	11:MC:220:MET:HB2	2.00	0.44
8:CN:62:ASN:OD1	8:CN:62:ASN:N	2.49	0.44
3:Cf:216:ILE:HD12	3:Cf:216:ILE:HA	1.81	0.44
2:DD:26:LYS:NZ	6:DL:110:GLN:O	2.45	0.44
1:JG:900:ILE:HD11	1:KG:865:THR:HG22	1.99	0.44
1:KG:925:GLU:H	1:KG:925:GLU:HG2	1.53	0.44
6:DL:133:PHE:HD1	6:DL:140:LEU:HA	1.83	0.44
1:AG:972:PHE:HD1	1:AG:972:PHE:HA	1.66	0.44
1:AG:1005:VAL:O	1:AG:1009:ALA:HB2	2.18	0.44
5:EK:46:ASP:OD1	5:EK:46:ASP:N	2.47	0.44
3:FF:243:MET:O	3:FF:257:SER:N	2.50	0.44
1:Fg:818:GLN:HG3	4:FH:205:GLN:HE22	1.82	0.44
5:GK:150:ASP:O	5:GK:152:ARG:NH2	2.51	0.44
3:Gf:209:ILE:H	3:Gf:225:SER:HG	1.63	0.44
2:ID:111:LYS:HA	2:ID:111:LYS:HD2	1.87	0.44
2:ID:123:THR:OG1	2:ID:126:GLU:OE1	2.33	0.44
1:Ig:800:ASP:N	1:Ig:800:ASP:OD1	2.50	0.44
4:JH:190:PRO:HA	4:JH:211:ASN:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:JK:115:THR:HB	5:JK:183:THR:HG23	2.00	0.44
4:AH:226:LEU:HB2	4:AH:241:LEU:HD21	2.00	0.44
3:KF:219:ARG:HG2	4:YH:148:PRO:HD2	1.98	0.44
7:KM:301:MET:HE3	7:KM:301:MET:HB3	1.89	0.44
2:LD:155:GLU:OE2	2:LD:157:ARG:NH2	2.51	0.44
3:LF:237:LYS:NZ	3:LF:243:MET:SD	2.90	0.44
4:LH:152:THR:OG1	4:LH:249:ASP:OD1	2.34	0.44
4:LH:182:LEU:HA	4:LH:188:PRO:HA	2.00	0.44
4:MH:289:PRO:O	4:MH:292:SER:OG	2.34	0.44
7:MM:290:ASP:HB2	7:MM:298:VAL:HG21	1.99	0.44
4:VH:207:ASP:N	4:VH:207:ASP:OD1	2.49	0.44
5:BK:121:SER:OG	5:BK:122:LYS:N	2.51	0.44
4:DH:322:PRO:HG2	4:DH:339:MET:HE1	1.98	0.44
6:DL:94:VAL:HA	6:DL:97:ILE:HG12	1.99	0.44
1:Eg:806:THR:O	1:Eg:810:GLN:NE2	2.45	0.44
1:BG:884:PRO:HA	1:BG:901:GLY:O	2.18	0.44
2:GD:97:ARG:HH12	5:GK:112:ILE:HD12	1.82	0.44
7:GM:275:ASP:HA	7:GM:295:ASN:H	1.83	0.44
2:Gd:78:ASN:N	2:Gd:78:ASN:OD1	2.50	0.44
6:HL:91:VAL:HA	6:HL:94:VAL:HG22	1.98	0.44
8:HN:45:MET:HE3	8:HN:45:MET:HB2	1.89	0.44
5:IK:138:ARG:HH21	7:IM:319:PHE:HA	1.82	0.44
4:AH:239:LEU:O	4:BH:250:TYR:OH	2.33	0.44
1:Mg:820:TYR:OH	4:MH:207:ASP:OD2	2.31	0.44
4:VH:213:LEU:HB3	4:VH:215:ILE:HD11	2.00	0.44
4:BH:134:TYR:HE1	1:Ag:813:LYS:HE2	1.83	0.44
4:BH:236:PRO:HG3	4:CH:212:THR:HG21	1.98	0.44
11:EC:216:LEU:HG	11:EC:221:MET:HB2	1.99	0.44
1:Cg:818:GLN:NE2	4:CH:205:GLN:OE1	2.47	0.44
5:CK:151:SER:OG	5:CK:153:ILE:O	2.35	0.44
7:CM:209:SER:HB3	7:CM:228:VAL:HG22	1.99	0.44
7:CM:229:ASN:HA	7:CM:249:GLN:HG2	2.00	0.44
5:DK:120:SER:N	5:DK:160:GLY:O	2.44	0.44
5:DK:130:ARG:NH2	5:DK:162:ASP:OD2	2.50	0.44
1:HG:878:ASN:HD22	1:HG:1030:GLU:HB2	1.83	0.44
11:AC:173:GLU:HA	11:AC:176:ILE:HG12	1.99	0.44
1:AG:969:GLY:HA3	1:AG:1009:ALA:HB2	2.00	0.44
6:EL:91:VAL:HA	6:EL:94:VAL:HG12	2.00	0.44
6:EL:193:LEU:HD13	6:EL:193:LEU:HA	1.87	0.44
7:EM:191:LEU:HB3	7:EM:212:LEU:HD11	1.99	0.44
2:FD:73:ILE:O	2:FD:133:ARG:NH2	2.45	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Fg:818:GLN:NE2	4:FH:205:GLN:OE1	2.50	0.44
8:FN:58:LEU:HD12	8:FN:68:CYS:HB2	1.99	0.44
6:HL:190:MET:HG2	6:HL:205:ALA:HB2	2.00	0.44
11:KC:170:LYS:HA	11:KC:173:LYS:HE2	2.00	0.44
6:JL:109:LEU:HD21	6:JL:125:LEU:HD11	1.99	0.44
3:Jf:223:ILE:HD12	3:Jf:223:ILE:HA	1.85	0.44
4:AH:292:SER:OG	4:AH:293:ARG:N	2.51	0.44
2:Kd:160:LYS:HE3	2:Kd:160:LYS:HB2	1.76	0.44
4:LH:211:ASN:OD1	4:YH:234:ASN:ND2	2.43	0.44
6:LL:94:VAL:HA	6:LL:97:ILE:HG12	2.00	0.44
7:LM:281:TYR:HE1	7:LM:298:VAL:HB	1.83	0.44
2:Ld:95:THR:HA	2:Ld:98:ILE:HG22	2.00	0.44
2:Ld:141:LYS:HA	2:Ld:141:LYS:HD3	1.89	0.44
4:MH:166:PRO:HG3	4:ZH:151:PRO:HB2	1.98	0.44
7:MM:275:ASP:OD1	7:MM:275:ASP:N	2.49	0.44
2:Md:82:ARG:HH21	2:Md:126:GLU:HA	1.83	0.44
4:XH:172:SER:HB2	4:XH:248:VAL:HG11	1.99	0.44
1:FG:925:GLU:HB3	1:GG:862:ILE:HG21	1.99	0.44
11:DC:193:THR:H	11:DC:193:THR:HG1	1.52	0.44
3:BF:268:ASP:HA	4:BH:150:LYS:HD3	1.99	0.44
4:BH:149:PRO:HB2	4:BH:248:VAL:HG12	2.00	0.44
7:BM:275:ASP:OD1	7:BM:275:ASP:N	2.50	0.44
2:Bd:52:MET:SD	11:JC:99:SER:OG	2.69	0.44
11:IC:139:HIS:ND1	11:IC:140:PHE:O	2.46	0.44
7:CM:131:THR:HG23	7:CM:151:GLY:H	1.82	0.44
7:CM:173:LEU:O	7:CM:174:GLN:NE2	2.51	0.44
1:OG:886:LEU:HA	1:OG:899:LEU:O	2.17	0.44
1:AG:917:ASN:OD1	1:AG:917:ASN:N	2.49	0.44
1:AG:920:SER:HB2	1:BG:865:THR:HB	2.00	0.44
6:FL:227:ARG:H	6:FL:227:ARG:HG2	1.43	0.44
11:BC:261:GLU:OE1	11:BC:261:GLU:N	2.51	0.44
11:GC:108:PRO:HD3	11:GC:138:ALA:HB2	2.00	0.44
4:HH:207:ASP:HB2	4:HH:210:SER:HB3	2.00	0.44
5:HK:48:ALA:HA	5:HK:108:GLN:HE22	1.83	0.44
2:ID:117:VAL:HG22	2:ID:142:LYS:HD3	2.00	0.44
4:IH:324:TRP:HA	4:IH:339:MET:HB3	2.00	0.44
5:KK:185:ARG:NH1	6:LL:216:ASP:OD1	2.51	0.44
4:LH:190:PRO:HD3	4:LH:261:PRO:HG3	1.99	0.44
4:LH:204:ILE:HG12	4:LH:215:ILE:HG23	2.00	0.44
3:WF:210:TYR:HB3	3:WF:222:LEU:HB3	1.98	0.44
4:WH:355:GLN:HE22	4:WH:357:LYS:HG2	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:XH:332:ASP:OD1	4:XH:332:ASP:N	2.50	0.44
4:YH:170:ARG:HH12	4:YH:247:ALA:HB3	1.82	0.44
4:ZH:105:GLU:OE1	4:ZH:109:LYS:NZ	2.39	0.44
7:AM:282:TYR:OH	7:AM:301:MET:SD	2.69	0.44
6:BL:124:THR:HA	6:BL:231:ILE:O	2.18	0.44
6:BL:213:ALA:HA	6:BL:228:ARG:HH22	1.82	0.44
2:CD:87:TRP:CD1	2:CD:89:GLY:H	2.36	0.44
1:HG:921:ILE:HD12	1:HG:926:LYS:HD2	1.99	0.44
1:IG:904:ASN:OD1	1:IG:904:ASN:N	2.51	0.44
1:OG:947:ARG:NH2	1:OG:1030:GLU:HB3	2.33	0.44
4:EH:108:ASP:OD1	4:DH:126:GLN:NE2	2.51	0.44
4:GH:319:ILE:HA	4:GH:347:VAL:HG12	1.99	0.44
6:GL:121:ASP:O	6:GL:235:THR:OG1	2.33	0.44
6:GL:163:ILE:HB	6:GL:203:LEU:HD13	1.99	0.44
1:CG:969:GLY:O	1:CG:973:GLN:HB2	2.17	0.44
2:ID:39:ILE:HG23	6:IL:220:ILE:HG13	1.99	0.44
6:IL:102:LYS:HA	6:IL:105:ILE:HD12	2.00	0.44
11:KC:215:LEU:HG	11:KC:220:MET:HB2	2.00	0.44
6:JL:91:VAL:HA	6:JL:94:VAL:HG12	1.99	0.44
6:JL:219:ILE:HD12	6:JL:219:ILE:HA	1.80	0.44
7:JM:203:SER:HA	7:JM:223:GLN:O	2.17	0.44
1:DG:1006:ILE:O	1:DG:1010:THR:OG1	2.36	0.44
7:MM:146:LEU:HD13	7:MM:146:LEU:HA	1.90	0.44
2:Md:150:ASN:OD1	2:Md:150:ASN:N	2.51	0.44
3:WF:211:TYR:HB2	3:WF:223:ILE:HG23	1.99	0.44
4:WH:229:ARG:HE	4:WH:229:ARG:HB3	1.60	0.44
7:AM:271:SER:OG	7:AM:290:ASP:OD1	2.34	0.44
5:BK:148:GLY:H	2:Bd:30:ILE:HD13	1.83	0.44
11:JC:222:VAL:HA	11:JC:255:GLU:O	2.18	0.44
11:LC:95:ASP:OD2	11:LC:98:SER:OG	2.34	0.44
11:MC:219:ASN:ND2	11:MC:261:GLU:O	2.51	0.44
5:CK:87:GLN:HB3	5:CK:128:ARG:HH22	1.83	0.44
5:CK:87:GLN:N	5:CK:173:ASP:OD2	2.50	0.44
2:DD:52:MET:HE2	2:Dd:52:MET:HG2	1.99	0.44
5:DK:60:LEU:HG	5:DK:65:ILE:HB	2.00	0.44
1:JG:931:SER:O	1:JG:1042:THR:OG1	2.36	0.44
1:KG:946:SER:OG	1:KG:1030:GLU:O	2.30	0.44
1:NG:1019:ALA:O	1:NG:1023:PHE:HB2	2.18	0.44
1:AG:1005:VAL:O	1:AG:1009:ALA:CB	2.66	0.43
6:EL:191:THR:HG21	7:EM:289:ALA:HB3	2.00	0.43
11:BC:172:GLU:HA	11:BC:175:ILE:HG12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:HD:55:MET:HE2	2:HD:55:MET:HB2	1.80	0.43
1:Hg:794:ILE:O	1:Hg:798:THR:N	2.51	0.43
2:ID:147:VAL:HG22	2:ID:154:VAL:HG22	2.00	0.43
2:Jd:131:ILE:HD13	2:Jd:131:ILE:HA	1.90	0.43
4:LH:126:GLN:HA	4:LH:129:LYS:HE3	1.99	0.43
1:VG:798:THR:HG23	1:VG:801:MET:HE2	1.98	0.43
3:YF:243:MET:N	3:YF:257:SER:OG	2.44	0.43
1:FG:876:SER:N	1:GG:940:ALA:O	2.50	0.43
8:AN:63:GLY:HA3	2:BD:27:LYS:HB2	2.00	0.43
2:Bd:87:TRP:HZ2	2:Bd:90:PRO:HD2	1.82	0.43
1:GG:891:THR:OG1	1:GG:892:GLY:N	2.51	0.43
11:HC:261:GLU:N	11:HC:261:GLU:OE1	2.51	0.43
11:JC:163:ASN:OD1	11:JC:163:ASN:N	2.37	0.43
11:MC:228:HIS:HB3	11:MC:247:LEU:HD13	1.99	0.43
4:CH:238:MET:HB2	4:CH:238:MET:HE3	1.79	0.43
7:CM:158:VAL:HA	7:CM:178:LYS:HZ3	1.83	0.43
1:MG:951:HIS:H	1:MG:1027:THR:HG22	1.82	0.43
4:EH:208:LYS:HE2	1:Fg:824:THR:H	1.83	0.43
6:EL:124:THR:HA	6:EL:231:ILE:O	2.17	0.43
11:CC:116:THR:HG22	4:HH:328:MET:HE1	1.99	0.43
1:Gg:802:LEU:O	1:Gg:806:THR:OG1	2.29	0.43
4:GH:158:VAL:HG22	4:GH:167:PRO:HG2	1.99	0.43
4:GH:191:ILE:O	4:GH:231:ARG:NH1	2.52	0.43
4:GH:198:ASP:OD1	4:GH:200:SER:OG	2.37	0.43
4:HH:171:LEU:HD11	4:HH:241:LEU:HB3	1.99	0.43
2:Hd:71:LEU:HD22	2:Hd:145:ILE:HG13	2.00	0.43
5:IK:66:LYS:O	5:IK:76:ILE:HA	2.18	0.43
2:JD:55:MET:HA	2:JD:58:VAL:HG12	2.00	0.43
3:JF:216:ILE:HD11	3:JF:219:ARG:HB2	2.00	0.43
3:LF:247:ILE:HG12	3:LF:254:ILE:HG23	2.00	0.43
8:MN:89:GLY:HA3	8:MN:104:ASN:HB2	1.99	0.43
1:VG:817:THR:OG1	4:VH:203:ASN:ND2	2.51	0.43
1:FG:931:SER:O	1:FG:1042:THR:OG1	2.36	0.43
7:AM:208:LYS:HD3	7:AM:208:LYS:HA	1.74	0.43
3:Af:245:LYS:HE2	3:Af:245:LYS:HB2	1.75	0.43
4:BH:274:PRO:O	11:JC:119:ASN:ND2	2.49	0.43
11:LC:169:THR:HG23	11:LC:172:GLU:H	1.83	0.43
1:PG:1006:ILE:O	1:PG:1010:THR:OG1	2.36	0.43
7:DM:117:ARG:HG2	7:DM:137:TYR:HB3	2.00	0.43
1:AG:951:HIS:O	1:AG:955:ARG:NE	2.51	0.43
4:EH:200:SER:OG	1:Fg:816:GLU:OE2	2.36	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FL:109:LEU:HD12	6:FL:114:ILE:HB	2.01	0.43
11:BC:154:ASP:OD2	8:GN:85:CYS:N	2.45	0.43
1:BG:917:ASN:HA	1:BG:931:SER:HA	2.00	0.43
7:GM:123:VAL:HG22	7:GM:143:THR:HB	2.00	0.43
4:HH:117:ARG:NH1	4:HH:117:ARG:O	2.52	0.43
6:IL:150:ASN:OD1	6:IL:153:ARG:NH2	2.42	0.43
6:IL:169:THR:OG1	6:IL:170:ASP:OD1	2.36	0.43
1:DG:885:ILE:O	1:DG:900:ILE:HA	2.19	0.43
1:DG:968:PHE:CG	1:DG:1008:LEU:HD13	2.53	0.43
4:LH:174:GLY:N	4:LH:217:ALA:O	2.45	0.43
4:LH:191:ILE:HB	4:LH:206:TRP:HE1	1.83	0.43
6:LL:168:PHE:HB2	6:LL:228:ARG:HG2	2.00	0.43
2:Ld:148:TYR:HB2	2:Ld:153:VAL:HG12	2.00	0.43
1:EG:966:GLN:O	1:EG:970:ASN:ND2	2.51	0.43
4:MH:130:LEU:HA	4:MH:133:ILE:HG22	1.99	0.43
4:VH:203:ASN:N	4:VH:203:ASN:OD1	2.51	0.43
4:WH:284:LEU:HD22	4:WH:328:MET:HB3	2.00	0.43
4:XH:190:PRO:HB2	4:XH:231:ARG:HH22	1.83	0.43
4:YH:246:LYS:HD3	4:YH:246:LYS:HA	1.82	0.43
11:DC:110:LEU:HD23	11:DC:212:TYR:HB2	1.98	0.43
11:EC:174:LYS:HG2	11:FC:38:ALA:HB1	2.00	0.43
11:HC:88:ARG:HD2	11:HC:88:ARG:HA	1.87	0.43
11:IC:203:LYS:NZ	2:AD:47:SER:OG	2.50	0.43
2:DD:123:THR:OG1	2:DD:124:LYS:N	2.51	0.43
5:DK:116:VAL:HB	5:DK:182:ILE:HG22	2.00	0.43
1:HG:1024:ASN:OD1	1:HG:1024:ASN:N	2.51	0.43
1:KG:891:THR:OG1	1:KG:892:GLY:N	2.51	0.43
6:DL:49:ASN:ND2	7:DM:293:ALA:O	2.50	0.43
7:DM:271:SER:OG	7:DM:290:ASP:OD1	2.37	0.43
2:Dd:98:ILE:HD13	2:Dd:98:ILE:HA	1.89	0.43
7:EM:136:LEU:HD23	7:EM:155:LEU:HD12	2.01	0.43
7:FM:165:ILE:HB	7:FM:185:ILE:HG23	2.00	0.43
3:AF:207:ARG:NH2	3:AF:208:ILE:O	2.51	0.43
7:GM:224:LEU:HB2	7:GM:246:LEU:HD22	1.99	0.43
2:Gd:79:LEU:HA	2:Gd:128:LEU:HD11	1.99	0.43
4:HH:125:GLU:H	4:HH:125:GLU:HG3	1.61	0.43
3:IF:233:ARG:NH1	3:JF:266:GLN:OE1	2.51	0.43
1:Jg:801:MET:HG2	4:KH:121:PRO:HB2	2.00	0.43
4:AH:302:ALA:O	4:AH:303:ARG:NH1	2.43	0.43
4:AH:343:PRO:HA	4:AH:358:VAL:HB	2.00	0.43
6:KL:91:VAL:HA	6:KL:94:VAL:HG22	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:LK:115:THR:HG23	5:LK:155:PHE:HB2	2.00	0.43
3:Lf:253:ARG:HG3	3:Lf:263:LYS:HD2	1.99	0.43
1:EG:1011:VAL:HG12	1:FG:963:SER:HB2	1.99	0.43
4:MH:192:ALA:HB2	4:MH:231:ARG:HG3	2.00	0.43
4:VH:236:PRO:HD2	4:DH:251:ARG:HH21	1.83	0.43
4:VH:278:ASP:OD1	4:VH:278:ASP:N	2.50	0.43
4:VH:296:VAL:O	4:VH:359:GLU:N	2.49	0.43
4:YH:207:ASP:OD1	4:YH:207:ASP:N	2.44	0.43
4:ZH:168:VAL:HA	4:ZH:240:THR:O	2.18	0.43
11:FC:146:THR:OG1	11:FC:147:TRP:N	2.52	0.43
4:CH:233:LEU:HD23	4:CH:233:LEU:HA	1.90	0.43
5:DK:50:ASP:HA	5:DK:53:ILE:HD12	2.00	0.43
1:JG:966:GLN:O	1:JG:970:ASN:ND2	2.51	0.43
2:ED:107:ARG:HE	2:ED:155:GLU:HG3	1.83	0.43
7:EM:292:MET:SD	7:EM:292:MET:N	2.92	0.43
3:Ef:210:TYR:HB3	3:Ef:222:LEU:HD12	2.00	0.43
11:CC:226:VAL:HA	11:CC:249:ILE:HA	1.99	0.43
11:CC:244:ASP:OD2	11:DC:126:ARG:NE	2.41	0.43
5:FK:63:LYS:HA	5:FK:63:LYS:HD3	1.80	0.43
8:FN:103:CYS:N	8:FN:107:TYR:O	2.45	0.43
4:GH:225:ASN:HD22	4:GH:225:ASN:H	1.66	0.43
7:GM:117:ARG:HE	7:GM:117:ARG:HB3	1.55	0.43
1:Hg:800:ASP:N	1:Hg:800:ASP:OD1	2.47	0.43
2:JD:148:TYR:O	2:JD:152:GLN:N	2.52	0.43
3:KF:245:LYS:H	3:KF:256:THR:HA	1.83	0.43
1:Kg:813:LYS:HD3	1:Kg:813:LYS:HA	1.83	0.43
7:KM:191:LEU:HD21	7:KM:194:LEU:HD23	2.00	0.43
4:BH:207:ASP:OD1	4:BH:207:ASP:N	2.48	0.43
6:BL:49:ASN:ND2	7:BM:293:ALA:O	2.40	0.43
7:BM:121:ALA:HA	7:BM:141:GLU:HB3	1.99	0.43
2:DD:55:MET:HE2	2:DD:55:MET:HB3	1.75	0.43
4:DH:114:ASP:HA	4:DH:117:ARG:HH11	1.83	0.43
1:OG:968:PHE:HB3	1:OG:1008:LEU:HD13	2.00	0.43
7:DM:257:ASP:OD1	7:DM:257:ASP:N	2.51	0.43
2:ED:86:ASP:HA	2:ED:121:ILE:O	2.19	0.43
4:EH:306:LEU:HD11	4:EH:309:GLU:HA	2.01	0.43
7:EM:183:VAL:HB	7:EM:185:ILE:HD11	2.01	0.43
6:FL:109:LEU:HD13	6:FL:109:LEU:HA	1.86	0.43
2:Fd:69:ASN:OD1	2:Fd:69:ASN:N	2.51	0.43
3:Gf:253:ARG:HG2	3:Gf:263:LYS:HD2	2.00	0.43
5:HK:73:ASN:N	5:HK:73:ASN:OD1	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:ID:29:PRO:HG2	6:IL:225:GLN:HA	2.01	0.43
5:IK:142:GLU:OE2	6:IL:139:ARG:NH1	2.51	0.43
11:KC:50:LYS:HB3	1:MG:938:ASN:HD21	1.82	0.43
11:KC:106:LEU:HD12	11:KC:107:PRO:HD2	2.00	0.43
7:JM:123:VAL:HG22	7:JM:143:THR:HB	2.00	0.43
4:AH:138:GLU:OE1	4:ZH:221:TYR:OH	2.32	0.43
3:LF:245:LYS:HD3	3:LF:257:SER:HB3	2.01	0.43
2:Ld:71:LEU:HD22	2:Ld:145:ILE:HG13	2.01	0.43
5:MK:150:ASP:O	5:MK:152:ARG:NH1	2.50	0.43
3:Mf:243:MET:HE3	3:Mf:243:MET:HB3	1.82	0.43
3:Af:216:ILE:HD12	3:Af:216:ILE:HA	1.80	0.43
3:Af:237:LYS:HZ2	3:Af:243:MET:HB2	1.84	0.43
6:BL:102:LYS:HA	6:BL:105:ILE:HD12	2.01	0.43
7:BM:275:ASP:HA	7:BM:295:ASN:H	1.83	0.43
11:HC:233:VAL:HG11	11:IC:262:TRP:HH2	1.84	0.43
11:IC:147:TRP:O	11:IC:151:LEU:HB2	2.18	0.43
11:MC:91:ASP:OD1	11:MC:91:ASP:N	2.41	0.43
2:CD:36:ASP:HA	2:CD:39:ILE:HD12	2.00	0.43
5:CK:65:ILE:HG13	5:CK:78:ILE:HA	2.01	0.43
1:JG:1006:ILE:O	1:JG:1010:THR:OG1	2.37	0.43
1:MG:1019:ALA:O	1:MG:1023:PHE:HB2	2.19	0.43
2:ED:121:ILE:HD13	2:ED:121:ILE:HA	1.85	0.43
4:EH:282:HIS:HB3	4:EH:287:VAL:HG13	2.00	0.43
2:Ed:105:ARG:HB2	2:Ed:153:VAL:HG23	2.00	0.43
11:BC:45:ALA:HA	11:BC:48:LYS:HE2	2.01	0.43
4:HH:171:LEU:HB2	4:HH:243:PRO:HB3	2.01	0.43
7:HM:225:ALA:HA	7:HM:246:LEU:HB2	2.01	0.43
7:HM:301:MET:HE2	7:HM:301:MET:HB2	1.90	0.43
1:CG:876:SER:OG	1:CG:1031:VAL:O	2.34	0.43
4:IH:207:ASP:OD1	4:IH:207:ASP:N	2.52	0.43
10:IX:13:UNK:O	10:IX:17:UNK:CB	2.67	0.43
11:KC:226:VAL:HB	11:KC:249:ILE:HG23	1.99	0.43
8:JN:87:TRP:O	8:JN:88:HIS:ND1	2.51	0.43
4:AH:127:VAL:HG11	4:ZH:141:LYS:HA	2.01	0.43
4:AH:292:SER:HB2	4:AH:307:SER:HB3	2.00	0.43
5:KK:90:ARG:HH12	5:KK:92:ASN:HA	1.83	0.43
2:Kd:132:LEU:HD11	2:Kd:145:ILE:HG21	2.01	0.43
8:MN:95:LEU:HG	1:JG:923:GLY:HA2	2.00	0.43
3:Mf:219:ARG:HA	3:Mf:232:VAL:O	2.18	0.43
4:VH:172:SER:HB2	4:VH:248:VAL:HG11	1.99	0.43
4:WH:169:ILE:HD12	4:WH:252:VAL:HG21	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:DC:79:ILE:HD12	11:DC:195:LEU:HD22	2.01	0.43
2:Ad:91:ILE:HD11	2:Ad:135:ILE:HD12	2.01	0.43
4:BH:174:GLY:N	4:BH:217:ALA:O	2.52	0.43
4:BH:181:PHE:HE2	4:BH:228:VAL:HG11	1.83	0.43
8:BN:96:ASN:OD1	8:BN:98:SER:OG	2.33	0.43
11:HC:175:ILE:HA	11:HC:178:ILE:HG12	2.00	0.43
11:JC:65:LEU:HD22	11:JC:180:TYR:HB3	2.01	0.43
2:CD:136:ASP:O	2:Cd:60:LYS:NZ	2.43	0.43
1:JG:886:LEU:HD21	1:KG:868:ILE:HG12	2.01	0.43
6:DL:141:ASN:HD21	6:DL:143:ILE:HB	1.84	0.43
3:Df:254:ILE:HB	3:Df:262:ILE:HG23	2.00	0.43
2:FD:150:ASN:OD1	2:FD:150:ASN:N	2.51	0.43
3:FF:246:LEU:HB3	3:FF:255:LEU:HB2	2.01	0.43
3:Ff:247:ILE:HA	3:Ff:254:ILE:HG22	2.00	0.43
7:GM:196:MET:HG2	7:GM:220:ALA:HB2	2.01	0.43
7:GM:215:ARG:HD2	7:GM:234:GLU:HB3	2.00	0.43
11:GC:114:ARG:HG2	11:GC:130:ARG:HG2	2.00	0.43
8:HN:62:ASN:HD21	8:HN:64:PHE:HB2	1.84	0.43
5:IK:148:GLY:H	2:Id:30:ILE:HD13	1.84	0.43
7:IM:300:ASP:OD1	7:IM:302:ARG:NE	2.39	0.43
8:IN:58:LEU:HD12	8:IN:68:CYS:HB2	2.00	0.43
8:JN:103:CYS:N	8:JN:107:TYR:O	2.49	0.43
2:Jd:142:LYS:HE2	2:Jd:142:LYS:HB2	1.92	0.43
5:KK:144:LEU:HD13	5:KK:144:LEU:HA	1.88	0.43
7:KM:146:LEU:HD13	7:KM:146:LEU:HA	1.91	0.43
7:KM:154:LYS:HD3	7:KM:154:LYS:HA	1.84	0.43
4:LH:122:LEU:HG	1:YG:801:MET:HG3	2.01	0.43
2:MD:57:LYS:HE2	2:MD:57:LYS:HB2	1.89	0.43
3:VF:243:MET:O	3:VF:257:SER:N	2.52	0.43
1:FG:876:SER:OG	1:FG:1031:VAL:O	2.33	0.43
5:BK:87:GLN:NE2	5:BK:173:ASP:OD1	2.51	0.43
7:BM:127:ASN:HB3	7:BM:147:ALA:HB3	2.01	0.43
11:HC:86:GLN:OE1	11:HC:89:ASN:ND2	2.41	0.43
4:CH:203:ASN:ND2	4:CH:216:GLN:OE1	2.52	0.43
4:CH:341:LYS:HB2	4:CH:361:LEU:HD21	2.00	0.43
4:DH:219:LYS:HD2	4:DH:219:LYS:HA	1.91	0.43
1:LG:885:ILE:O	1:LG:900:ILE:HA	2.18	0.43
1:MG:931:SER:H	1:MG:1043:GLN:HE22	1.67	0.43
1:PG:948:THR:HG22	1:PG:1029:VAL:HG12	2.00	0.43
6:DL:91:VAL:HA	6:DL:94:VAL:HG12	2.00	0.43
1:AG:872:VAL:HG11	11:AC:165:THR:HB	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:FH:294:ARG:HA	4:FH:305:TRP:HD1	1.84	0.43
1:BG:916:PHE:HD1	1:BG:916:PHE:HA	1.68	0.43
4:HH:166:PRO:HG3	4:XH:151:PRO:HB2	2.00	0.43
7:HM:157:ALA:O	7:HM:178:LYS:NZ	2.38	0.43
2:Hd:36:ASP:OD1	2:Hd:36:ASP:N	2.50	0.43
1:CG:1030:GLU:HG2	1:DG:941:ARG:HH21	1.83	0.43
7:IM:138:LEU:O	7:IM:157:ALA:HA	2.19	0.43
5:JK:90:ARG:NH1	7:JM:292:MET:O	2.51	0.43
4:KH:281:LEU:HD13	11:FC:111:LEU:HB3	2.00	0.43
7:LM:280:TYR:HB3	7:LM:282:TYR:HE1	1.84	0.43
2:Ld:150:ASN:OD1	2:Ld:150:ASN:N	2.51	0.43
5:MK:87:GLN:NE2	5:MK:173:ASP:OD1	2.52	0.43
7:MM:137:TYR:HA	7:MM:156:GLU:O	2.19	0.43
3:Mf:208:ILE:HB	3:Mf:209:ILE:H	1.71	0.43
4:VH:203:ASN:ND2	4:VH:216:GLN:OE1	2.37	0.43
4:YH:115:MET:HE3	4:YH:115:MET:HB3	1.87	0.43
4:BH:275:SER:OG	4:BH:276:ALA:N	2.52	0.43
6:BL:91:VAL:HA	6:BL:94:VAL:HG12	2.00	0.43
11:LC:60:LYS:HE2	11:LC:60:LYS:HB2	1.83	0.43
4:CH:190:PRO:HA	4:CH:211:ASN:HB3	2.01	0.43
4:CH:302:ALA:O	4:CH:303:ARG:NH1	2.40	0.43
6:CL:54:ARG:HE	6:CL:57:VAL:HG22	1.84	0.43
2:DD:82:ARG:HH21	2:DD:126:GLU:HA	1.83	0.43
2:DD:131:ILE:HD13	2:DD:131:ILE:HA	1.92	0.43
1:Dg:820:TYR:HB3	4:DH:205:GLN:HG2	2.00	0.43
1:JG:886:LEU:HA	1:JG:899:LEU:O	2.18	0.43
1:JG:935:ILE:HG22	1:JG:942:THR:HG22	2.00	0.43
1:KG:1002:GLU:H	1:KG:1002:GLU:HG3	1.60	0.43
1:NG:880:ASP:OD1	1:NG:880:ASP:N	2.52	0.43
11:AC:118:LEU:HB2	11:AC:128:ILE:HG22	2.00	0.43
7:DM:194:LEU:O	7:DM:214:ILE:HA	2.19	0.43
4:EH:166:PRO:HA	4:EH:167:PRO:HD3	1.91	0.43
4:EH:343:PRO:HA	4:EH:358:VAL:HB	2.00	0.43
6:EL:44:HIS:HB3	6:EL:48:ASN:HA	2.01	0.43
4:GH:151:PRO:HA	4:GH:248:VAL:HG13	2.01	0.43
5:HK:102:ILE:HD13	5:HK:102:ILE:HA	1.88	0.43
11:KC:261:GLU:N	11:KC:261:GLU:OE1	2.52	0.43
4:AH:281:LEU:HD13	11:IC:111:LEU:HB3	2.01	0.43
2:KD:74:PRO:HD2	2:KD:147:VAL:HB	2.01	0.43
6:KL:99:ARG:HA	6:KL:104:LYS:HG2	2.01	0.43
6:KL:113:ASP:N	6:KL:113:ASP:OD1	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Lf:219:ARG:HB3	3:Lf:233:ARG:HD3	2.01	0.43
5:MK:54:ILE:O	5:MK:58:THR:OG1	2.33	0.43
11:DC:106:LEU:HD12	11:DC:107:PRO:HD2	1.99	0.43
3:ZF:243:MET:N	3:ZF:257:SER:OG	2.45	0.43
2:BD:150:ASN:O	2:BD:152:GLN:NE2	2.52	0.43
4:BH:183:ASP:OD1	4:BH:187:ALA:N	2.52	0.43
11:IC:147:TRP:HB2	11:IC:151:LEU:HD23	2.01	0.43
11:MC:258:ASN:OD1	11:MC:258:ASN:N	2.51	0.43
6:CL:193:LEU:HD13	6:CL:193:LEU:HA	1.88	0.43
4:DH:256:VAL:HG13	4:DH:258:GLY:H	1.83	0.43
1:MG:916:PHE:HD1	1:MG:916:PHE:HA	1.75	0.43
1:MG:966:GLN:O	1:MG:970:ASN:ND2	2.51	0.43
6:DL:129:THR:OG1	6:DL:130:ASP:OD1	2.35	0.43
4:EH:288:PRO:HB3	4:EH:305:TRP:CD2	2.54	0.42
3:Ff:255:LEU:HD22	3:Ff:255:LEU:HA	1.90	0.42
2:GD:27:LYS:HD3	2:GD:27:LYS:HA	1.84	0.42
3:GF:214:ALA:O	3:GF:221:TRP:N	2.48	0.42
1:Gg:800:ASP:OD1	1:Gg:800:ASP:N	2.50	0.42
4:HH:238:MET:SD	4:XH:178:SER:OG	2.67	0.42
4:HH:311:MET:HG3	4:HH:341:LYS:HA	2.01	0.42
7:IM:254:LYS:HE3	7:IM:254:LYS:HB2	1.80	0.42
11:KC:189:ASP:O	11:KC:193:THR:OG1	2.37	0.42
2:KD:26:LYS:HE2	6:KL:110:GLN:HG2	2.00	0.42
4:KH:190:PRO:HA	4:KH:211:ASN:HB3	2.00	0.42
7:KM:136:LEU:HD23	7:KM:155:LEU:HD12	2.00	0.42
3:Kf:238:ILE:HG13	3:Kf:241:TYR:HB2	2.01	0.42
2:Ld:98:ILE:HD12	2:Ld:98:ILE:HA	1.90	0.42
8:MN:49:ASN:HB3	8:MN:59:VAL:HB	2.01	0.42
3:Mf:223:ILE:HD12	3:Mf:223:ILE:HA	1.89	0.42
3:XF:221:TRP:CD1	3:XF:231:THR:HB	2.54	0.42
11:DC:164:THR:OG1	11:DC:165:LEU:N	2.51	0.42
2:Ad:67:LYS:HB3	2:Ad:67:LYS:HE2	1.81	0.42
11:LC:112:GLU:OE2	11:LC:130:ARG:NH1	2.47	0.42
5:CK:150:ASP:OD1	5:CK:150:ASP:N	2.47	0.42
4:DH:281:LEU:H	4:DH:281:LEU:HG	1.68	0.42
11:AC:148:TRP:HB2	11:AC:152:LEU:HD23	2.01	0.42
2:FD:162:TYR:OH	11:AC:105:ASN:OD1	2.34	0.42
5:FK:119:TYR:HB2	5:FK:179:ARG:HG2	2.00	0.42
1:BG:1025:THR:HA	1:BG:1026:PRO:HD3	1.90	0.42
3:AF:208:ILE:HG13	3:AF:225:SER:H	1.84	0.42
11:GC:88:ARG:HD2	11:GC:88:ARG:HA	1.91	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:GC:126:ARG:NH1	4:LH:273:PRO:O	2.42	0.42
11:GC:249:ILE:HB	11:HC:123:GLN:HG2	2.00	0.42
5:JK:179:ARG:NE	5:JK:181:GLU:OE2	2.47	0.42
6:JL:219:ILE:HG23	6:JL:222:GLY:H	1.83	0.42
5:KK:63:LYS:HD3	5:KK:63:LYS:HA	1.83	0.42
7:KM:136:LEU:HB2	7:KM:155:LEU:HG	2.00	0.42
3:Kf:243:MET:N	3:Kf:257:SER:OG	2.49	0.42
5:AK:54:ILE:HD11	8:AN:44:LYS:HG3	2.01	0.42
1:EG:1025:THR:HA	1:EG:1026:PRO:HD3	1.88	0.42
4:VH:321:SER:OG	11:JC:226:TYR:OH	2.30	0.42
6:AL:129:THR:OG1	6:AL:130:ASP:OD1	2.34	0.42
11:DC:129:ASP:OD1	11:DC:129:ASP:N	2.44	0.42
6:BL:193:LEU:HD13	6:BL:193:LEU:HA	1.86	0.42
1:Cg:810:GLN:H	1:Cg:810:GLN:HG3	1.58	0.42
1:LG:863:ILE:HB	1:LG:1045:VAL:HG22	2.00	0.42
1:LG:874:ASP:OD1	1:LG:874:ASP:N	2.51	0.42
1:PG:899:LEU:HD21	1:PG:916:PHE:HB3	2.01	0.42
11:AC:167:LEU:HD13	11:AC:167:LEU:HA	1.87	0.42
4:EH:191:ILE:HD12	4:EH:206:TRP:HE1	1.83	0.42
2:FD:67:LYS:HB3	2:Fd:62:ILE:HD11	2.02	0.42
7:FM:153:GLN:HA	7:FM:173:LEU:HA	2.02	0.42
2:Fd:92:GLU:OE1	2:Fd:93:GLU:N	2.53	0.42
7:GM:271:SER:OG	7:GM:290:ASP:OD1	2.37	0.42
2:HD:55:MET:HA	2:HD:58:VAL:HG12	2.01	0.42
11:GC:168:LYS:N	11:GC:172:GLU:OE2	2.44	0.42
5:HK:49:CYS:O	5:HK:52:THR:OG1	2.30	0.42
1:Bg:794:ILE:O	1:Bg:798:THR:OG1	2.31	0.42
2:ID:79:LEU:HA	2:ID:128:LEU:HD12	2.01	0.42
2:ID:83:ALA:HA	5:IK:154:ILE:O	2.19	0.42
11:KC:117:LEU:HA	11:KC:127:ILE:HG22	2.02	0.42
4:JH:229:ARG:NH2	4:JH:233:LEU:O	2.53	0.42
6:JL:162:THR:HA	6:JL:202:ARG:HB3	2.01	0.42
1:DG:919:MET:HG3	1:DG:930:ILE:HG23	2.00	0.42
1:DG:972:PHE:HB3	1:DG:1005:VAL:HG22	2.01	0.42
4:AH:181:PHE:HE2	4:AH:228:VAL:HG11	1.84	0.42
2:KD:73:ILE:O	2:KD:133:ARG:NH2	2.44	0.42
1:Kg:797:ARG:HD2	1:Kg:797:ARG:HA	1.70	0.42
7:LM:130:ARG:HE	7:LM:149:ASN:HD21	1.68	0.42
8:LN:52:ASP:OD2	8:LN:55:ALA:N	2.46	0.42
2:Ld:93:GLU:OE2	11:HC:263:ARG:NH1	2.51	0.42
4:VH:185:THR:HG21	4:VH:263:ALA:HA	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:XF:243:MET:O	3:XF:257:SER:N	2.52	0.42
4:XH:322:PRO:HG2	4:XH:339:MET:HE1	2.02	0.42
4:YH:292:SER:HB2	4:YH:305:TRP:HB3	2.01	0.42
11:DC:151:LEU:HD21	11:DC:202:ILE:HG21	2.00	0.42
8:AN:49:ASN:HB3	8:AN:59:VAL:HG23	2.01	0.42
2:Ad:111:LYS:HB2	2:Ad:111:LYS:HE2	1.86	0.42
2:BD:82:ARG:NH2	2:BD:125:ASP:O	2.53	0.42
3:BF:243:MET:O	3:BF:257:SER:N	2.51	0.42
7:BM:238:PHE:N	7:BM:258:LYS:O	2.48	0.42
11:IC:115:ASN:N	11:IC:129:ASP:O	2.38	0.42
3:CF:214:ALA:H	3:CF:221:TRP:HB2	1.84	0.42
4:CH:292:SER:OG	4:CH:293:ARG:N	2.53	0.42
5:CK:61:ASN:HD21	5:CK:67:VAL:HB	1.84	0.42
7:CM:256:HIS:O	7:CM:259:SER:OG	2.31	0.42
3:Cf:243:MET:N	3:Cf:257:SER:OG	2.49	0.42
3:DF:216:ILE:HD11	3:DF:219:ARG:HB2	2.02	0.42
4:DH:282:HIS:O	4:DH:287:VAL:N	2.53	0.42
1:IG:916:PHE:HD1	1:IG:916:PHE:HA	1.77	0.42
1:LG:878:ASN:HA	1:LG:1030:GLU:HG3	2.01	0.42
1:OG:931:SER:H	1:OG:1043:GLN:HE22	1.67	0.42
4:EH:307:SER:OG	4:EH:308:ASN:N	2.51	0.42
7:EM:163:THR:HB	7:EM:183:VAL:HG12	2.01	0.42
6:FL:219:ILE:HD12	6:FL:219:ILE:HA	1.92	0.42
7:FM:178:LYS:HZ2	7:FM:178:LYS:H	1.66	0.42
6:GL:114:ILE:HG22	6:GL:125:LEU:HD12	2.01	0.42
8:GN:101:VAL:HG12	8:GN:113:SER:HB2	2.01	0.42
2:Gd:95:THR:HA	2:Gd:98:ILE:HG22	2.01	0.42
5:HK:72:GLN:HE22	6:IL:216:ASP:H	1.68	0.42
1:CG:1017:GLN:HE21	1:CG:1017:GLN:HB2	1.66	0.42
4:IH:313:VAL:O	4:IH:336:ALA:HA	2.19	0.42
7:IM:207:ILE:HG13	7:IM:226:GLY:HA3	2.01	0.42
7:IM:209:SER:HB3	7:IM:228:VAL:HG22	2.01	0.42
8:IN:51:CYS:HB2	8:IN:58:LEU:HD23	2.01	0.42
11:KC:37:MET:SD	11:KC:37:MET:N	2.93	0.42
2:JD:86:ASP:OD1	11:EC:89:ARG:NH2	2.53	0.42
3:JF:233:ARG:NE	3:JF:235:GLY:O	2.46	0.42
3:JF:245:LYS:HB3	3:JF:255:LEU:HB2	2.01	0.42
5:JK:66:LYS:HD2	5:JK:66:LYS:HA	1.87	0.42
2:KD:35:ASP:O	2:KD:38:THR:OG1	2.33	0.42
2:KD:59:GLU:OE2	2:KD:63:THR:OG1	2.30	0.42
2:LD:52:MET:HG3	2:Ld:48:VAL:HG23	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:YF:209:ILE:H	3:YF:225:SER:HB3	1.84	0.42
2:Ad:105:ARG:HB2	2:Ad:153:VAL:HG23	2.01	0.42
5:BK:99:LEU:HD12	5:BK:99:LEU:HA	1.90	0.42
7:BM:222:ILE:HG22	7:BM:224:LEU:HG	2.02	0.42
8:BN:86:LEU:HD13	8:BN:86:LEU:HA	1.90	0.42
11:FC:113:GLY:O	11:FC:130:ARG:HA	2.19	0.42
11:MC:259:SER:HA	11:MC:262:TRP:CE2	2.54	0.42
4:CH:320:LEU:N	4:CH:346:LEU:O	2.47	0.42
7:CM:180:ASP:O	7:CM:182:LYS:NZ	2.43	0.42
1:HG:1042:THR:OG1	1:HG:1043:GLN:OE1	2.31	0.42
1:IG:874:ASP:OD1	1:IG:874:ASP:N	2.48	0.42
11:AC:100:LEU:HD13	11:AC:100:LEU:HA	1.92	0.42
7:DM:145:ARG:HH22	7:DM:162:VAL:HG23	1.85	0.42
3:Df:216:ILE:HD12	3:Df:216:ILE:HA	1.81	0.42
7:EM:174:GLN:HB2	7:EM:192:ARG:HH22	1.83	0.42
3:FF:267:GLU:O	4:FH:150:LYS:NZ	2.43	0.42
3:GF:266:GLN:NE2	3:WF:235:GLY:O	2.42	0.42
5:GK:45:VAL:HG12	8:GN:67:THR:HB	2.00	0.42
2:Gd:98:ILE:HD12	2:Gd:98:ILE:HA	1.92	0.42
11:GC:168:LYS:O	11:GC:173:LYS:NZ	2.52	0.42
7:IM:284:LEU:HD22	7:IM:302:ARG:HH12	1.84	0.42
8:JN:84:CYS:HB2	11:EC:155:ASP:HB2	2.01	0.42
4:AH:226:LEU:HD23	4:AH:239:LEU:HD13	2.00	0.42
8:KN:89:GLY:HA3	8:KN:104:ASN:HB2	2.02	0.42
7:LM:288:ARG:NH2	7:LM:318:GLN:O	2.39	0.42
5:AK:40:LYS:HB2	5:AK:40:LYS:HE2	1.84	0.42
2:MD:79:LEU:HD12	2:MD:79:LEU:HA	1.89	0.42
5:MK:92:ASN:OD1	5:MK:95:SER:N	2.53	0.42
7:MM:117:ARG:HG2	7:MM:137:TYR:HB3	2.01	0.42
2:Md:41:LEU:HD13	2:Md:41:LEU:HA	1.90	0.42
3:XF:226:ASN:OD1	3:XF:226:ASN:N	2.47	0.42
1:FG:891:THR:OG1	1:FG:892:GLY:N	2.52	0.42
11:FC:189:ASP:O	11:FC:193:THR:OG1	2.35	0.42
11:LC:108:PRO:HD3	11:LC:138:ALA:HB2	2.01	0.42
4:CH:313:VAL:HG23	4:CH:337:TYR:HB2	2.02	0.42
3:Cf:246:LEU:HD23	3:Cf:255:LEU:HD23	2.01	0.42
2:DD:82:ARG:HB2	5:DK:156:THR:HG23	2.01	0.42
1:LG:1019:ALA:HA	1:LG:1022:LEU:HG	2.02	0.42
5:FK:73:ASN:OD1	5:FK:185:ARG:NE	2.51	0.42
6:FL:219:ILE:HG23	6:FL:222:GLY:H	1.84	0.42
2:GD:150:ASN:OD1	2:GD:150:ASN:N	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:GH:225:ASN:HD22	4:GH:225:ASN:N	2.17	0.42
3:Gf:238:ILE:HG13	3:Gf:241:TYR:HB2	2.02	0.42
2:HD:42:ALA:HB1	2:Hd:40:LYS:HD2	2.00	0.42
5:HK:111:LYS:HD3	5:HK:114:ILE:HD11	2.00	0.42
2:ID:63:THR:HA	2:ID:64:PRO:HD3	1.91	0.42
4:IH:108:ASP:OD1	4:IH:108:ASP:N	2.51	0.42
5:IK:111:LYS:HE3	5:IK:111:LYS:HB3	1.86	0.42
1:DG:1017:GLN:HE21	1:DG:1017:GLN:HB2	1.63	0.42
4:AH:275:SER:HA	11:IC:126:ARG:HD3	2.02	0.42
2:KD:121:ILE:HD13	2:KD:121:ILE:HA	1.94	0.42
3:KF:235:GLY:HA2	3:KF:243:MET:HE1	2.01	0.42
4:KH:190:PRO:HB2	4:KH:231:ARG:HE	1.85	0.42
2:LD:150:ASN:OD1	2:LD:150:ASN:N	2.52	0.42
4:LH:213:LEU:HD23	4:LH:213:LEU:HA	1.89	0.42
4:LH:311:MET:HE1	4:LH:358:VAL:HG11	2.02	0.42
6:LL:175:ARG:HE	6:LL:175:ARG:HB2	1.67	0.42
8:LN:92:TYR:HD1	8:LN:94:GLN:H	1.67	0.42
3:Lf:216:ILE:HD12	3:Lf:216:ILE:HA	1.84	0.42
5:AK:162:ASP:N	5:AK:162:ASP:OD1	2.51	0.42
5:MK:150:ASP:OD1	5:MK:152:ARG:NH2	2.50	0.42
4:XH:196:LEU:HB2	4:XH:226:LEU:HD12	2.02	0.42
1:FG:884:PRO:HG2	1:GG:1040:LEU:HD21	2.01	0.42
5:BK:51:ALA:HB1	8:BN:44:LYS:HE3	2.01	0.42
3:Bf:251:GLN:OE1	3:Bf:253:ARG:NE	2.53	0.42
11:EC:173:GLU:HA	11:EC:176:ILE:HG12	2.01	0.42
11:HC:168:LYS:N	11:HC:172:GLU:OE1	2.51	0.42
11:MC:153:MET:HE2	11:MC:153:MET:HB3	1.97	0.42
2:CD:82:ARG:NE	2:CD:125:ASP:OD1	2.45	0.42
2:CD:111:LYS:HZ3	2:CD:111:LYS:H	1.66	0.42
2:DD:127:SER:N	2:DD:130:GLU:OE2	2.47	0.42
4:DH:151:PRO:HA	4:DH:248:VAL:HG13	2.00	0.42
5:DK:74:TYR:HE1	5:DK:186:ARG:HB2	1.84	0.42
1:IG:899:LEU:HD21	1:IG:916:PHE:HB3	2.01	0.42
11:AC:89:ARG:HD2	11:AC:89:ARG:HA	1.87	0.42
6:DL:210:ASP:OD1	6:DL:210:ASP:N	2.40	0.42
1:Ag:794:ILE:O	1:Ag:798:THR:OG1	2.34	0.42
1:AG:910:ASP:OD1	1:AG:910:ASP:N	2.52	0.42
4:EH:131:LYS:HB3	4:EH:131:LYS:HE2	1.80	0.42
4:EH:196:LEU:HD11	4:EH:202:PHE:HB2	2.01	0.42
5:EK:50:ASP:OD1	5:EK:50:ASP:N	2.53	0.42
5:FK:76:ILE:HB	5:FK:182:ILE:HG13	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:GK:81:SER:OG	5:GK:173:ASP:O	2.37	0.42
1:Ig:797:ARG:HD2	1:Ig:797:ARG:HA	1.87	0.42
7:IM:180:ASP:OD1	7:IM:199:LYS:N	2.48	0.42
3:KF:246:LEU:O	3:KF:255:LEU:N	2.53	0.42
2:Kd:27:LYS:HE2	2:Kd:27:LYS:HB2	1.93	0.42
2:Kd:119:ILE:HD12	2:Kd:135:ILE:HD12	2.01	0.42
4:LH:304:ALA:HA	4:LH:312:TYR:O	2.20	0.42
5:AK:78:ILE:HB	5:AK:180:VAL:HG23	2.01	0.42
5:AK:144:LEU:HD13	5:AK:144:LEU:HA	1.92	0.42
7:MM:175:ILE:HG23	7:MM:194:LEU:HD13	2.02	0.42
7:AM:268:HIS:ND1	7:AM:287:THR:OG1	2.38	0.42
2:BD:158:TYR:O	2:Bd:137:TYR:OH	2.27	0.42
5:BK:115:THR:HG22	5:BK:155:PHE:HB2	2.02	0.42
11:FC:147:TRP:HB2	11:FC:151:LEU:HD23	2.02	0.42
11:IC:61:GLU:O	11:IC:65:SER:OG	2.35	0.42
11:IC:94:TYR:HB3	11:IC:96:PHE:HE1	1.84	0.42
11:MC:240:ILE:HD12	11:MC:240:ILE:HA	1.90	0.42
7:CM:249:GLN:OE1	7:CM:267:ASN:ND2	2.52	0.42
1:HG:910:ASP:OD1	1:HG:910:ASP:N	2.38	0.42
1:LG:880:ASP:OD1	1:LG:880:ASP:N	2.53	0.42
11:AC:107:LEU:HD12	11:AC:108:PRO:HD2	2.01	0.42
2:Dd:85:VAL:O	2:Dd:122:SER:HA	2.19	0.42
2:ED:122:SER:OG	11:MC:88:ARG:NH2	2.53	0.42
4:EH:110:LYS:HA	4:EH:113:LYS:HG2	2.01	0.42
4:EH:159:ASN:OD1	4:EH:159:ASN:N	2.42	0.42
4:EH:325:LEU:HD23	4:EH:340:GLN:HE22	1.85	0.42
4:FH:192:ALA:HB2	4:FH:231:ARG:HA	2.01	0.42
11:BC:121:ASP:N	11:BC:124:SER:OG	2.46	0.42
2:GD:94:LEU:HD12	2:GD:94:LEU:HA	1.89	0.42
1:CG:898:LYS:HE2	1:DG:867:ASP:HB3	2.02	0.42
4:IH:184:SER:HB2	4:IH:259:TYR:HE1	1.84	0.42
11:KC:89:ASN:N	11:KC:89:ASN:OD1	2.53	0.42
11:KC:104:ASN:OD1	2:CD:162:TYR:OH	2.37	0.42
2:JD:27:LYS:HD3	2:JD:27:LYS:HA	1.86	0.42
6:JL:161:SER:O	6:JL:202:ARG:NH2	2.37	0.42
7:JM:129:LEU:HB2	7:JM:150:ILE:HD11	2.01	0.42
4:AH:157:PHE:HD1	4:AH:255:ARG:HB3	1.85	0.42
7:KM:254:LYS:HE2	7:KM:272:LEU:HD23	2.02	0.42
5:LK:113:ALA:HA	5:LK:153:ILE:O	2.20	0.42
1:EG:962:SER:HA	1:EG:965:LEU:HD22	2.01	0.42
4:VH:223:TYR:HB3	4:VH:242:ILE:HG13	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YH:230:LEU:HB2	4:YH:233:LEU:HB2	2.01	0.42
4:YH:349:TRP:CD1	4:YH:352:LYS:HZ2	2.38	0.42
4:ZH:191:ILE:HG13	4:ZH:211:ASN:HA	2.01	0.42
7:AM:138:LEU:O	7:AM:157:ALA:HA	2.19	0.42
5:BK:62:LYS:HE2	5:BK:62:LYS:HB2	1.93	0.42
7:BM:221:LYS:HA	7:BM:221:LYS:HD3	1.97	0.42
2:Bd:82:ARG:HH21	2:Bd:126:GLU:HA	1.85	0.42
11:EC:246:ARG:HE	11:EC:246:ARG:HB3	1.69	0.42
11:FC:106:LEU:HD12	11:FC:107:PRO:HD2	2.02	0.42
11:HC:91:ASP:HB3	11:HC:147:TRP:HE1	1.85	0.42
3:CF:245:LYS:NZ	3:CF:256:THR:O	2.44	0.42
7:CM:233:VAL:HG13	7:CM:253:VAL:HA	2.01	0.42
2:Cd:98:ILE:HD13	2:Cd:98:ILE:HA	1.88	0.42
11:AC:103:GLU:OE2	11:AC:104:HIS:ND1	2.53	0.42
2:AD:121:ILE:HD13	2:AD:121:ILE:HA	1.93	0.42
4:EH:264:LYS:HD3	4:EH:264:LYS:HA	1.79	0.42
4:EH:319:ILE:HA	4:EH:347:VAL:HG12	2.01	0.42
2:Ed:136:ASP:HB2	2:Ed:145:ILE:HD11	2.01	0.42
6:FL:192:PHE:O	6:FL:196:ASN:ND2	2.33	0.42
3:AF:241:TYR:HB3	3:AF:256:THR:HG21	2.02	0.42
11:GC:54:ILE:HG23	1:HG:872:VAL:HG13	2.02	0.42
2:Hd:85:VAL:HG22	11:DC:266:VAL:HA	2.02	0.42
7:IM:210:ASP:HA	7:IM:229:ASN:H	1.85	0.42
11:KC:176:TRP:O	11:KC:180:THR:OG1	2.29	0.42
4:JH:192:ALA:HB2	4:JH:231:ARG:HA	2.02	0.42
5:JK:127:LYS:H	5:JK:127:LYS:HZ3	1.68	0.42
4:AH:320:LEU:HB2	4:AH:346:LEU:HB3	2.01	0.42
4:KH:109:LYS:HB2	4:KH:109:LYS:HE2	1.81	0.42
4:LH:196:LEU:HD13	4:LH:226:LEU:HD12	2.02	0.42
6:LL:169:THR:HG1	6:LL:170:ASP:H	1.66	0.42
3:Lf:246:LEU:HB3	3:Lf:255:LEU:HD21	2.01	0.42
1:EG:876:SER:OG	1:EG:1031:VAL:O	2.34	0.42
1:Mg:795:GLN:HE21	1:Mg:795:GLN:HB2	1.60	0.42
4:WH:312:TYR:HD1	4:WH:338:GLU:HG2	1.85	0.42
4:YH:213:LEU:HD13	4:YH:215:ILE:HD11	2.02	0.42
3:ZF:243:MET:O	3:ZF:257:SER:N	2.48	0.42
2:BD:121:ILE:HD13	2:BD:121:ILE:HA	1.89	0.42
11:EC:75:TRP:NE1	11:FC:28:THR:OG1	2.53	0.42
7:CM:158:VAL:HG13	7:CM:178:LYS:HE2	2.01	0.42
1:JG:871:ALA:HB2	1:JG:889:ILE:HD13	2.02	0.42
1:KG:880:ASP:OD1	1:KG:880:ASP:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:AC:154:MET:HE2	11:AC:154:MET:HB3	1.81	0.42
2:AD:119:ILE:HD12	2:AD:119:ILE:HA	1.94	0.42
2:ED:135:ILE:HD13	2:ED:135:ILE:HA	1.87	0.42
4:EH:324:TRP:HA	4:EH:339:MET:HB3	2.01	0.42
5:EK:148:GLY:H	2:Ed:30:ILE:HD13	1.84	0.42
2:FD:79:LEU:N	2:FD:80:GLN:OE1	2.50	0.42
11:CC:255:LEU:HD13	11:BC:240:ILE:HG12	2.02	0.42
5:FK:122:LYS:HA	5:FK:122:LYS:HD2	1.91	0.42
1:BG:902:SER:O	1:BG:915:THR:N	2.52	0.42
2:GD:107:ARG:O	2:GD:155:GLU:HA	2.19	0.42
4:GH:143:ALA:O	4:HH:131:LYS:NZ	2.41	0.42
4:GH:170:ARG:N	4:GH:249:ASP:OD2	2.52	0.42
7:GM:235:LEU:HB2	7:GM:255:THR:HG22	2.01	0.42
11:GC:97:ASN:ND2	2:LD:118:LEU:O	2.53	0.42
3:HF:219:ARG:HH22	4:XH:150:LYS:HZ2	1.68	0.42
4:HH:140:ALA:HB2	4:XH:124:PRO:HB3	2.02	0.42
6:IL:91:VAL:HA	6:IL:94:VAL:HG22	2.01	0.42
11:KC:57:MET:HA	11:KC:60:LYS:HG3	2.01	0.42
4:JH:166:PRO:HA	4:JH:167:PRO:HD3	1.91	0.42
5:JK:46:ASP:OD1	5:JK:46:ASP:N	2.52	0.42
2:Jd:86:ASP:OD1	11:FC:130:ARG:NH2	2.50	0.42
4:KH:160:LEU:O	4:YH:251:ARG:NH2	2.53	0.42
5:KK:78:ILE:HB	5:KK:180:VAL:HG23	2.01	0.42
6:LL:91:VAL:HA	6:LL:94:VAL:HG12	2.02	0.42
6:LL:116:TYR:OH	6:LL:118:GLU:OE1	2.34	0.42
2:MD:75:ASN:HA	2:MD:79:LEU:HD23	2.00	0.42
7:MM:278:ASP:OD1	7:MM:297:SER:OG	2.38	0.42
3:VF:222:LEU:HD13	3:VF:262:ILE:HD13	2.00	0.42
3:VF:233:ARG:NH1	3:DF:269:SER:OG	2.53	0.42
4:VH:160:LEU:H	4:VH:160:LEU:HG	1.60	0.42
3:YF:207:ARG:HB3	3:YF:208:ILE:H	1.58	0.42
6:AL:190:MET:HE2	6:AL:190:MET:HB2	1.82	0.42
4:YH:233:LEU:HD23	4:YH:233:LEU:HA	1.94	0.42
4:YH:278:ASP:OD1	4:YH:278:ASP:N	2.53	0.42
4:BH:288:PRO:HB3	4:BH:305:TRP:CE2	2.54	0.42
7:BM:256:HIS:O	7:BM:259:SER:OG	2.30	0.42
11:FC:220:MET:HE3	11:FC:220:MET:HB3	1.90	0.42
11:JC:169:LYS:O	11:JC:174:LYS:NZ	2.53	0.42
11:MC:234:THR:O	11:MC:241:HIS:ND1	2.51	0.42
7:CM:243:GLY:H	7:CM:262:GLU:HG2	1.85	0.42
8:CN:47:GLY:O	8:CN:61:ASN:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MG:898:LYS:HE2	1:MG:898:LYS:HB2	1.80	0.42
11:AC:145:PRO:HA	11:AC:146:PRO:HD3	1.95	0.42
7:DM:256:HIS:O	7:DM:259:SER:OG	2.34	0.42
4:EH:147:THR:HA	4:EH:148:PRO:HD3	1.94	0.41
8:FN:116:LYS:O	8:FN:116:LYS:NZ	2.50	0.41
7:GM:256:HIS:O	7:GM:277:SER:OG	2.38	0.41
7:HM:125:THR:HG23	7:HM:145:ARG:HB2	2.01	0.41
1:CG:969:GLY:HA3	1:CG:1009:ALA:HB2	2.02	0.41
6:IL:128:PRO:O	6:IL:132:TYR:HB2	2.20	0.41
8:IN:72:ARG:NH1	4:JH:297:VAL:O	2.53	0.41
11:KC:53:LYS:HA	11:KC:56:GLU:HB3	2.02	0.41
11:KC:243:ASP:HB3	11:LC:129:ASP:HB2	2.02	0.41
2:Jd:29:PRO:HB2	2:Jd:32:ASN:HB2	2.02	0.41
2:KD:55:MET:HA	2:KD:58:VAL:HG12	2.02	0.41
3:KF:243:MET:N	3:KF:257:SER:OG	2.50	0.41
7:KM:149:ASN:OD1	7:KM:149:ASN:N	2.46	0.41
5:LK:66:LYS:HB3	5:LK:77:SER:HB3	2.01	0.41
6:LL:204:LYS:HA	6:LL:204:LYS:HD3	1.86	0.41
7:LM:214:ILE:HB	7:LM:233:VAL:HG22	2.02	0.41
5:AK:163:LYS:HA	5:AK:163:LYS:HD2	1.85	0.41
4:MH:204:ILE:HG23	4:MH:215:ILE:HG12	2.01	0.41
6:ML:129:THR:OG1	6:ML:130:ASP:OD1	2.37	0.41
4:VH:176:VAL:HG22	4:VH:216:GLN:HB2	2.02	0.41
4:YH:280:LEU:HA	4:YH:283:VAL:HG12	2.00	0.41
2:Ad:128:LEU:HA	2:Ad:131:ILE:HB	2.02	0.41
2:BD:47:SER:O	2:BD:51:SER:OG	2.32	0.41
4:BH:325:LEU:HD21	4:BH:340:GLN:HE22	1.85	0.41
7:BM:275:ASP:O	7:BM:277:SER:OG	2.37	0.41
11:FC:150:TYR:HB2	11:FC:151:LEU:HD22	2.02	0.41
11:JC:219:MET:HB3	11:JC:221:MET:HG2	2.01	0.41
2:CD:41:LEU:HB3	2:Cd:41:LEU:HD21	2.02	0.41
6:CL:125:LEU:HD13	6:CL:125:LEU:HA	1.95	0.41
5:DK:40:LYS:HE2	5:DK:40:LYS:HB2	1.87	0.41
5:DK:124:VAL:N	5:DK:129:GLU:OE2	2.41	0.41
1:KG:1025:THR:HA	1:KG:1026:PRO:HD3	1.88	0.41
1:NG:898:LYS:HE2	1:NG:898:LYS:HB2	1.86	0.41
11:AC:171:LYS:HA	11:AC:174:LYS:HE2	2.02	0.41
7:DM:280:TYR:HA	7:DM:299:LEU:O	2.20	0.41
3:Df:220:ALA:HB3	3:Df:232:VAL:HG13	2.02	0.41
3:EF:248:ASP:HB3	3:EF:253:ARG:HG3	2.02	0.41
5:EK:122:LYS:HZ2	5:EK:122:LYS:HG3	1.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:EL:109:LEU:HD13	6:EL:109:LEU:HA	1.88	0.41
7:EM:229:ASN:HA	7:EM:249:GLN:HG2	2.02	0.41
11:BC:210:ILE:HD12	11:BC:210:ILE:HA	1.91	0.41
2:GD:67:LYS:HZ2	2:Gd:64:PRO:HD3	1.85	0.41
6:GL:49:ASN:O	6:GL:51:GLN:NE2	2.42	0.41
7:GM:210:ASP:O	7:GM:230:ARG:N	2.52	0.41
3:Gf:216:ILE:HD12	3:Gf:216:ILE:HA	1.94	0.41
2:HD:135:ILE:HD13	2:HD:135:ILE:HA	1.89	0.41
7:HM:208:LYS:HA	7:HM:208:LYS:HD3	1.77	0.41
1:Bg:794:ILE:H	1:Bg:794:ILE:HG12	1.68	0.41
3:IF:254:ILE:HB	3:IF:262:ILE:HB	2.02	0.41
6:IL:109:LEU:HD13	6:IL:109:LEU:HA	1.90	0.41
4:JH:191:ILE:HG13	4:JH:211:ASN:HA	2.01	0.41
4:AH:154:THR:O	4:AH:252:VAL:HA	2.20	0.41
1:Kg:794:ILE:H	1:Kg:794:ILE:HG12	1.61	0.41
7:KM:157:ALA:O	7:KM:178:LYS:NZ	2.46	0.41
3:LF:267:GLU:O	4:LH:150:LYS:NZ	2.44	0.41
4:LH:238:MET:SD	4:MH:178:SER:OG	2.72	0.41
6:LL:184:ALA:O	6:LL:188:THR:OG1	2.35	0.41
2:MD:127:SER:OG	2:MD:128:LEU:N	2.50	0.41
4:MH:173:GLN:HA	4:MH:217:ALA:HB3	2.01	0.41
7:MM:273:ALA:O	7:MM:292:MET:HA	2.20	0.41
1:XG:794:ILE:H	1:XG:794:ILE:HG12	1.54	0.41
4:ZH:330:SER:HG	4:ZH:334:THR:HG1	1.67	0.41
6:BL:183:GLN:NE2	6:BL:207:GLY:O	2.41	0.41
2:Bd:78:ASN:OD1	2:Bd:78:ASN:N	2.51	0.41
11:EC:155:ASP:N	11:EC:155:ASP:OD1	2.53	0.41
11:FC:110:LEU:HD13	11:FC:110:LEU:HA	1.91	0.41
11:IC:79:ILE:HD11	11:IC:195:LEU:HD22	2.02	0.41
11:IC:157:LYS:HD2	11:IC:157:LYS:HA	1.84	0.41
1:Dg:805:ALA:HA	1:Dg:808:LEU:HB2	2.01	0.41
5:DK:163:LYS:O	5:DK:179:ARG:NH2	2.41	0.41
7:DM:273:ALA:O	7:DM:292:MET:HA	2.20	0.41
2:ED:82:ARG:HA	2:ED:82:ARG:HD2	1.91	0.41
4:EH:173:GLN:NE2	4:EH:218:THR:O	2.41	0.41
5:EK:166:THR:HG22	5:EK:168:TYR:H	1.86	0.41
7:EM:238:PHE:N	7:EM:258:LYS:O	2.49	0.41
8:EN:45:MET:HE3	8:EN:62:ASN:HD21	1.84	0.41
2:Ed:98:ILE:HD13	2:Ed:98:ILE:HA	1.89	0.41
3:Ef:243:MET:N	3:Ef:257:SER:OG	2.46	0.41
1:BG:891:THR:OG1	1:BG:892:GLY:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AF:219:ARG:HG2	4:BH:148:PRO:HD2	2.02	0.41
3:AF:233:ARG:NH1	3:BF:266:GLN:O	2.41	0.41
7:GM:229:ASN:OD1	7:GM:229:ASN:N	2.54	0.41
6:HL:125:LEU:HB2	6:HL:231:ILE:HB	2.02	0.41
1:CG:1006:ILE:O	1:CG:1010:THR:OG1	2.38	0.41
1:Jg:794:ILE:O	1:Jg:798:THR:OG1	2.35	0.41
4:JH:253:ASP:OD1	4:JH:253:ASP:N	2.51	0.41
7:JM:146:LEU:HB2	7:JM:165:ILE:HG12	2.02	0.41
7:JM:275:ASP:OD1	7:JM:275:ASP:N	2.52	0.41
2:KD:109:LEU:HB3	2:KD:157:ARG:HA	2.03	0.41
2:KD:161:ILE:HD12	2:KD:161:ILE:HA	1.87	0.41
5:KK:122:LYS:NZ	5:KK:125:SER:O	2.52	0.41
7:KM:193:GLN:HG3	7:KM:213:THR:HB	2.03	0.41
2:LD:71:LEU:HD12	2:LD:72:THR:HG23	2.01	0.41
4:LH:325:LEU:HD21	4:LH:340:GLN:HE22	1.85	0.41
2:Ld:124:LYS:HE3	2:Ld:124:LYS:HB2	1.92	0.41
3:Mf:243:MET:O	3:Mf:257:SER:N	2.53	0.41
3:VF:245:LYS:HA	3:VF:245:LYS:HD3	1.91	0.41
4:VH:292:SER:HB3	4:VH:307:SER:HB2	2.00	0.41
4:YH:280:LEU:HD23	4:YH:328:MET:HG2	2.02	0.41
1:ZG:794:ILE:HD13	4:BH:107:ILE:HG23	2.02	0.41
1:ZG:806:THR:HA	1:ZG:809:VAL:HG12	2.02	0.41
2:Ad:72:THR:OG1	2:Ad:73:ILE:N	2.49	0.41
3:Af:220:ALA:HB3	3:Af:232:VAL:HB	2.02	0.41
6:BL:94:VAL:HA	6:BL:97:ILE:HG12	2.02	0.41
11:FC:153:MET:HE3	11:FC:153:MET:HB3	1.94	0.41
11:IC:214:LYS:HZ2	2:AD:55:MET:HB3	1.84	0.41
11:MC:266:VAL:HG12	2:Dd:97:ARG:HH12	1.85	0.41
5:CK:88:SER:H	5:CK:136:ARG:HH21	1.68	0.41
2:Ed:110:GLY:HA3	2:Ed:158:TYR:HB2	2.01	0.41
4:GH:309:GLU:HB2	4:GH:341:LYS:HE3	2.02	0.41
5:GK:46:ASP:OD1	5:GK:46:ASP:N	2.47	0.41
6:GL:170:ASP:HB2	6:GL:217:ASN:HD21	1.85	0.41
6:GL:174:SER:HB3	6:GL:177:HIS:HB3	2.02	0.41
7:GM:154:LYS:HD3	7:GM:154:LYS:HA	1.93	0.41
4:IH:226:LEU:O	4:IH:238:MET:HA	2.21	0.41
2:Id:98:ILE:HD13	2:Id:98:ILE:HA	1.89	0.41
2:Id:135:ILE:HD13	2:Id:135:ILE:HA	1.86	0.41
2:JD:47:SER:OG	11:EC:204:LYS:NZ	2.41	0.41
6:LL:114:ILE:HG22	6:LL:125:LEU:HD12	2.03	0.41
7:LM:303:GLU:HG2	7:LM:305:GLY:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AK:54:ILE:HA	5:AK:57:MET:HG2	2.03	0.41
4:MH:297:VAL:HG11	4:MH:302:ALA:HB3	2.02	0.41
4:VH:311:MET:O	4:VH:338:GLU:HA	2.21	0.41
1:XG:794:ILE:O	1:XG:798:THR:OG1	2.38	0.41
1:XG:817:THR:OG1	1:XG:818:GLN:N	2.53	0.41
6:AL:193:LEU:HD13	6:AL:193:LEU:HA	1.93	0.41
11:DC:60:LYS:HB3	11:DC:179:TYR:HE2	1.85	0.41
3:Af:214:ALA:H	3:Af:221:TRP:HB3	1.86	0.41
5:BK:169:THR:O	5:BK:169:THR:OG1	2.36	0.41
7:BM:114:ASN:HB3	7:BM:115:ARG:HE	1.86	0.41
2:Bd:67:LYS:HE3	2:Bd:67:LYS:HB2	1.83	0.41
11:FC:172:GLU:HA	11:FC:175:ILE:HG12	2.02	0.41
11:LC:153:MET:HB2	11:LC:153:MET:HE2	1.71	0.41
11:LC:203:LYS:HE3	11:LC:203:LYS:HB3	1.77	0.41
4:CH:167:PRO:HB2	4:CH:239:LEU:HD23	2.02	0.41
7:CM:210:ASP:OD1	7:CM:210:ASP:N	2.53	0.41
2:Cd:148:TYR:HB2	2:Cd:153:VAL:HG12	2.02	0.41
1:HG:864:LYS:HB3	1:HG:864:LYS:HE2	1.84	0.41
1:NG:862:ILE:HD13	1:NG:1046:THR:HA	2.01	0.41
11:CC:261:GLU:N	11:CC:261:GLU:OE1	2.53	0.41
5:FK:78:ILE:HB	5:FK:180:VAL:HG13	2.02	0.41
6:FL:48:ASN:ND2	6:FL:51:GLN:OE1	2.53	0.41
6:FL:124:THR:HG22	6:FL:232:GLN:HG2	2.02	0.41
3:Ff:213:GLN:HE22	3:Ff:223:ILE:H	1.68	0.41
11:BC:157:LYS:H	8:GN:82:MET:HE3	1.85	0.41
1:BG:876:SER:OG	1:BG:1031:VAL:O	2.31	0.41
3:AF:209:ILE:H	3:AF:225:SER:HB3	1.85	0.41
1:Gg:823:GLY:HA3	4:WH:206:TRP:HH2	1.84	0.41
11:GC:113:GLY:O	11:GC:130:ARG:HA	2.21	0.41
2:Hd:41:LEU:HD13	2:Hd:41:LEU:HA	1.89	0.41
3:IF:207:ARG:HB3	3:IF:208:ILE:H	1.51	0.41
4:IH:157:PHE:HA	4:IH:255:ARG:HB3	2.01	0.41
8:IN:63:GLY:HA3	2:JD:27:LYS:HB2	2.01	0.41
4:JH:203:ASN:N	4:JH:216:GLN:O	2.48	0.41
4:JH:354:MET:HE2	4:JH:354:MET:HB2	1.87	0.41
7:JM:144:THR:HB	7:JM:163:THR:HG23	2.02	0.41
2:LD:29:PRO:HG2	6:LL:225:GLN:HA	2.01	0.41
6:LL:59:ARG:HD2	6:LL:59:ARG:HA	1.87	0.41
2:MD:131:ILE:HD13	2:MD:131:ILE:HA	1.88	0.41
3:MF:212:ILE:HD12	3:MF:263:LYS:HA	2.02	0.41
3:MF:265:SER:HB3	3:MF:268:ASP:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:MM:177:LEU:HD12	7:MM:196:MET:HG2	2.03	0.41
8:MN:44:LYS:HA	8:MN:44:LYS:HD3	1.81	0.41
1:VG:824:THR:H	4:CH:208:LYS:HG3	1.85	0.41
3:YF:248:ASP:HB3	3:YF:253:ARG:HG3	2.02	0.41
7:AM:137:TYR:HA	7:AM:156:GLU:O	2.21	0.41
7:AM:229:ASN:HA	7:AM:249:GLN:HG2	2.02	0.41
1:GG:1013:LYS:HE3	1:GG:1013:LYS:HB2	1.85	0.41
11:IC:114:ARG:HG2	11:IC:130:ARG:HG2	2.03	0.41
7:CM:115:ARG:HG3	7:CM:135:ASP:HB3	2.02	0.41
7:CM:210:ASP:O	7:CM:230:ARG:N	2.42	0.41
7:CM:235:LEU:HG	7:CM:239:ALA:HB3	2.02	0.41
1:IG:931:SER:O	1:IG:1042:THR:OG1	2.39	0.41
1:LG:1017:GLN:HE21	1:LG:1017:GLN:HB2	1.66	0.41
1:Ag:807:GLN:H	1:Ag:807:GLN:HG3	1.69	0.41
1:AG:937:PRO:HD3	1:AG:1037:LEU:HA	2.02	0.41
4:EH:280:LEU:HD21	4:EH:338:GLU:HB2	2.02	0.41
11:CC:106:LEU:HD12	11:CC:107:PRO:HD2	2.03	0.41
1:BG:944:LEU:HD11	1:BG:1031:VAL:HA	2.02	0.41
2:GD:55:MET:HA	2:GD:58:VAL:HG12	2.01	0.41
4:GH:171:LEU:HB2	4:GH:243:PRO:HB3	2.01	0.41
7:HM:218:LYS:HE2	7:HM:218:LYS:HB2	1.90	0.41
3:Hf:216:ILE:HD12	3:Hf:216:ILE:HA	1.84	0.41
1:CG:972:PHE:HD1	1:CG:972:PHE:HA	1.79	0.41
5:IK:81:SER:OG	5:IK:173:ASP:O	2.38	0.41
2:Id:92:GLU:OE2	2:Id:158:TYR:OH	2.38	0.41
5:JK:66:LYS:HB3	5:JK:77:SER:HB2	2.03	0.41
5:JK:107:LYS:NZ	5:JK:148:GLY:O	2.42	0.41
7:JM:254:LYS:HE3	7:JM:254:LYS:HB2	1.88	0.41
5:KK:138:ARG:HH21	7:KM:319:PHE:HA	1.86	0.41
3:Kf:263:LYS:HE2	3:Kf:263:LYS:HB3	1.95	0.41
4:LH:171:LEU:HB2	4:LH:243:PRO:HA	2.03	0.41
4:LH:208:LYS:O	4:LH:208:LYS:NZ	2.45	0.41
8:LN:51:CYS:HA	8:LN:58:LEU:HA	2.02	0.41
1:XG:818:GLN:N	4:XH:216:GLN:OE1	2.54	0.41
1:FG:871:ALA:HB2	1:FG:889:ILE:HD13	2.01	0.41
1:FG:898:LYS:HE3	1:GG:864:LYS:HZ2	1.86	0.41
1:FG:944:LEU:HD21	1:FG:1031:VAL:HG12	2.02	0.41
1:FG:951:HIS:H	1:FG:1027:THR:HG22	1.85	0.41
4:CH:229:ARG:HG2	4:CH:236:PRO:HB3	2.02	0.41
2:Cd:105:ARG:HB2	2:Cd:153:VAL:HG23	2.03	0.41
2:Cd:150:ASN:OD1	2:Cd:150:ASN:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JG:898:LYS:NZ	1:KG:865:THR:O	2.49	0.41
1:JG:910:ASP:OD1	1:JG:910:ASP:N	2.52	0.41
1:LG:876:SER:OG	1:MG:941:ARG:NH2	2.53	0.41
1:NG:910:ASP:OD1	1:NG:910:ASP:N	2.53	0.41
1:AG:962:SER:HB3	1:AG:1015:TRP:HB3	2.03	0.41
2:ED:148:TYR:O	2:ED:152:GLN:N	2.54	0.41
3:EF:224:GLY:N	3:EF:228:SER:O	2.44	0.41
5:FK:181:GLU:OE2	6:GL:119:TYR:OH	2.38	0.41
8:FN:45:MET:SD	8:FN:62:ASN:ND2	2.87	0.41
1:BG:897:SER:HA	1:BG:922:PRO:HD3	2.02	0.41
6:GL:114:ILE:HD13	6:GL:128:PRO:HD2	2.03	0.41
3:HF:243:MET:O	3:HF:257:SER:N	2.54	0.41
1:Hg:801:MET:O	1:Hg:805:ALA:N	2.48	0.41
5:HK:87:GLN:N	5:HK:173:ASP:OD2	2.51	0.41
6:HL:150:ASN:OD1	6:HL:153:ARG:NH2	2.41	0.41
3:IF:213:GLN:HB2	3:IF:223:ILE:HG22	2.01	0.41
7:IM:129:LEU:HB3	7:IM:150:ILE:HD11	2.02	0.41
5:JK:50:ASP:OD1	8:JN:67:THR:OG1	2.29	0.41
3:Jf:216:ILE:HD12	3:Jf:216:ILE:HA	1.89	0.41
4:KH:264:LYS:HD2	4:KH:264:LYS:HA	1.80	0.41
3:Kf:210:TYR:HE2	3:Kf:238:ILE:HB	1.85	0.41
2:LD:161:ILE:HD12	2:LD:161:ILE:HA	1.86	0.41
7:MM:212:LEU:HD13	7:MM:212:LEU:HA	1.94	0.41
1:VG:797:ARG:HD2	1:VG:797:ARG:HA	1.95	0.41
4:WH:320:LEU:HD11	11:MC:251:ALA:HB2	2.03	0.41
1:FG:968:PHE:CG	1:FG:1008:LEU:HD13	2.56	0.41
1:FG:968:PHE:O	1:FG:972:PHE:HB2	2.21	0.41
2:Ad:65:PRO:HD3	2:Ad:71:LEU:HD13	2.03	0.41
2:Ad:131:ILE:HD13	2:Ad:131:ILE:HA	1.94	0.41
6:BL:174:SER:HB3	6:BL:177:HIS:HB3	2.03	0.41
2:Bd:76:ALA:HB3	2:Bd:79:LEU:HD23	2.02	0.41
11:EC:216:LEU:HD12	11:EC:216:LEU:HA	1.87	0.41
11:HC:111:LEU:HD13	11:HC:111:LEU:HA	1.91	0.41
2:CD:135:ILE:HD13	2:CD:135:ILE:HA	1.85	0.41
7:CM:209:SER:OG	7:CM:210:ASP:N	2.53	0.41
2:DD:98:ILE:HD13	2:DD:98:ILE:HA	1.92	0.41
4:DH:284:LEU:HD22	4:DH:328:MET:HG3	2.01	0.41
1:MG:1030:GLU:HG2	1:NG:941:ARG:HH21	1.85	0.41
1:OG:885:ILE:O	1:OG:900:ILE:HA	2.20	0.41
1:OG:916:PHE:HD1	1:OG:916:PHE:HA	1.74	0.41
11:AC:171:LYS:H	11:AC:171:LYS:HG2	1.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:CC:97:ASN:ND2	2:HD:118:LEU:O	2.54	0.41
4:FH:341:LYS:HE3	4:FH:341:LYS:HB3	1.98	0.41
5:FK:96:TYR:HA	5:FK:99:LEU:HB2	2.01	0.41
2:GD:98:ILE:HD13	2:GD:98:ILE:HA	1.92	0.41
4:GH:209:THR:HA	4:GH:231:ARG:HH22	1.85	0.41
6:GL:109:LEU:HD13	6:GL:109:LEU:HA	1.87	0.41
8:GN:78:LEU:HB3	4:HH:355:GLN:HB2	2.03	0.41
6:HL:169:THR:OG1	6:HL:170:ASP:N	2.54	0.41
3:Hf:238:ILE:HB	3:Hf:241:TYR:HB2	2.03	0.41
6:IL:134:MET:HB2	6:IL:139:ARG:HB2	2.03	0.41
1:Jg:797:ARG:HD2	1:Jg:797:ARG:HA	1.84	0.41
5:JK:183:THR:HG21	9:JU:123:UNK:HA	2.02	0.41
6:JL:155:LEU:HD13	6:JL:155:LEU:HA	1.91	0.41
6:KL:123:ARG:HD2	6:KL:233:TRP:HE1	1.85	0.41
2:Kd:72:THR:OG1	2:Kd:73:ILE:N	2.53	0.41
2:Ld:136:ASP:HB2	2:Ld:145:ILE:HD11	2.03	0.41
3:Lf:244:VAL:HA	3:Lf:256:THR:HA	2.02	0.41
3:VF:219:ARG:HG2	4:DH:148:PRO:HD2	2.03	0.41
4:VH:226:LEU:HB2	4:VH:241:LEU:HD11	2.02	0.41
1:FG:1013:LYS:HE3	1:FG:1013:LYS:HB2	1.88	0.41
11:DC:250:THR:OG1	11:DC:251:ALA:N	2.53	0.41
4:BH:229:ARG:HH22	4:CH:210:SER:HB2	1.85	0.41
11:EC:185:TRP:HZ3	11:FC:30:SER:HB3	1.86	0.41
11:IC:75:ARG:HA	11:IC:75:ARG:HD2	1.86	0.41
11:IC:106:LEU:HD12	11:IC:107:PRO:HD2	2.03	0.41
11:JC:102:LEU:HB2	11:JC:106:ILE:HG13	2.03	0.41
11:JC:151:TYR:HB2	11:JC:152:LEU:HD22	2.03	0.41
6:CL:94:VAL:HA	6:CL:97:ILE:HG12	2.01	0.41
8:CN:89:GLY:HA3	8:CN:104:ASN:HB2	2.03	0.41
2:Cd:142:LYS:HE2	2:Cd:142:LYS:HB2	1.94	0.41
6:DL:109:LEU:HD13	6:DL:109:LEU:HA	1.87	0.41
1:Eg:797:ARG:NH1	1:Eg:801:MET:SD	2.83	0.41
4:EH:221:TYR:HE2	4:FH:138:GLU:HB3	1.86	0.41
2:Ed:73:ILE:HD12	2:Ed:129:ALA:HB1	2.02	0.41
2:Ed:147:VAL:HG22	2:Ed:154:VAL:HG12	2.02	0.41
3:Ef:254:ILE:O	3:Ef:261:VAL:HA	2.20	0.41
3:FF:265:SER:OG	3:FF:266:GLN:N	2.54	0.41
11:CC:240:ILE:HG12	11:DC:255:LEU:HD13	2.02	0.41
4:FH:171:LEU:HD11	4:FH:241:LEU:HB3	2.01	0.41
5:FK:44:ARG:HA	8:FN:68:CYS:HA	2.02	0.41
7:FM:290:ASP:HB3	7:FM:298:VAL:HG21	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:FN:104:ASN:OD1	8:FN:104:ASN:N	2.53	0.41
10:FX:23:UNK:HA	10:FX:33:UNK:HA	2.02	0.41
2:Fd:110:GLY:HA3	2:Fd:158:TYR:HB2	2.03	0.41
1:BG:911:LYS:HA	1:BG:943:ALA:HA	2.03	0.41
5:GK:174:ARG:HD3	5:GK:174:ARG:HA	1.84	0.41
6:GL:94:VAL:HA	6:GL:97:ILE:HG12	2.02	0.41
7:GM:191:LEU:HD21	7:GM:194:LEU:HD23	2.02	0.41
11:GC:261:GLU:OE1	11:GC:261:GLU:N	2.54	0.41
4:HH:191:ILE:HB	4:HH:206:TRP:HE1	1.85	0.41
4:HH:341:LYS:HB3	4:HH:341:LYS:HE2	1.83	0.41
6:HL:102:LYS:HE3	6:HL:102:LYS:HB2	1.92	0.41
7:HM:210:ASP:O	7:HM:230:ARG:N	2.53	0.41
7:HM:284:LEU:HD22	7:HM:302:ARG:HH12	1.85	0.41
3:Hf:219:ARG:HH22	3:Hf:233:ARG:HH21	1.68	0.41
8:IN:52:ASP:HB3	8:IN:55:ALA:HB3	2.03	0.41
2:Id:84:SER:H	11:EC:268:ALA:HB3	1.86	0.41
11:KC:64:LEU:HG	11:KC:179:TYR:HB3	2.02	0.41
2:JD:131:ILE:HD13	2:JD:131:ILE:HA	1.87	0.41
4:JH:317:LEU:HA	4:JH:317:LEU:HD13	1.84	0.41
8:JN:58:LEU:HD12	8:JN:68:CYS:HB2	2.02	0.41
4:AH:115:MET:HB2	1:Mg:798:THR:HG23	2.02	0.41
4:AH:204:ILE:HD11	4:AH:213:LEU:HD22	2.03	0.41
2:KD:29:PRO:HG2	6:KL:225:GLN:HA	2.03	0.41
2:KD:141:LYS:HE2	2:KD:141:LYS:HB3	1.84	0.41
4:KH:138:GLU:HA	4:KH:141:LYS:HE3	2.02	0.41
4:KH:166:PRO:HA	4:KH:167:PRO:HD3	1.90	0.41
4:KH:183:ASP:OD1	4:KH:187:ALA:N	2.52	0.41
7:KM:303:GLU:HG3	7:KM:305:GLY:H	1.86	0.41
5:LK:60:LEU:HD23	5:LK:60:LEU:HA	1.83	0.41
7:LM:229:ASN:HA	7:LM:249:GLN:HG2	2.03	0.41
4:MH:320:LEU:HD12	4:MH:346:LEU:HG	2.01	0.41
6:ML:168:PHE:HE2	6:ML:230:GLU:HB3	1.86	0.41
7:MM:149:ASN:OD1	7:MM:149:ASN:N	2.42	0.41
7:MM:215:ARG:NH1	7:MM:232:ASP:OD2	2.53	0.41
2:Md:87:TRP:O	2:Md:120:SER:HA	2.21	0.41
4:VH:121:PRO:HB2	1:Cg:801:MET:HE3	2.03	0.41
3:XF:210:TYR:HA	3:XF:224:GLY:HA2	2.03	0.41
4:XH:191:ILE:HG13	4:XH:211:ASN:HA	2.03	0.41
4:XH:196:LEU:HD21	4:XH:202:PHE:HB2	2.03	0.41
4:XH:303:ARG:HA	4:XH:303:ARG:HD3	1.87	0.41
4:ZH:159:ASN:OD1	4:ZH:164:SER:OG	2.27	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Af:265:SER:OG	3:Af:266:GLN:N	2.54	0.41
3:BF:233:ARG:NH1	3:CF:269:SER:OG	2.54	0.41
4:BH:130:LEU:HA	4:BH:133:ILE:HG22	2.02	0.41
4:BH:199:PRO:HG3	1:Cg:819:VAL:HG22	2.03	0.41
7:BM:313:ASP:OD1	7:BM:314:ARG:N	2.53	0.41
11:IC:170:LYS:HA	11:IC:173:LYS:HD2	2.02	0.41
11:JC:114:GLY:O	11:JC:131:ARG:HA	2.20	0.41
4:CH:109:LYS:HA	4:CH:109:LYS:HD3	1.87	0.41
5:DK:127:LYS:HB3	5:DK:127:LYS:HE2	1.87	0.41
1:HG:884:PRO:HG2	1:IG:1040:LEU:HD21	2.03	0.41
1:IG:1025:THR:HA	1:IG:1026:PRO:HD3	1.91	0.41
1:MG:891:THR:OG1	1:MG:892:GLY:N	2.54	0.41
1:MG:969:GLY:HA3	1:MG:1009:ALA:HB2	2.02	0.41
1:NG:1025:THR:HA	1:NG:1026:PRO:HD3	1.95	0.41
1:OG:931:SER:H	1:OG:1043:GLN:NE2	2.19	0.41
1:OG:1024:ASN:OD1	1:OG:1024:ASN:N	2.47	0.41
1:PG:947:ARG:H	1:PG:947:ARG:HE	1.68	0.41
7:DM:154:LYS:HD3	7:DM:154:LYS:HA	1.85	0.41
7:DM:189:VAL:HB	7:DM:207:ILE:HG22	2.03	0.41
1:AG:876:SER:OG	1:AG:877:VAL:N	2.53	0.41
2:FD:41:LEU:HD13	2:FD:41:LEU:HA	1.98	0.41
3:FF:208:ILE:HD11	3:FF:224:GLY:HA3	2.03	0.41
6:FL:114:ILE:HG23	6:FL:127:ILE:HG13	2.03	0.41
7:FM:119:GLU:HG3	7:FM:139:ALA:HB3	2.03	0.41
7:GM:275:ASP:OD1	7:GM:275:ASP:N	2.54	0.41
2:ID:131:ILE:HA	2:ID:131:ILE:HD13	1.86	0.41
11:KC:47:LYS:O	1:MG:938:ASN:ND2	2.54	0.41
4:KH:113:LYS:HE2	4:KH:113:LYS:HB2	1.90	0.41
7:LM:129:LEU:HB2	7:LM:150:ILE:HD11	2.03	0.41
7:LM:230:ARG:HA	7:LM:250:ARG:HB2	2.03	0.41
1:EG:919:MET:HG3	1:EG:930:ILE:HG23	2.02	0.41
3:MF:243:MET:HE3	3:MF:243:MET:HB3	1.96	0.41
4:MH:169:ILE:HD12	4:MH:252:VAL:HG11	2.03	0.41
4:MH:198:ASP:OD2	4:MH:201:SER:OG	2.30	0.41
3:VF:263:LYS:HE2	3:VF:263:LYS:HB3	1.84	0.41
4:VH:195:ASP:HB3	4:VH:227:ALA:HB3	2.02	0.41
4:XH:191:ILE:HB	4:XH:206:TRP:HE1	1.87	0.41
6:BL:170:ASP:OD2	6:BL:227:ARG:NH2	2.49	0.41
7:BM:274:THR:HA	7:BM:293:ALA:HB3	2.03	0.41
2:Bd:142:LYS:HE2	2:Bd:142:LYS:HB2	1.93	0.41
3:Bf:263:LYS:HE2	3:Bf:263:LYS:HB2	1.99	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:EC:86:LYS:HD2	11:EC:86:LYS:HA	1.90	0.41
11:FC:263:ARG:HA	11:FC:263:ARG:HD2	1.85	0.41
4:CH:207:ASP:OD1	4:CH:207:ASP:N	2.43	0.41
5:CK:70:VAL:HA	2:DD:27:LYS:HE2	2.03	0.41
6:CL:170:ASP:N	6:CL:170:ASP:OD1	2.48	0.41
7:CM:165:ILE:HB	7:CM:185:ILE:HG23	2.03	0.41
3:Cf:263:LYS:HE2	3:Cf:263:LYS:HB2	1.91	0.41
11:AC:211:ILE:HD12	11:AC:211:ILE:HA	1.92	0.41
7:DM:275:ASP:HA	7:DM:295:ASN:H	1.86	0.41
2:Dd:155:GLU:OE2	2:Dd:157:ARG:NE	2.52	0.41
4:EH:151:PRO:HA	4:EH:248:VAL:HG13	2.02	0.40
11:CC:210:ILE:HD12	11:CC:210:ILE:HA	1.95	0.40
2:GD:121:ILE:HD13	2:GD:121:ILE:HA	1.94	0.40
4:GH:109:LYS:HB2	4:GH:109:LYS:HE2	1.93	0.40
4:GH:166:PRO:HA	4:GH:167:PRO:HD3	1.89	0.40
7:GM:302:ARG:HH11	7:GM:309:LEU:HD11	1.86	0.40
2:Gd:111:LYS:HE3	2:Gd:111:LYS:HB3	1.91	0.40
4:HH:342:SER:OG	4:HH:344:VAL:O	2.31	0.40
1:Bg:807:GLN:H	1:Bg:807:GLN:HG3	1.72	0.40
7:IM:275:ASP:HA	7:IM:295:ASN:H	1.86	0.40
7:IM:318:GLN:NE2	7:IM:319:PHE:O	2.46	0.40
1:Jg:808:LEU:H	1:Jg:808:LEU:HG	1.70	0.40
6:JL:129:THR:O	6:JL:133:PHE:CB	2.69	0.40
7:JM:228:VAL:HG12	7:JM:230:ARG:H	1.85	0.40
4:KH:295:LEU:HB2	4:KH:304:ALA:HB3	2.03	0.40
4:KH:320:LEU:N	4:KH:346:LEU:O	2.49	0.40
7:KM:199:LYS:HG3	7:KM:219:ALA:HB3	2.03	0.40
5:LK:73:ASN:OD1	5:LK:73:ASN:N	2.55	0.40
4:MH:251:ARG:HE	4:MH:251:ARG:HB2	1.57	0.40
2:Md:107:ARG:HE	2:Md:109:LEU:HD11	1.86	0.40
4:WH:189:TRP:HZ3	4:WH:256:VAL:HG11	1.87	0.40
4:ZH:218:THR:HB	4:ZH:219:LYS:HD2	2.03	0.40
4:BH:319:ILE:HA	4:BH:347:VAL:HG12	2.03	0.40
7:BM:235:LEU:HB2	7:BM:255:THR:HG22	2.03	0.40
1:GG:1006:ILE:O	1:GG:1010:THR:OG1	2.39	0.40
11:FC:52:GLY:O	11:FC:56:GLU:HB3	2.21	0.40
11:LC:109:VAL:HG13	11:LC:136:LYS:H	1.86	0.40
4:CH:106:VAL:HG23	4:CH:110:LYS:HZ2	1.86	0.40
7:CM:290:ASP:HB3	7:CM:298:VAL:HG21	2.02	0.40
8:CN:114:LEU:HD13	8:CN:114:LEU:HA	1.95	0.40
2:DD:52:MET:HG3	2:Dd:48:VAL:HG23	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:DH:339:MET:HE3	4:DH:339:MET:HB2	1.91	0.40
1:HG:874:ASP:OD1	1:HG:874:ASP:N	2.54	0.40
1:HG:900:ILE:HD11	1:IG:865:THR:HG22	2.03	0.40
1:HG:1025:THR:HA	1:HG:1026:PRO:HD3	1.96	0.40
1:LG:956:TYR:HD1	1:LG:956:TYR:HA	1.81	0.40
1:OG:948:THR:HG22	1:OG:1029:VAL:HG12	2.03	0.40
1:PG:1017:GLN:HE21	1:PG:1017:GLN:HB2	1.66	0.40
2:Gd:73:ILE:HG22	2:Gd:75:ASN:H	1.85	0.40
4:HH:311:MET:HE3	4:HH:339:MET:HE3	2.04	0.40
2:ID:119:ILE:HD13	2:ID:119:ILE:HA	1.92	0.40
11:KC:147:TRP:CD1	11:KC:147:TRP:H	2.40	0.40
3:If:246:LEU:HB3	3:If:255:LEU:HD21	2.03	0.40
4:JH:191:ILE:HA	4:JH:230:LEU:HA	2.03	0.40
5:JK:127:LYS:HE2	5:JK:127:LYS:HB2	1.90	0.40
7:JM:317:LYS:HE3	7:JM:317:LYS:HB2	1.88	0.40
4:KH:154:THR:HB	4:KH:156:GLN:HE22	1.86	0.40
6:KL:167:GLY:H	6:KL:207:GLY:HA2	1.86	0.40
4:LH:154:THR:HB	4:LH:156:GLN:HE22	1.86	0.40
5:LK:144:LEU:HD13	5:LK:144:LEU:HA	1.91	0.40
1:EG:867:ASP:OD1	1:EG:867:ASP:N	2.53	0.40
4:MH:233:LEU:HD23	4:MH:233:LEU:HA	1.92	0.40
5:MK:44:ARG:HD2	5:MK:48:ALA:HB3	2.03	0.40
6:ML:129:THR:HG22	6:ML:229:ILE:HG12	2.03	0.40
6:ML:193:LEU:HD13	6:ML:193:LEU:HA	1.87	0.40
7:MM:153:GLN:NE2	7:MM:172:ASN:OD1	2.50	0.40
8:MN:45:MET:SD	8:MN:62:ASN:ND2	2.83	0.40
8:MN:85:CYS:N	11:HC:154:ASP:OD2	2.54	0.40
2:Md:73:ILE:HA	2:Md:74:PRO:HD3	1.92	0.40
4:XH:242:ILE:HD12	4:XH:243:PRO:HD2	2.03	0.40
11:DC:111:LEU:HD23	11:DC:135:ALA:HB2	2.04	0.40
4:ZH:280:LEU:HA	4:ZH:283:VAL:HG22	2.03	0.40
7:AM:123:VAL:HG22	7:AM:143:THR:HB	2.03	0.40
8:BN:46:GLY:HA3	8:BN:61:ASN:HB2	2.03	0.40
11:EC:152:LEU:HD13	11:EC:152:LEU:HA	1.95	0.40
4:CH:249:ASP:HB3	4:CH:252:VAL:HG22	2.03	0.40
6:CL:187:GLU:HA	6:CL:190:MET:HB3	2.03	0.40
6:CL:208:TYR:HD1	6:CL:211:LYS:HD3	1.86	0.40
7:CM:306:GLN:HB2	3:Cf:251:GLN:HE22	1.86	0.40
1:LG:1025:THR:HA	1:LG:1026:PRO:HD3	1.90	0.40
1:MG:874:ASP:OD1	1:MG:874:ASP:N	2.54	0.40
1:NG:878:ASN:OD1	1:NG:879:SER:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:ED:144:SER:HB2	2:ED:157:ARG:HG3	2.03	0.40
4:EH:183:ASP:OD1	4:EH:187:ALA:N	2.54	0.40
4:EH:294:ARG:HH22	11:MC:193:THR:HB	1.86	0.40
11:CC:214:LYS:HE2	2:HD:58:VAL:HG11	2.03	0.40
4:FH:178:SER:OG	4:FH:250:TYR:O	2.36	0.40
5:FK:41:LEU:HD13	5:FK:41:LEU:HA	1.96	0.40
5:GK:91:LEU:HD13	5:GK:91:LEU:HA	1.92	0.40
5:GK:107:LYS:HE3	5:GK:107:LYS:HB3	1.93	0.40
11:GC:102:GLU:O	2:LD:162:TYR:OH	2.34	0.40
4:JH:313:VAL:HG13	4:JH:337:TYR:HB2	2.03	0.40
4:AH:201:SER:O	4:AH:218:THR:N	2.43	0.40
4:KH:168:VAL:HA	4:KH:240:THR:O	2.21	0.40
8:LN:81:LEU:HD13	8:LN:81:LEU:HA	1.94	0.40
6:ML:105:ILE:H	6:ML:105:ILE:HG13	1.73	0.40
4:WH:157:PHE:HD1	4:WH:255:ARG:HB2	1.85	0.40
4:WH:230:LEU:HB2	4:WH:233:LEU:HB3	2.04	0.40
1:FG:875:THR:HG22	1:GG:940:ALA:HB1	2.03	0.40
1:YG:800:ASP:O	1:YG:803:THR:OG1	2.37	0.40
4:ZH:147:THR:HA	4:ZH:148:PRO:HD3	1.91	0.40
10:ZX:21:UNK:O	10:ZX:77:UNK:HA	2.22	0.40
2:BD:135:ILE:HD13	2:BD:135:ILE:HA	1.88	0.40
1:GG:944:LEU:HD11	1:GG:1031:VAL:HG12	2.04	0.40
11:FC:176:TRP:O	11:FC:180:THR:OG1	2.36	0.40
4:CH:192:ALA:N	4:CH:229:ARG:O	2.54	0.40
5:CK:119:TYR:O	5:CK:178:ALA:HA	2.21	0.40
7:CM:123:VAL:HG22	7:CM:143:THR:HB	2.04	0.40
7:CM:271:SER:OG	7:CM:290:ASP:OD1	2.32	0.40
4:DH:166:PRO:HA	4:DH:167:PRO:HD3	1.94	0.40
4:DH:328:MET:HE3	4:DH:329:THR:H	1.86	0.40
1:KG:898:LYS:HE2	1:KG:898:LYS:HB2	1.89	0.40
1:MG:946:SER:OG	1:MG:1030:GLU:O	2.27	0.40
1:MG:1017:GLN:HE21	1:MG:1017:GLN:HB2	1.64	0.40
11:AC:116:ASN:N	11:AC:130:ASP:O	2.52	0.40
2:ED:60:LYS:HE3	2:ED:65:PRO:HG3	2.02	0.40
4:EH:289:PRO:O	4:EH:292:SER:OG	2.36	0.40
6:EL:187:GLU:O	6:EL:191:THR:OG1	2.37	0.40
7:EM:207:ILE:HD11	7:EM:224:LEU:HB3	2.03	0.40
4:FH:170:ARG:HA	4:FH:242:ILE:O	2.21	0.40
5:FK:81:SER:OG	5:FK:173:ASP:O	2.39	0.40
7:FM:180:ASP:OD1	7:FM:199:LYS:N	2.48	0.40
7:FM:254:LYS:HE3	7:FM:254:LYS:HB2	1.92	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Ff:256:THR:OG1	3:Ff:260:GLN:N	2.52	0.40
2:GD:84:SER:HA	2:GD:125:ASP:H	1.86	0.40
2:Gd:97:ARG:HD3	2:Gd:97:ARG:HA	1.98	0.40
8:HN:48:ILE:HD13	8:HN:58:LEU:HB3	2.02	0.40
5:IK:57:MET:HE3	5:IK:57:MET:HB3	1.77	0.40
6:IL:165:VAL:O	6:IL:205:ALA:HA	2.21	0.40
1:Jg:818:GLN:O	4:JH:205:GLN:NE2	2.55	0.40
3:Jf:256:THR:OG1	3:Jf:257:SER:N	2.54	0.40
2:LD:126:GLU:HB2	2:LD:131:ILE:HG12	2.04	0.40
8:LN:103:CYS:N	8:LN:107:TYR:O	2.42	0.40
5:AK:54:ILE:O	5:AK:58:THR:OG1	2.30	0.40
4:MH:157:PHE:HA	4:MH:255:ARG:HB2	2.02	0.40
10:MX:24:UNK:N	10:MX:32:UNK:O	2.55	0.40
2:Md:109:LEU:O	2:Md:157:ARG:HA	2.22	0.40
3:XF:247:ILE:HA	3:XF:254:ILE:HG12	2.03	0.40
3:ZF:243:MET:HE3	3:ZF:243:MET:HB3	1.90	0.40
1:ZG:798:THR:O	1:ZG:802:LEU:HB2	2.22	0.40
4:BH:173:GLN:HG3	4:BH:220:LEU:HD22	2.04	0.40
11:EC:173:GLU:O	11:EC:177:TRP:HB2	2.22	0.40
11:EC:256:LEU:HD13	11:EC:256:LEU:HA	1.90	0.40
11:HC:225:TYR:HB3	11:HC:251:ALA:HB3	2.04	0.40
11:IC:175:ILE:HA	11:IC:178:ILE:HG12	2.02	0.40
4:CH:282:HIS:O	4:CH:287:VAL:N	2.54	0.40
4:CH:316:ASN:OD1	4:CH:316:ASN:N	2.55	0.40
6:CL:215:SER:N	6:CL:226:ASN:OD1	2.55	0.40
1:JG:916:PHE:HD1	1:JG:916:PHE:HA	1.71	0.40
1:JG:1025:THR:HA	1:JG:1026:PRO:HD3	1.97	0.40
1:LG:869:MET:HB2	1:LG:1041:PHE:HE1	1.86	0.40
8:DN:62:ASN:OD1	8:DN:62:ASN:N	2.35	0.40
2:Dd:150:ASN:OD1	2:Dd:150:ASN:N	2.53	0.40
2:AD:98:ILE:HD13	2:AD:98:ILE:HA	1.92	0.40
2:FD:62:ILE:HD13	2:FD:62:ILE:HA	1.88	0.40
1:Fg:791:GLN:NE2	1:Fg:793:GLU:OE2	2.55	0.40
4:FH:107:ILE:HG23	1:Dg:794:ILE:HD13	2.02	0.40
4:FH:193:ALA:HA	1:WG:822:GLU:HA	2.03	0.40
2:Fd:64:PRO:HG2	2:Fd:67:LYS:HG2	2.02	0.40
1:BG:874:ASP:OD1	1:BG:874:ASP:N	2.53	0.40
1:BG:1005:VAL:O	1:BG:1009:ALA:CB	2.70	0.40
6:GL:145:TYR:HA	6:GL:148:LEU:HB2	2.03	0.40
6:HL:204:LYS:HD3	6:HL:204:LYS:HA	1.82	0.40
7:HM:235:LEU:HB2	7:HM:255:THR:HG22	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Hf:246:LEU:HD23	3:Hf:246:LEU:HA	1.91	0.40
1:CG:966:GLN:O	1:CG:970:ASN:ND2	2.54	0.40
1:CG:1005:VAL:O	1:CG:1009:ALA:HB2	2.22	0.40
5:IK:65:ILE:HG23	5:IK:78:ILE:HG13	2.04	0.40
8:JN:66:SER:OG	8:JN:67:THR:N	2.54	0.40
2:Jd:52:MET:HE2	2:Jd:52:MET:HB2	1.92	0.40
4:AH:149:PRO:HB2	4:AH:248:VAL:HG12	2.04	0.40
2:KD:67:LYS:HD3	2:Kd:62:ILE:HG12	2.03	0.40
5:KK:148:GLY:H	2:Kd:30:ILE:HD13	1.86	0.40
7:KM:124:VAL:O	7:KM:144:THR:HA	2.21	0.40
7:KM:276:ALA:H	7:KM:295:ASN:HB2	1.86	0.40
6:LL:114:ILE:HG23	6:LL:127:ILE:HG13	2.04	0.40
8:LN:116:LYS:HE3	8:LN:116:LYS:HB3	1.87	0.40
3:WF:216:ILE:HD11	3:WF:219:ARG:HB2	2.04	0.40
4:YH:158:VAL:HB	4:YH:256:VAL:HA	2.04	0.40
1:GG:1034:GLY:O	11:FC:55:ARG:NH2	2.50	0.40
11:IC:151:LEU:HD13	11:IC:151:LEU:HA	1.92	0.40
11:JC:195:ILE:HD13	11:JC:195:ILE:HA	1.94	0.40
11:LC:240:ILE:HG12	11:MC:255:LEU:HD13	2.03	0.40
6:CL:109:LEU:HD13	6:CL:109:LEU:HA	1.89	0.40
7:CM:154:LYS:HA	7:CM:154:LYS:HD3	1.79	0.40
1:KG:1003:ASN:HA	1:KG:1006:ILE:HD12	2.02	0.40
3:Df:246:LEU:HD21	3:Df:255:LEU:HD23	2.03	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%)	154 (96%)	7 (4%)	0	100	100
1	Ag	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BG	161/1048 (15%)	155 (96%)	6 (4%)	0	100	100
1	Bg	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	CG	161/1048 (15%)	152 (94%)	9 (6%)	0	100	100
1	Cg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	DG	161/1048 (15%)	154 (96%)	7 (4%)	0	100	100
1	Dg	32/1048 (3%)	32 (100%)	0	0	100	100
1	EG	161/1048 (15%)	156 (97%)	5 (3%)	0	100	100
1	Eg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	FG	161/1048 (15%)	153 (95%)	8 (5%)	0	100	100
1	Fg	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	GG	161/1048 (15%)	151 (94%)	10 (6%)	0	100	100
1	Gg	32/1048 (3%)	32 (100%)	0	0	100	100
1	HG	161/1048 (15%)	153 (95%)	8 (5%)	0	100	100
1	Hg	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	IG	161/1048 (15%)	153 (95%)	8 (5%)	0	100	100
1	Ig	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	JG	161/1048 (15%)	156 (97%)	5 (3%)	0	100	100
1	Jg	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	KG	161/1048 (15%)	155 (96%)	6 (4%)	0	100	100
1	Kg	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	LG	161/1048 (15%)	149 (92%)	12 (8%)	0	100	100
1	Lg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	MG	161/1048 (15%)	154 (96%)	7 (4%)	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%)	157 (98%)	4 (2%)	0	100	100
1	PG	161/1048 (15%)	156 (97%)	5 (3%)	0	100	100
1	VG	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	WG	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	XG	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	YG	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	ZG	32/1048 (3%)	32 (100%)	0	0	100	100
2	AD	138/163 (85%)	127 (92%)	11 (8%)	0	100	100
2	Ad	135/163 (83%)	128 (95%)	7 (5%)	0	100	100
2	BD	138/163 (85%)	133 (96%)	5 (4%)	0	100	100
2	Bd	135/163 (83%)	127 (94%)	8 (6%)	0	100	100
2	CD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
2	Cd	135/163 (83%)	130 (96%)	5 (4%)	0	100	100
2	DD	138/163 (85%)	133 (96%)	5 (4%)	0	100	100
2	Dd	135/163 (83%)	130 (96%)	5 (4%)	0	100	100
2	ED	138/163 (85%)	130 (94%)	8 (6%)	0	100	100
2	Ed	135/163 (83%)	130 (96%)	5 (4%)	0	100	100
2	FD	138/163 (85%)	130 (94%)	8 (6%)	0	100	100
2	Fd	135/163 (83%)	127 (94%)	8 (6%)	0	100	100
2	GD	138/163 (85%)	130 (94%)	8 (6%)	0	100	100
2	Gd	135/163 (83%)	128 (95%)	7 (5%)	0	100	100
2	HD	138/163 (85%)	130 (94%)	8 (6%)	0	100	100
2	Hd	135/163 (83%)	130 (96%)	5 (4%)	0	100	100
2	ID	138/163 (85%)	127 (92%)	11 (8%)	0	100	100
2	Id	135/163 (83%)	131 (97%)	4 (3%)	0	100	100
2	JD	138/163 (85%)	132 (96%)	6 (4%)	0	100	100
2	Jd	135/163 (83%)	126 (93%)	9 (7%)	0	100	100
2	KD	138/163 (85%)	126 (91%)	12 (9%)	0	100	100
2	Kd	135/163 (83%)	131 (97%)	4 (3%)	0	100	100
2	LD	138/163 (85%)	134 (97%)	4 (3%)	0	100	100
2	Ld	135/163 (83%)	130 (96%)	5 (4%)	0	100	100
2	MD	138/163 (85%)	130 (94%)	8 (6%)	0	100	100
2	Md	135/163 (83%)	130 (96%)	5 (4%)	0	100	100
3	AF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
3	Af	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
3	BF	61/269 (23%)	56 (92%)	5 (8%)	0	100	100
3	Bf	57/269 (21%)	54 (95%)	3 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	CF	61/269 (23%)	56 (92%)	5 (8%)	0	100	100
3	Cf	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
3	DF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
3	Df	57/269 (21%)	52 (91%)	5 (9%)	0	100	100
3	EF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
3	Ef	57/269 (21%)	52 (91%)	5 (9%)	0	100	100
3	FF	61/269 (23%)	60 (98%)	1 (2%)	0	100	100
3	Ff	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
3	GF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
3	Gf	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
3	HF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
3	Hf	57/269 (21%)	51 (90%)	6 (10%)	0	100	100
3	IF	61/269 (23%)	56 (92%)	5 (8%)	0	100	100
3	If	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
3	JF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
3	Jf	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
3	KF	61/269 (23%)	55 (90%)	6 (10%)	0	100	100
3	Kf	57/269 (21%)	55 (96%)	2 (4%)	0	100	100
3	LF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
3	Lf	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
3	MF	61/269 (23%)	60 (98%)	1 (2%)	0	100	100
3	Mf	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
3	VF	61/269 (23%)	61 (100%)	0	0	100	100
3	WF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
3	XF	61/269 (23%)	60 (98%)	1 (2%)	0	100	100
3	YF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
3	ZF	61/269 (23%)	60 (98%)	1 (2%)	0	100	100
4	AH	256/361 (71%)	240 (94%)	16 (6%)	0	100	100
4	BH	256/361 (71%)	244 (95%)	12 (5%)	0	100	100
4	CH	256/361 (71%)	241 (94%)	15 (6%)	0	100	100
4	DH	256/361 (71%)	241 (94%)	15 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	EH	256/361 (71%)	248 (97%)	8 (3%)	0	100	100
4	FH	256/361 (71%)	246 (96%)	10 (4%)	0	100	100
4	GH	256/361 (71%)	238 (93%)	18 (7%)	0	100	100
4	HH	256/361 (71%)	244 (95%)	12 (5%)	0	100	100
4	IH	256/361 (71%)	239 (93%)	17 (7%)	0	100	100
4	JH	256/361 (71%)	245 (96%)	11 (4%)	0	100	100
4	KH	256/361 (71%)	239 (93%)	17 (7%)	0	100	100
4	LH	256/361 (71%)	239 (93%)	17 (7%)	0	100	100
4	MH	256/361 (71%)	244 (95%)	12 (5%)	0	100	100
4	VH	239/361 (66%)	229 (96%)	10 (4%)	0	100	100
4	WH	239/361 (66%)	230 (96%)	9 (4%)	0	100	100
4	XH	239/361 (66%)	232 (97%)	7 (3%)	0	100	100
4	YH	239/361 (66%)	229 (96%)	10 (4%)	0	100	100
4	ZH	239/361 (66%)	229 (96%)	10 (4%)	0	100	100
5	AK	149/189 (79%)	145 (97%)	4 (3%)	0	100	100
5	BK	149/189 (79%)	145 (97%)	4 (3%)	0	100	100
5	CK	149/189 (79%)	141 (95%)	8 (5%)	0	100	100
5	DK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
5	EK	149/189 (79%)	146 (98%)	3 (2%)	0	100	100
5	FK	149/189 (79%)	144 (97%)	5 (3%)	0	100	100
5	GK	149/189 (79%)	142 (95%)	7 (5%)	0	100	100
5	HK	149/189 (79%)	140 (94%)	9 (6%)	0	100	100
5	IK	149/189 (79%)	141 (95%)	8 (5%)	0	100	100
5	JK	149/189 (79%)	142 (95%)	7 (5%)	0	100	100
5	KK	149/189 (79%)	142 (95%)	7 (5%)	0	100	100
5	LK	149/189 (79%)	142 (95%)	7 (5%)	0	100	100
5	MK	149/189 (79%)	142 (95%)	7 (5%)	0	100	100
6	AL	169/249 (68%)	165 (98%)	4 (2%)	0	100	100
6	BL	169/249 (68%)	162 (96%)	7 (4%)	0	100	100
6	CL	169/249 (68%)	162 (96%)	7 (4%)	0	100	100
6	DL	169/249 (68%)	158 (94%)	11 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	EL	169/249 (68%)	158 (94%)	11 (6%)	0	100	100
6	FL	169/249 (68%)	162 (96%)	7 (4%)	0	100	100
6	GL	169/249 (68%)	160 (95%)	9 (5%)	0	100	100
6	HL	169/249 (68%)	158 (94%)	11 (6%)	0	100	100
6	IL	169/249 (68%)	163 (96%)	6 (4%)	0	100	100
6	JL	169/249 (68%)	159 (94%)	10 (6%)	0	100	100
6	KL	169/249 (68%)	158 (94%)	11 (6%)	0	100	100
6	LL	169/249 (68%)	160 (95%)	9 (5%)	0	100	100
6	ML	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
7	AM	206/320 (64%)	190 (92%)	16 (8%)	0	100	100
7	BM	206/320 (64%)	191 (93%)	15 (7%)	0	100	100
7	CM	206/320 (64%)	194 (94%)	12 (6%)	0	100	100
7	DM	206/320 (64%)	196 (95%)	10 (5%)	0	100	100
7	EM	206/320 (64%)	193 (94%)	13 (6%)	0	100	100
7	FM	206/320 (64%)	188 (91%)	18 (9%)	0	100	100
7	GM	206/320 (64%)	193 (94%)	13 (6%)	0	100	100
7	HM	206/320 (64%)	191 (93%)	15 (7%)	0	100	100
7	IM	206/320 (64%)	188 (91%)	18 (9%)	0	100	100
7	JM	206/320 (64%)	189 (92%)	17 (8%)	0	100	100
7	KM	206/320 (64%)	189 (92%)	17 (8%)	0	100	100
7	LM	206/320 (64%)	192 (93%)	14 (7%)	0	100	100
7	MM	206/320 (64%)	191 (93%)	15 (7%)	0	100	100
8	AN	76/124 (61%)	66 (87%)	10 (13%)	0	100	100
8	BN	76/124 (61%)	68 (90%)	8 (10%)	0	100	100
8	CN	76/124 (61%)	70 (92%)	6 (8%)	0	100	100
8	DN	76/124 (61%)	71 (93%)	5 (7%)	0	100	100
8	EN	76/124 (61%)	68 (90%)	8 (10%)	0	100	100
8	FN	76/124 (61%)	68 (90%)	8 (10%)	0	100	100
8	GN	76/124 (61%)	71 (93%)	5 (7%)	0	100	100
8	HN	76/124 (61%)	70 (92%)	6 (8%)	0	100	100
8	IN	76/124 (61%)	71 (93%)	5 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	JN	76/124 (61%)	68 (90%)	8 (10%)	0	100	100
8	KN	76/124 (61%)	70 (92%)	6 (8%)	0	100	100
8	LN	76/124 (61%)	68 (90%)	8 (10%)	0	100	100
8	MN	76/124 (61%)	70 (92%)	6 (8%)	0	100	100
11	AC	207/303 (68%)	194 (94%)	13 (6%)	0	100	100
11	BC	241/303 (80%)	231 (96%)	10 (4%)	0	100	100
11	CC	241/303 (80%)	230 (95%)	11 (5%)	0	100	100
11	DC	207/303 (68%)	194 (94%)	13 (6%)	0	100	100
11	EC	207/303 (68%)	202 (98%)	5 (2%)	0	100	100
11	FC	241/303 (80%)	230 (95%)	11 (5%)	0	100	100
11	GC	241/303 (80%)	234 (97%)	7 (3%)	0	100	100
11	HC	207/303 (68%)	193 (93%)	14 (7%)	0	100	100
11	IC	207/303 (68%)	192 (93%)	15 (7%)	0	100	100
11	JC	207/303 (68%)	198 (96%)	9 (4%)	0	100	100
11	KC	241/303 (80%)	230 (95%)	11 (5%)	0	100	100
11	LC	207/303 (68%)	190 (92%)	17 (8%)	0	100	100
11	MC	207/303 (68%)	192 (93%)	15 (7%)	0	100	100
All	All	23724/70112 (34%)	22457 (95%)	1267 (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%)	117 (87%)	18 (13%)	4	16
1	Ag	31/765 (4%)	23 (74%)	8 (26%)	0	4
1	BG	135/765 (18%)	114 (84%)	21 (16%)	2	13
1	Bg	31/765 (4%)	26 (84%)	5 (16%)	2	12

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CG	135/765 (18%)	116 (86%)	19 (14%)	3	15
1	Cg	31/765 (4%)	25 (81%)	6 (19%)	1	8
1	DG	135/765 (18%)	117 (87%)	18 (13%)	4	16
1	Dg	31/765 (4%)	24 (77%)	7 (23%)	1	6
1	EG	135/765 (18%)	114 (84%)	21 (16%)	2	13
1	Eg	31/765 (4%)	21 (68%)	10 (32%)	0	2
1	FG	135/765 (18%)	121 (90%)	14 (10%)	7	22
1	Fg	31/765 (4%)	23 (74%)	8 (26%)	0	4
1	GG	135/765 (18%)	113 (84%)	22 (16%)	2	12
1	Gg	31/765 (4%)	23 (74%)	8 (26%)	0	4
1	HG	135/765 (18%)	118 (87%)	17 (13%)	4	17
1	Hg	31/765 (4%)	26 (84%)	5 (16%)	2	12
1	IG	135/765 (18%)	115 (85%)	20 (15%)	3	14
1	Ig	31/765 (4%)	26 (84%)	5 (16%)	2	12
1	JG	135/765 (18%)	117 (87%)	18 (13%)	4	16
1	Jg	31/765 (4%)	24 (77%)	7 (23%)	1	6
1	KG	135/765 (18%)	114 (84%)	21 (16%)	2	13
1	Kg	31/765 (4%)	22 (71%)	9 (29%)	0	3
1	LG	135/765 (18%)	115 (85%)	20 (15%)	3	14
1	Lg	31/765 (4%)	24 (77%)	7 (23%)	1	6
1	MG	135/765 (18%)	119 (88%)	16 (12%)	5	19
1	Mg	31/765 (4%)	26 (84%)	5 (16%)	2	12
1	NG	135/765 (18%)	124 (92%)	11 (8%)	11	31
1	OG	135/765 (18%)	116 (86%)	19 (14%)	3	15
1	PG	135/765 (18%)	114 (84%)	21 (16%)	2	13
1	VG	31/765 (4%)	28 (90%)	3 (10%)	8	25
1	WG	31/765 (4%)	25 (81%)	6 (19%)	1	8
1	XG	31/765 (4%)	25 (81%)	6 (19%)	1	8
1	YG	31/765 (4%)	25 (81%)	6 (19%)	1	8
1	ZG	31/765 (4%)	27 (87%)	4 (13%)	4	17
2	AD	121/139 (87%)	104 (86%)	17 (14%)	3	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	Ad	118/139 (85%)	103 (87%)	15 (13%)	4	17
2	BD	121/139 (87%)	112 (93%)	9 (7%)	13	33
2	Bd	118/139 (85%)	101 (86%)	17 (14%)	3	14
2	CD	121/139 (87%)	101 (84%)	20 (16%)	2	12
2	Cd	118/139 (85%)	105 (89%)	13 (11%)	6	21
2	DD	121/139 (87%)	111 (92%)	10 (8%)	10	30
2	Dd	118/139 (85%)	103 (87%)	15 (13%)	4	17
2	ED	121/139 (87%)	112 (93%)	9 (7%)	13	33
2	Ed	118/139 (85%)	102 (86%)	16 (14%)	3	15
2	FD	121/139 (87%)	106 (88%)	15 (12%)	4	18
2	Fd	118/139 (85%)	105 (89%)	13 (11%)	6	21
2	GD	121/139 (87%)	109 (90%)	12 (10%)	7	24
2	Gd	118/139 (85%)	104 (88%)	14 (12%)	5	19
2	HD	121/139 (87%)	108 (89%)	13 (11%)	6	22
2	Hd	118/139 (85%)	105 (89%)	13 (11%)	6	21
2	ID	121/139 (87%)	112 (93%)	9 (7%)	13	33
2	Id	118/139 (85%)	106 (90%)	12 (10%)	7	23
2	JD	121/139 (87%)	109 (90%)	12 (10%)	7	24
2	Jd	118/139 (85%)	108 (92%)	10 (8%)	10	29
2	KD	121/139 (87%)	110 (91%)	11 (9%)	9	28
2	Kd	118/139 (85%)	106 (90%)	12 (10%)	7	23
2	LD	121/139 (87%)	103 (85%)	18 (15%)	3	14
2	Ld	118/139 (85%)	105 (89%)	13 (11%)	6	21
2	MD	121/139 (87%)	102 (84%)	19 (16%)	2	12
2	Md	118/139 (85%)	102 (86%)	16 (14%)	3	15
3	AF	53/237 (22%)	44 (83%)	9 (17%)	2	11
3	Af	49/237 (21%)	40 (82%)	9 (18%)	1	10
3	BF	53/237 (22%)	44 (83%)	9 (17%)	2	11
3	Bf	49/237 (21%)	44 (90%)	5 (10%)	7	23
3	CF	53/237 (22%)	48 (91%)	5 (9%)	8	26
3	Cf	49/237 (21%)	41 (84%)	8 (16%)	2	12

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	DF	53/237 (22%)	44 (83%)	9 (17%)	2	11
3	Df	49/237 (21%)	42 (86%)	7 (14%)	3	14
3	EF	53/237 (22%)	45 (85%)	8 (15%)	3	13
3	Ef	49/237 (21%)	41 (84%)	8 (16%)	2	12
3	FF	53/237 (22%)	43 (81%)	10 (19%)	1	9
3	Ff	49/237 (21%)	40 (82%)	9 (18%)	1	10
3	GF	53/237 (22%)	45 (85%)	8 (15%)	3	13
3	Gf	49/237 (21%)	41 (84%)	8 (16%)	2	12
3	HF	53/237 (22%)	43 (81%)	10 (19%)	1	9
3	Hf	49/237 (21%)	45 (92%)	4 (8%)	10	31
3	IF	53/237 (22%)	44 (83%)	9 (17%)	2	11
3	If	49/237 (21%)	39 (80%)	10 (20%)	1	7
3	JF	53/237 (22%)	44 (83%)	9 (17%)	2	11
3	Jf	49/237 (21%)	43 (88%)	6 (12%)	5	18
3	KF	53/237 (22%)	45 (85%)	8 (15%)	3	13
3	Kf	49/237 (21%)	40 (82%)	9 (18%)	1	10
3	LF	53/237 (22%)	45 (85%)	8 (15%)	3	13
3	Lf	49/237 (21%)	38 (78%)	11 (22%)	1	6
3	MF	53/237 (22%)	44 (83%)	9 (17%)	2	11
3	Mf	49/237 (21%)	43 (88%)	6 (12%)	5	18
3	VF	53/237 (22%)	47 (89%)	6 (11%)	5	20
3	WF	53/237 (22%)	46 (87%)	7 (13%)	4	16
3	XF	53/237 (22%)	47 (89%)	6 (11%)	5	20
3	YF	53/237 (22%)	45 (85%)	8 (15%)	3	13
3	ZF	53/237 (22%)	47 (89%)	6 (11%)	5	20
4	AH	220/300 (73%)	191 (87%)	29 (13%)	4	16
4	BH	220/300 (73%)	201 (91%)	19 (9%)	10	29
4	CH	220/300 (73%)	194 (88%)	26 (12%)	5	19
4	DH	220/300 (73%)	189 (86%)	31 (14%)	3	15
4	EH	220/300 (73%)	185 (84%)	35 (16%)	2	12
4	FH	220/300 (73%)	196 (89%)	24 (11%)	6	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	GH	220/300 (73%)	197 (90%)	23 (10%)	6	22
4	HH	220/300 (73%)	193 (88%)	27 (12%)	4	18
4	IH	220/300 (73%)	194 (88%)	26 (12%)	5	19
4	JH	220/300 (73%)	192 (87%)	28 (13%)	4	17
4	KH	220/300 (73%)	200 (91%)	20 (9%)	9	28
4	LH	220/300 (73%)	198 (90%)	22 (10%)	7	24
4	MH	220/300 (73%)	193 (88%)	27 (12%)	4	18
4	VH	207/300 (69%)	180 (87%)	27 (13%)	4	16
4	WH	207/300 (69%)	176 (85%)	31 (15%)	3	13
4	XH	207/300 (69%)	185 (89%)	22 (11%)	6	22
4	YH	207/300 (69%)	181 (87%)	26 (13%)	4	17
4	ZH	207/300 (69%)	179 (86%)	28 (14%)	4	15
5	AK	129/163 (79%)	109 (84%)	20 (16%)	2	13
5	BK	129/163 (79%)	107 (83%)	22 (17%)	2	11
5	CK	129/163 (79%)	111 (86%)	18 (14%)	3	15
5	DK	129/163 (79%)	118 (92%)	11 (8%)	10	29
5	EK	129/163 (79%)	113 (88%)	16 (12%)	4	18
5	FK	129/163 (79%)	112 (87%)	17 (13%)	4	16
5	GK	129/163 (79%)	120 (93%)	9 (7%)	14	36
5	HK	129/163 (79%)	115 (89%)	14 (11%)	6	21
5	IK	129/163 (79%)	108 (84%)	21 (16%)	2	12
5	JK	129/163 (79%)	116 (90%)	13 (10%)	7	23
5	KK	129/163 (79%)	110 (85%)	19 (15%)	3	14
5	LK	129/163 (79%)	112 (87%)	17 (13%)	4	16
5	MK	129/163 (79%)	107 (83%)	22 (17%)	2	11
6	AL	148/203 (73%)	135 (91%)	13 (9%)	9	29
6	BL	148/203 (73%)	132 (89%)	16 (11%)	6	22
6	CL	148/203 (73%)	131 (88%)	17 (12%)	5	19
6	DL	148/203 (73%)	136 (92%)	12 (8%)	11	31
6	EL	148/203 (73%)	129 (87%)	19 (13%)	4	17
6	FL	148/203 (73%)	131 (88%)	17 (12%)	5	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	GL	148/203 (73%)	129 (87%)	19 (13%)	4	17
6	HL	148/203 (73%)	132 (89%)	16 (11%)	6	22
6	IL	148/203 (73%)	134 (90%)	14 (10%)	8	25
6	JL	148/203 (73%)	131 (88%)	17 (12%)	5	19
6	KL	148/203 (73%)	135 (91%)	13 (9%)	9	29
6	LL	148/203 (73%)	134 (90%)	14 (10%)	8	25
6	ML	148/203 (73%)	130 (88%)	18 (12%)	5	18
7	AM	175/276 (63%)	154 (88%)	21 (12%)	5	18
7	BM	175/276 (63%)	148 (85%)	27 (15%)	2	13
7	CM	175/276 (63%)	147 (84%)	28 (16%)	2	12
7	DM	175/276 (63%)	151 (86%)	24 (14%)	3	15
7	EM	175/276 (63%)	150 (86%)	25 (14%)	3	14
7	FM	175/276 (63%)	151 (86%)	24 (14%)	3	15
7	GM	175/276 (63%)	153 (87%)	22 (13%)	4	17
7	HM	175/276 (63%)	147 (84%)	28 (16%)	2	12
7	IM	175/276 (63%)	146 (83%)	29 (17%)	2	11
7	JM	175/276 (63%)	144 (82%)	31 (18%)	2	10
7	KM	175/276 (63%)	148 (85%)	27 (15%)	2	13
7	LM	175/276 (63%)	152 (87%)	23 (13%)	4	16
7	MM	175/276 (63%)	158 (90%)	17 (10%)	8	25
8	AN	66/107 (62%)	60 (91%)	6 (9%)	9	28
8	BN	66/107 (62%)	54 (82%)	12 (18%)	2	10
8	CN	66/107 (62%)	60 (91%)	6 (9%)	9	28
8	DN	66/107 (62%)	55 (83%)	11 (17%)	2	11
8	EN	66/107 (62%)	56 (85%)	10 (15%)	3	13
8	FN	66/107 (62%)	53 (80%)	13 (20%)	1	8
8	GN	66/107 (62%)	56 (85%)	10 (15%)	3	13
8	HN	66/107 (62%)	57 (86%)	9 (14%)	3	15
8	IN	66/107 (62%)	57 (86%)	9 (14%)	3	15
8	JN	66/107 (62%)	60 (91%)	6 (9%)	9	28
8	KN	66/107 (62%)	58 (88%)	8 (12%)	5	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	LN	66/107 (62%)	57 (86%)	9 (14%)	3	15
8	MN	66/107 (62%)	57 (86%)	9 (14%)	3	15
11	AC	178/257 (69%)	157 (88%)	21 (12%)	5	19
11	BC	203/257 (79%)	181 (89%)	22 (11%)	6	22
11	CC	203/257 (79%)	176 (87%)	27 (13%)	4	16
11	DC	178/257 (69%)	155 (87%)	23 (13%)	4	17
11	EC	178/257 (69%)	159 (89%)	19 (11%)	6	22
11	FC	203/257 (79%)	183 (90%)	20 (10%)	7	24
11	GC	203/257 (79%)	178 (88%)	25 (12%)	4	18
11	HC	178/257 (69%)	157 (88%)	21 (12%)	5	19
11	IC	178/257 (69%)	146 (82%)	32 (18%)	2	10
11	JC	178/257 (69%)	158 (89%)	20 (11%)	6	20
11	KC	203/257 (79%)	170 (84%)	33 (16%)	2	12
11	LC	178/257 (69%)	156 (88%)	22 (12%)	4	18
11	MC	178/257 (69%)	150 (84%)	28 (16%)	2	12
All	All	20484/55449 (37%)	17824 (87%)	2660 (13%)	6	16

All (2660) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AG	864	LYS
1	AG	869	MET
1	AG	873	LEU
1	AG	886	LEU
1	AG	898	LYS
1	AG	900	ILE
1	AG	911	LYS
1	AG	930	ILE
1	AG	933	TYR
1	AG	935	ILE
1	AG	944	LEU
1	AG	947	ARG
1	AG	956	TYR
1	AG	962	SER
1	AG	965	LEU
1	AG	972	PHE
1	AG	1010	THR

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Mol	Chain	Res	Type
1	AG	1028	THR
2	ED	41	LEU
2	ED	51	SER
2	ED	53	LEU
2	ED	85	VAL
2	ED	86	ASP
2	ED	108	VAL
2	ED	109	LEU
2	ED	115	VAL
2	ED	150	ASN
3	EF	208	ILE
3	EF	215	VAL
3	EF	223	ILE
3	EF	230	LEU
3	EF	231	THR
3	EF	238	ILE
3	EF	250	LEU
3	EF	263	LYS
1	Eg	797	ARG
1	Eg	801	MET
1	Eg	802	LEU
1	Eg	808	LEU
1	Eg	809	VAL
1	Eg	810	GLN
1	Eg	814	GLN
1	Eg	815	VAL
1	Eg	817	THR
1	Eg	819	VAL
4	EH	105	GLU
4	EH	107	ILE
4	EH	112	PHE
4	EH	135	GLU
4	EH	147	THR
4	EH	159	ASN
4	EH	160	LEU
4	EH	168	VAL
4	EH	176	VAL
4	EH	180	VAL
4	EH	184	SER
4	EH	196	LEU
4	EH	204	ILE
4	EH	207	ASP

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Mol	Chain	Res	Type
4	EH	211	ASN
4	EH	213	LEU
4	EH	226	LEU
4	EH	233	LEU
4	EH	240	THR
4	EH	242	ILE
4	EH	248	VAL
4	EH	249	ASP
4	EH	253	ASP
4	EH	256	VAL
4	EH	262	ASN
4	EH	266	MET
4	EH	270	GLU
4	EH	277	ASN
4	EH	287	VAL
4	EH	313	VAL
4	EH	320	LEU
4	EH	325	LEU
4	EH	329	THR
4	EH	344	VAL
4	EH	354	MET
5	EK	41	LEU
5	EK	70	VAL
5	EK	91	LEU
5	EK	92	ASN
5	EK	93	TRP
5	EK	106	LEU
5	EK	111	LYS
5	EK	129	GLU
5	EK	134	LEU
5	EK	144	LEU
5	EK	149	VAL
5	EK	153	ILE
5	EK	156	THR
5	EK	180	VAL
5	EK	182	ILE
5	EK	183	THR
6	EL	44	HIS
6	EL	93	LEU
6	EL	109	LEU
6	EL	113	ASP
6	EL	125	LEU

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Mol	Chain	Res	Type
6	EL	130	ASP
6	EL	133	PHE
6	EL	140	LEU
6	EL	143	ILE
6	EL	154	LEU
6	EL	155	LEU
6	EL	163	ILE
6	EL	172	VAL
6	EL	174	SER
6	EL	193	LEU
6	EL	203	LEU
6	EL	212	ASN
6	EL	216	ASP
6	EL	219	ILE
7	EM	123	VAL
7	EM	129	LEU
7	EM	131	THR
7	EM	134	LEU
7	EM	146	LEU
7	EM	149	ASN
7	EM	150	ILE
7	EM	152	LEU
7	EM	173	LEU
7	EM	176	VAL
7	EM	177	LEU
7	EM	180	ASP
7	EM	183	VAL
7	EM	184	LEU
7	EM	190	ASN
7	EM	204	LEU
7	EM	207	ILE
7	EM	210	ASP
7	EM	212	LEU
7	EM	221	LYS
7	EM	222	ILE
7	EM	263	ILE
7	EM	271	SER
7	EM	292	MET
7	EM	299	LEU
8	EN	45	MET
8	EN	69	TYR
8	EN	70	CYS

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Mol	Chain	Res	Type
8	EN	75	VAL
8	EN	81	LEU
8	EN	94	GLN
8	EN	95	LEU
8	EN	100	LEU
8	EN	101	VAL
8	EN	108	VAL
2	Ed	41	LEU
2	Ed	53	LEU
2	Ed	61	VAL
2	Ed	70	THR
2	Ed	79	LEU
2	Ed	80	GLN
2	Ed	91	ILE
2	Ed	108	VAL
2	Ed	109	LEU
2	Ed	115	VAL
2	Ed	126	GLU
2	Ed	141	LYS
2	Ed	150	ASN
2	Ed	153	VAL
2	Ed	154	VAL
2	Ed	156	LEU
3	Ef	209	ILE
3	Ef	216	ILE
3	Ef	222	LEU
3	Ef	223	ILE
3	Ef	244	VAL
3	Ef	254	ILE
3	Ef	255	LEU
3	Ef	262	ILE
2	FD	30	ILE
2	FD	41	LEU
2	FD	47	SER
2	FD	63	THR
2	FD	70	THR
2	FD	73	ILE
2	FD	80	GLN
2	FD	85	VAL
2	FD	91	ILE
2	FD	108	VAL
2	FD	118	LEU

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Mol	Chain	Res	Type
2	FD	123	THR
2	FD	126	GLU
2	FD	136	ASP
2	FD	160	LYS
3	FF	208	ILE
3	FF	215	VAL
3	FF	223	ILE
3	FF	230	LEU
3	FF	231	THR
3	FF	238	ILE
3	FF	243	MET
3	FF	245	LYS
3	FF	261	VAL
3	FF	263	LYS
1	Fg	796	GLN
1	Fg	798	THR
1	Fg	802	LEU
1	Fg	806	THR
1	Fg	808	LEU
1	Fg	809	VAL
1	Fg	815	VAL
1	Fg	819	VAL
11	CC	28	THR
11	CC	41	LYS
11	CC	42	TYR
11	CC	44	ARG
11	CC	59	LEU
11	CC	86	GLN
11	CC	100	VAL
11	CC	105	ILE
11	CC	112	GLU
11	CC	116	THR
11	CC	127	ILE
11	CC	143	THR
11	CC	148	ARG
11	CC	151	LEU
11	CC	154	ASP
11	CC	157	LYS
11	CC	165	LEU
11	CC	181	GLU
11	CC	182	ARG
11	CC	195	LEU

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Mol	Chain	Res	Type
11	CC	211	LEU
11	CC	221	VAL
11	CC	226	VAL
11	CC	233	VAL
11	CC	234	THR
11	CC	241	HIS
11	CC	243	ASP
4	FH	105	GLU
4	FH	115	MET
4	FH	130	LEU
4	FH	138	GLU
4	FH	139	TYR
4	FH	147	THR
4	FH	154	THR
4	FH	161	SER
4	FH	176	VAL
4	FH	180	VAL
4	FH	203	ASN
4	FH	238	MET
4	FH	240	THR
4	FH	242	ILE
4	FH	253	ASP
4	FH	257	GLN
4	FH	265	SER
4	FH	272	ILE
4	FH	278	ASP
4	FH	279	LEU
4	FH	296	VAL
4	FH	313	VAL
4	FH	344	VAL
4	FH	353	VAL
5	FK	41	LEU
5	FK	46	ASP
5	FK	63	LYS
5	FK	66	LYS
5	FK	67	VAL
5	FK	73	ASN
5	FK	75	LEU
5	FK	83	LEU
5	FK	92	ASN
5	FK	99	LEU
5	FK	111	LYS

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Mol	Chain	Res	Type
5	FK	126	VAL
5	FK	129	GLU
5	FK	144	LEU
5	FK	149	VAL
5	FK	156	THR
5	FK	180	VAL
6	FL	54	ARG
6	FL	91	VAL
6	FL	93	LEU
6	FL	109	LEU
6	FL	113	ASP
6	FL	121	ASP
6	FL	125	LEU
6	FL	131	LYS
6	FL	143	ILE
6	FL	155	LEU
6	FL	165	VAL
6	FL	169	THR
6	FL	172	VAL
6	FL	177	HIS
6	FL	193	LEU
6	FL	212	ASN
6	FL	225	GLN
7	FM	131	THR
7	FM	134	LEU
7	FM	143	THR
7	FM	146	LEU
7	FM	152	LEU
7	FM	155	LEU
7	FM	162	VAL
7	FM	175	ILE
7	FM	176	VAL
7	FM	177	LEU
7	FM	178	LYS
7	FM	180	ASP
7	FM	183	VAL
7	FM	189	VAL
7	FM	208	LYS
7	FM	221	LYS
7	FM	222	ILE
7	FM	229	ASN
7	FM	231	LEU

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Mol	Chain	Res	Type
7	FM	271	SER
7	FM	292	MET
7	FM	299	LEU
7	FM	314	ARG
7	FM	316	ASN
8	FN	45	MET
8	FN	48	ILE
8	FN	69	TYR
8	FN	70	CYS
8	FN	77	ASP
8	FN	78	LEU
8	FN	81	LEU
8	FN	94	GLN
8	FN	95	LEU
8	FN	101	VAL
8	FN	102	VAL
8	FN	104	ASN
8	FN	108	VAL
2	Fd	30	ILE
2	Fd	41	LEU
2	Fd	53	LEU
2	Fd	63	THR
2	Fd	85	VAL
2	Fd	92	GLU
2	Fd	93	GLU
2	Fd	98	ILE
2	Fd	108	VAL
2	Fd	115	VAL
2	Fd	132	LEU
2	Fd	142	LYS
2	Fd	150	ASN
3	Ff	208	ILE
3	Ff	215	VAL
3	Ff	216	ILE
3	Ff	222	LEU
3	Ff	232	VAL
3	Ff	238	ILE
3	Ff	244	VAL
3	Ff	250	LEU
3	Ff	255	LEU
11	BC	28	THR
11	BC	46	GLN

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Mol	Chain	Res	Type
11	BC	50	LYS
11	BC	83	LEU
11	BC	105	ILE
11	BC	116	THR
11	BC	117	LEU
11	BC	149	GLN
11	BC	151	LEU
11	BC	155	TYR
11	BC	166	LEU
11	BC	169	THR
11	BC	174	GLU
11	BC	193	THR
11	BC	195	LEU
11	BC	203	LYS
11	BC	215	LEU
11	BC	226	VAL
11	BC	229	THR
11	BC	234	THR
11	BC	244	ASP
11	BC	249	ILE
1	BG	864	LYS
1	BG	869	MET
1	BG	873	LEU
1	BG	886	LEU
1	BG	895	LYS
1	BG	911	LYS
1	BG	913	VAL
1	BG	915	THR
1	BG	916	PHE
1	BG	930	ILE
1	BG	938	ASN
1	BG	944	LEU
1	BG	949	ASN
1	BG	962	SER
1	BG	963	SER
1	BG	965	LEU
1	BG	966	GLN
1	BG	972	PHE
1	BG	1001	LEU
1	BG	1010	THR
1	BG	1024	ASN
3	AF	208	ILE

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Mol	Chain	Res	Type
3	AF	212	ILE
3	AF	215	VAL
3	AF	223	ILE
3	AF	230	LEU
3	AF	231	THR
3	AF	238	ILE
3	AF	263	LYS
3	AF	266	GLN
2	GD	30	ILE
2	GD	41	LEU
2	GD	50	ASP
2	GD	55	MET
2	GD	70	THR
2	GD	85	VAL
2	GD	109	LEU
2	GD	115	VAL
2	GD	119	ILE
2	GD	135	ILE
2	GD	155	GLU
2	GD	156	LEU
3	GF	208	ILE
3	GF	215	VAL
3	GF	223	ILE
3	GF	230	LEU
3	GF	231	THR
3	GF	238	ILE
3	GF	250	LEU
3	GF	261	VAL
1	Gg	793	GLU
1	Gg	794	ILE
1	Gg	802	LEU
1	Gg	803	THR
1	Gg	806	THR
1	Gg	811	ASP
1	Gg	815	VAL
1	Gg	819	VAL
4	GH	108	ASP
4	GH	114	ASP
4	GH	117	ARG
4	GH	122	LEU
4	GH	135	GLU
4	GH	147	THR

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Mol	Chain	Res	Type
4	GH	176	VAL
4	GH	180	VAL
4	GH	185	THR
4	GH	225	ASN
4	GH	233	LEU
4	GH	238	MET
4	GH	240	THR
4	GH	248	VAL
4	GH	264	LYS
4	GH	266	MET
4	GH	278	ASP
4	GH	284	LEU
4	GH	313	VAL
4	GH	314	ARG
4	GH	344	VAL
4	GH	353	VAL
4	GH	355	GLN
5	GK	70	VAL
5	GK	75	LEU
5	GK	86	ASP
5	GK	92	ASN
5	GK	99	LEU
5	GK	111	LYS
5	GK	126	VAL
5	GK	169	THR
5	GK	182	ILE
6	GL	93	LEU
6	GL	99	ARG
6	GL	109	LEU
6	GL	110	GLN
6	GL	121	ASP
6	GL	125	LEU
6	GL	129	THR
6	GL	130	ASP
6	GL	148	LEU
6	GL	172	VAL
6	GL	174	SER
6	GL	177	HIS
6	GL	183	GLN
6	GL	198	ILE
6	GL	212	ASN
6	GL	216	ASP

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Mol	Chain	Res	Type
6	GL	217	ASN
6	GL	234	PHE
6	GL	235	THR
7	GM	124	VAL
7	GM	128	ASN
7	GM	129	LEU
7	GM	134	LEU
7	GM	146	LEU
7	GM	152	LEU
7	GM	160	ASN
7	GM	173	LEU
7	GM	175	ILE
7	GM	176	VAL
7	GM	180	ASP
7	GM	184	LEU
7	GM	191	LEU
7	GM	194	LEU
7	GM	207	ILE
7	GM	212	LEU
7	GM	221	LYS
7	GM	229	ASN
7	GM	259	SER
7	GM	292	MET
7	GM	299	LEU
7	GM	303	GLU
8	GN	51	CYS
8	GN	69	TYR
8	GN	70	CYS
8	GN	71	THR
8	GN	81	LEU
8	GN	91	VAL
8	GN	94	GLN
8	GN	101	VAL
8	GN	111	GLU
8	GN	114	LEU
2	Gd	30	ILE
2	Gd	31	ASN
2	Gd	53	LEU
2	Gd	61	VAL
2	Gd	62	ILE
2	Gd	63	THR
2	Gd	94	LEU

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Mol	Chain	Res	Type
2	Gd	108	VAL
2	Gd	119	ILE
2	Gd	128	LEU
2	Gd	131	ILE
2	Gd	145	ILE
2	Gd	147	VAL
2	Gd	150	ASN
3	Gf	215	VAL
3	Gf	216	ILE
3	Gf	222	LEU
3	Gf	229	THR
3	Gf	244	VAL
3	Gf	250	LEU
3	Gf	255	LEU
3	Gf	263	LYS
2	HD	38	THR
2	HD	41	LEU
2	HD	50	ASP
2	HD	51	SER
2	HD	52	MET
2	HD	55	MET
2	HD	91	ILE
2	HD	108	VAL
2	HD	115	VAL
2	HD	124	LYS
2	HD	127	SER
2	HD	147	VAL
2	HD	154	VAL
11	GC	28	THR
11	GC	35	GLN
11	GC	37	MET
11	GC	41	LYS
11	GC	42	TYR
11	GC	44	ARG
11	GC	56	GLU
11	GC	60	LYS
11	GC	86	GLN
11	GC	99	LEU
11	GC	105	ILE
11	GC	110	LEU
11	GC	112	GLU
11	GC	117	LEU

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Mol	Chain	Res	Type
11	GC	143	THR
11	GC	146	THR
11	GC	151	LEU
11	GC	154	ASP
11	GC	166	LEU
11	GC	180	THR
11	GC	195	LEU
11	GC	196	GLU
11	GC	226	VAL
11	GC	229	THR
11	GC	241	HIS
3	HF	209	ILE
3	HF	215	VAL
3	HF	223	ILE
3	HF	229	THR
3	HF	230	LEU
3	HF	238	ILE
3	HF	255	LEU
3	HF	261	VAL
3	HF	263	LYS
3	HF	267	GLU
1	Hg	793	GLU
1	Hg	801	MET
1	Hg	808	LEU
1	Hg	815	VAL
1	Hg	819	VAL
4	HH	107	ILE
4	HH	116	THR
4	HH	125	GLU
4	HH	135	GLU
4	HH	136	THR
4	HH	139	TYR
4	HH	152	THR
4	HH	168	VAL
4	HH	180	VAL
4	HH	204	ILE
4	HH	212	THR
4	HH	215	ILE
4	HH	226	LEU
4	HH	233	LEU
4	HH	234	ASN
4	HH	237	VAL

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Mol	Chain	Res	Type
4	HH	238	MET
4	HH	240	THR
4	HH	248	VAL
4	HH	250	TYR
4	HH	253	ASP
4	HH	257	GLN
4	HH	278	ASP
4	HH	279	LEU
4	HH	319	ILE
4	HH	334	THR
4	HH	346	LEU
5	HK	45	VAL
5	HK	65	ILE
5	HK	70	VAL
5	HK	75	LEU
5	HK	101	GLU
5	HK	106	LEU
5	HK	111	LYS
5	HK	124	VAL
5	HK	144	LEU
5	HK	156	THR
5	HK	162	ASP
5	HK	166	THR
5	HK	180	VAL
5	HK	182	ILE
6	HL	53	ASP
6	HL	93	LEU
6	HL	100	ASP
6	HL	108	ASP
6	HL	109	LEU
6	HL	122	THR
6	HL	125	LEU
6	HL	130	ASP
6	HL	148	LEU
6	HL	160	GLN
6	HL	172	VAL
6	HL	174	SER
6	HL	181	LEU
6	HL	193	LEU
6	HL	206	GLU
6	HL	212	ASN
7	HM	129	LEU

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Mol	Chain	Res	Type
7	HM	131	THR
7	HM	134	LEU
7	HM	136	LEU
7	HM	144	THR
7	HM	146	LEU
7	HM	149	ASN
7	HM	152	LEU
7	HM	174	GLN
7	HM	176	VAL
7	HM	177	LEU
7	HM	178	LYS
7	HM	184	LEU
7	HM	191	LEU
7	HM	192	ARG
7	HM	199	LYS
7	HM	202	LEU
7	HM	207	ILE
7	HM	212	LEU
7	HM	222	ILE
7	HM	229	ASN
7	HM	242	LYS
7	HM	259	SER
7	HM	263	ILE
7	HM	271	SER
7	HM	277	SER
7	HM	292	MET
7	HM	308	ASP
8	HN	45	MET
8	HN	48	ILE
8	HN	69	TYR
8	HN	78	LEU
8	HN	95	LEU
8	HN	101	VAL
8	HN	105	ASP
8	HN	112	CYS
8	HN	114	LEU
2	Hd	41	LEU
2	Hd	51	SER
2	Hd	59	GLU
2	Hd	61	VAL
2	Hd	79	LEU
2	Hd	93	GLU

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Mol	Chain	Res	Type
2	Hd	115	VAL
2	Hd	118	LEU
2	Hd	120	SER
2	Hd	123	THR
2	Hd	142	LYS
2	Hd	147	VAL
2	Hd	150	ASN
3	Hf	211	TYR
3	Hf	216	ILE
3	Hf	219	ARG
3	Hf	244	VAL
1	CG	869	MET
1	CG	886	LEU
1	CG	889	ILE
1	CG	895	LYS
1	CG	898	LYS
1	CG	900	ILE
1	CG	911	LYS
1	CG	913	VAL
1	CG	916	PHE
1	CG	930	ILE
1	CG	939	THR
1	CG	944	LEU
1	CG	962	SER
1	CG	965	LEU
1	CG	966	GLN
1	CG	972	PHE
1	CG	1010	THR
1	CG	1017	GLN
1	CG	1044	ASP
1	Bg	795	GLN
1	Bg	808	LEU
1	Bg	809	VAL
1	Bg	815	VAL
1	Bg	819	VAL
2	ID	25	PHE
2	ID	52	MET
2	ID	73	ILE
2	ID	115	VAL
2	ID	124	LYS
2	ID	131	ILE
2	ID	137	TYR

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Mol	Chain	Res	Type
2	ID	155	GLU
2	ID	160	LYS
3	IF	207	ARG
3	IF	209	ILE
3	IF	215	VAL
3	IF	230	LEU
3	IF	231	THR
3	IF	238	ILE
3	IF	250	LEU
3	IF	255	LEU
3	IF	263	LYS
1	Ig	794	ILE
1	Ig	810	GLN
1	Ig	815	VAL
1	Ig	816	GLU
1	Ig	817	THR
4	IH	105	GLU
4	IH	108	ASP
4	IH	116	THR
4	IH	122	LEU
4	IH	134	TYR
4	IH	136	THR
4	IH	147	THR
4	IH	154	THR
4	IH	180	VAL
4	IH	183	ASP
4	IH	195	ASP
4	IH	201	SER
4	IH	207	ASP
4	IH	211	ASN
4	IH	214	MET
4	IH	228	VAL
4	IH	229	ARG
4	IH	239	LEU
4	IH	240	THR
4	IH	241	LEU
4	IH	248	VAL
4	IH	249	ASP
4	IH	253	ASP
4	IH	278	ASP
4	IH	280	LEU
4	IH	353	VAL

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Mol	Chain	Res	Type
5	IK	45	VAL
5	IK	46	ASP
5	IK	50	ASP
5	IK	57	MET
5	IK	70	VAL
5	IK	76	ILE
5	IK	83	LEU
5	IK	91	LEU
5	IK	92	ASN
5	IK	99	LEU
5	IK	111	LYS
5	IK	112	ILE
5	IK	117	THR
5	IK	125	SER
5	IK	126	VAL
5	IK	144	LEU
5	IK	156	THR
5	IK	162	ASP
5	IK	177	ASN
5	IK	180	VAL
5	IK	182	ILE
6	IL	51	GLN
6	IL	93	LEU
6	IL	109	LEU
6	IL	123	ARG
6	IL	125	LEU
6	IL	130	ASP
6	IL	155	LEU
6	IL	163	ILE
6	IL	172	VAL
6	IL	174	SER
6	IL	185	GLN
6	IL	193	LEU
6	IL	203	LEU
6	IL	212	ASN
7	IM	123	VAL
7	IM	127	ASN
7	IM	129	LEU
7	IM	134	LEU
7	IM	136	LEU
7	IM	146	LEU
7	IM	149	ASN

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Mol	Chain	Res	Type
7	IM	150	ILE
7	IM	152	LEU
7	IM	155	LEU
7	IM	170	SER
7	IM	176	VAL
7	IM	184	LEU
7	IM	192	ARG
7	IM	194	LEU
7	IM	201	THR
7	IM	207	ILE
7	IM	212	LEU
7	IM	221	LYS
7	IM	222	ILE
7	IM	232	ASP
7	IM	246	LEU
7	IM	251	SER
7	IM	255	THR
7	IM	263	ILE
7	IM	274	THR
7	IM	279	ILE
7	IM	280	TYR
7	IM	292	MET
8	IN	51	CYS
8	IN	78	LEU
8	IN	91	VAL
8	IN	95	LEU
8	IN	101	VAL
8	IN	108	VAL
8	IN	114	LEU
8	IN	115	GLN
8	IN	116	LYS
2	Id	41	LEU
2	Id	53	LEU
2	Id	61	VAL
2	Id	63	THR
2	Id	78	ASN
2	Id	91	ILE
2	Id	115	VAL
2	Id	119	ILE
2	Id	135	ILE
2	Id	145	ILE
2	Id	147	VAL

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Mol	Chain	Res	Type
2	Id	154	VAL
11	KC	28	THR
11	KC	30	SER
11	KC	31	LEU
11	KC	37	MET
11	KC	41	LYS
11	KC	42	TYR
11	KC	56	GLU
11	KC	82	GLN
11	KC	86	GLN
11	KC	99	LEU
11	KC	105	ILE
11	KC	110	LEU
11	KC	112	GLU
11	KC	117	LEU
11	KC	140	PHE
11	KC	143	THR
11	KC	149	GLN
11	KC	151	LEU
11	KC	154	ASP
11	KC	156	VAL
11	KC	170	LYS
11	KC	174	GLU
11	KC	193	THR
11	KC	195	LEU
11	KC	204	GLU
11	KC	215	LEU
11	KC	218	MET
11	KC	226	VAL
11	KC	230	ASP
11	KC	233	VAL
11	KC	234	THR
11	KC	240	ILE
11	KC	255	LEU
3	If	208	ILE
3	If	209	ILE
3	If	215	VAL
3	If	216	ILE
3	If	230	LEU
3	If	238	ILE
3	If	243	MET
3	If	244	VAL

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Mol	Chain	Res	Type
3	If	255	LEU
3	If	261	VAL
2	JD	23	MET
2	JD	35	ASP
2	JD	50	ASP
2	JD	51	SER
2	JD	55	MET
2	JD	63	THR
2	JD	71	LEU
2	JD	73	ILE
2	JD	91	ILE
2	JD	115	VAL
2	JD	127	SER
2	JD	131	ILE
3	JF	208	ILE
3	JF	215	VAL
3	JF	223	ILE
3	JF	230	LEU
3	JF	231	THR
3	JF	238	ILE
3	JF	243	MET
3	JF	246	LEU
3	JF	253	ARG
1	Jg	793	GLU
1	Jg	795	GLN
1	Jg	808	LEU
1	Jg	814	GLN
1	Jg	815	VAL
1	Jg	817	THR
1	Jg	819	VAL
4	JH	105	GLU
4	JH	108	ASP
4	JH	125	GLU
4	JH	139	TYR
4	JH	147	THR
4	JH	152	THR
4	JH	175	PHE
4	JH	176	VAL
4	JH	180	VAL
4	JH	204	ILE
4	JH	207	ASP
4	JH	220	LEU

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Mol	Chain	Res	Type
4	JH	226	LEU
4	JH	231	ARG
4	JH	233	LEU
4	JH	237	VAL
4	JH	238	MET
4	JH	241	LEU
4	JH	253	ASP
4	JH	256	VAL
4	JH	284	LEU
4	JH	313	VAL
4	JH	317	LEU
4	JH	319	ILE
4	JH	324	TRP
4	JH	339	MET
4	JH	344	VAL
4	JH	353	VAL
5	JK	41	LEU
5	JK	50	ASP
5	JK	75	LEU
5	JK	83	LEU
5	JK	98	LEU
5	JK	126	VAL
5	JK	138	ARG
5	JK	156	THR
5	JK	162	ASP
5	JK	166	THR
5	JK	170	LEU
5	JK	180	VAL
5	JK	183	THR
6	JL	93	LEU
6	JL	100	ASP
6	JL	113	ASP
6	JL	124	THR
6	JL	139	ARG
6	JL	140	LEU
6	JL	155	LEU
6	JL	163	ILE
6	JL	172	VAL
6	JL	175	ARG
6	JL	177	HIS
6	JL	181	LEU
6	JL	193	LEU

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Mol	Chain	Res	Type
6	JL	201	LYS
6	JL	203	LEU
6	JL	210	ASP
6	JL	212	ASN
7	JM	129	LEU
7	JM	130	ARG
7	JM	131	THR
7	JM	134	LEU
7	JM	144	THR
7	JM	146	LEU
7	JM	152	LEU
7	JM	154	LYS
7	JM	162	VAL
7	JM	173	LEU
7	JM	174	GLN
7	JM	175	ILE
7	JM	176	VAL
7	JM	178	LYS
7	JM	180	ASP
7	JM	184	LEU
7	JM	191	LEU
7	JM	202	LEU
7	JM	207	ILE
7	JM	208	LYS
7	JM	212	LEU
7	JM	221	LYS
7	JM	229	ASN
7	JM	275	ASP
7	JM	277	SER
7	JM	284	LEU
7	JM	292	MET
7	JM	299	LEU
7	JM	303	GLU
7	JM	313	ASP
7	JM	316	ASN
8	JN	44	LYS
8	JN	59	VAL
8	JN	78	LEU
8	JN	91	VAL
8	JN	102	VAL
8	JN	115	GLN
2	Jd	36	ASP

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Mol	Chain	Res	Type
2	Jd	61	VAL
2	Jd	63	THR
2	Jd	72	THR
2	Jd	79	LEU
2	Jd	91	ILE
2	Jd	93	GLU
2	Jd	108	VAL
2	Jd	115	VAL
2	Jd	119	ILE
3	Jf	216	ILE
3	Jf	221	TRP
3	Jf	222	LEU
3	Jf	230	LEU
3	Jf	246	LEU
3	Jf	261	VAL
1	DG	869	MET
1	DG	873	LEU
1	DG	893	LYS
1	DG	910	ASP
1	DG	913	VAL
1	DG	925	GLU
1	DG	930	ILE
1	DG	935	ILE
1	DG	944	LEU
1	DG	949	ASN
1	DG	953	LEU
1	DG	962	SER
1	DG	963	SER
1	DG	965	LEU
1	DG	972	PHE
1	DG	1010	THR
1	DG	1017	GLN
1	DG	1028	THR
4	AH	105	GLU
4	AH	115	MET
4	AH	122	LEU
4	AH	135	GLU
4	AH	147	THR
4	AH	160	LEU
4	AH	170	ARG
4	AH	177	SER
4	AH	180	VAL

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Mol	Chain	Res	Type
4	AH	202	PHE
4	AH	204	ILE
4	AH	215	ILE
4	AH	223	TYR
4	AH	239	LEU
4	AH	241	LEU
4	AH	248	VAL
4	AH	249	ASP
4	AH	254	LEU
4	AH	264	LYS
4	AH	280	LEU
4	AH	284	LEU
4	AH	285	GLU
4	AH	296	VAL
4	AH	313	VAL
4	AH	316	ASN
4	AH	317	LEU
4	AH	332	ASP
4	AH	334	THR
4	AH	361	LEU
2	KD	35	ASP
2	KD	50	ASP
2	KD	51	SER
2	KD	79	LEU
2	KD	91	ILE
2	KD	111	LYS
2	KD	132	LEU
2	KD	136	ASP
2	KD	138	GLN
2	KD	150	ASN
2	KD	154	VAL
3	KF	215	VAL
3	KF	223	ILE
3	KF	230	LEU
3	KF	231	THR
3	KF	238	ILE
3	KF	250	LEU
3	KF	253	ARG
3	KF	261	VAL
1	Kg	793	GLU
1	Kg	794	ILE
1	Kg	801	MET

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Mol	Chain	Res	Type
1	Kg	810	GLN
1	Kg	814	GLN
1	Kg	815	VAL
1	Kg	816	GLU
1	Kg	819	VAL
1	Kg	821	THR
4	KH	105	GLU
4	KH	107	ILE
4	KH	113	LYS
4	KH	139	TYR
4	KH	147	THR
4	KH	152	THR
4	KH	176	VAL
4	KH	180	VAL
4	KH	183	ASP
4	KH	218	THR
4	KH	221	TYR
4	KH	226	LEU
4	KH	238	MET
4	KH	242	ILE
4	KH	256	VAL
4	KH	257	GLN
4	KH	287	VAL
4	KH	313	VAL
4	KH	332	ASP
4	KH	334	THR
5	KK	41	LEU
5	KK	50	ASP
5	KK	63	LYS
5	KK	65	ILE
5	KK	67	VAL
5	KK	70	VAL
5	KK	76	ILE
5	KK	83	LEU
5	KK	88	SER
5	KK	91	LEU
5	KK	106	LEU
5	KK	111	LYS
5	KK	126	VAL
5	KK	144	LEU
5	KK	156	THR
5	KK	162	ASP

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Mol	Chain	Res	Type
5	KK	170	LEU
5	KK	181	GLU
5	KK	183	THR
6	KL	93	LEU
6	KL	100	ASP
6	KL	129	THR
6	KL	130	ASP
6	KL	133	PHE
6	KL	140	LEU
6	KL	165	VAL
6	KL	169	THR
6	KL	172	VAL
6	KL	175	ARG
6	KL	212	ASN
6	KL	216	ASP
6	KL	227	ARG
7	KM	123	VAL
7	KM	134	LEU
7	KM	146	LEU
7	KM	149	ASN
7	KM	152	LEU
7	KM	160	ASN
7	KM	173	LEU
7	KM	175	ILE
7	KM	176	VAL
7	KM	178	LYS
7	KM	180	ASP
7	KM	183	VAL
7	KM	184	LEU
7	KM	191	LEU
7	KM	194	LEU
7	KM	202	LEU
7	KM	205	TYR
7	KM	207	ILE
7	KM	212	LEU
7	KM	215	ARG
7	KM	221	LYS
7	KM	233	VAL
7	KM	249	GLN
7	KM	259	SER
7	KM	263	ILE
7	KM	292	MET

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Mol	Chain	Res	Type
7	KM	299	LEU
8	KN	69	TYR
8	KN	78	LEU
8	KN	81	LEU
8	KN	91	VAL
8	KN	95	LEU
8	KN	101	VAL
8	KN	108	VAL
8	KN	111	GLU
2	Kd	30	ILE
2	Kd	36	ASP
2	Kd	53	LEU
2	Kd	59	GLU
2	Kd	61	VAL
2	Kd	63	THR
2	Kd	73	ILE
2	Kd	78	ASN
2	Kd	93	GLU
2	Kd	118	LEU
2	Kd	128	LEU
2	Kd	145	ILE
3	Kf	209	ILE
3	Kf	212	ILE
3	Kf	215	VAL
3	Kf	216	ILE
3	Kf	232	VAL
3	Kf	245	LYS
3	Kf	247	ILE
3	Kf	260	GLN
3	Kf	261	VAL
2	LD	32	ASN
2	LD	35	ASP
2	LD	47	SER
2	LD	51	SER
2	LD	52	MET
2	LD	55	MET
2	LD	70	THR
2	LD	71	LEU
2	LD	85	VAL
2	LD	91	ILE
2	LD	115	VAL
2	LD	119	ILE

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Mol	Chain	Res	Type
2	LD	123	THR
2	LD	124	LYS
2	LD	126	GLU
2	LD	141	LYS
2	LD	147	VAL
2	LD	156	LEU
3	LF	208	ILE
3	LF	215	VAL
3	LF	223	ILE
3	LF	230	LEU
3	LF	231	THR
3	LF	238	ILE
3	LF	256	THR
3	LF	263	LYS
1	Lg	798	THR
1	Lg	806	THR
1	Lg	808	LEU
1	Lg	809	VAL
1	Lg	814	GLN
1	Lg	815	VAL
1	Lg	821	THR
4	LH	122	LEU
4	LH	138	GLU
4	LH	141	LYS
4	LH	147	THR
4	LH	160	LEU
4	LH	179	LEU
4	LH	180	VAL
4	LH	182	LEU
4	LH	215	ILE
4	LH	225	ASN
4	LH	228	VAL
4	LH	233	LEU
4	LH	248	VAL
4	LH	253	ASP
4	LH	256	VAL
4	LH	278	ASP
4	LH	279	LEU
4	LH	284	LEU
4	LH	301	ASP
4	LH	313	VAL
4	LH	332	ASP

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Mol	Chain	Res	Type
4	LH	353	VAL
5	LK	38	VAL
5	LK	50	ASP
5	LK	66	LYS
5	LK	70	VAL
5	LK	73	ASN
5	LK	76	ILE
5	LK	91	LEU
5	LK	92	ASN
5	LK	126	VAL
5	LK	129	GLU
5	LK	144	LEU
5	LK	156	THR
5	LK	159	LEU
5	LK	166	THR
5	LK	180	VAL
5	LK	182	ILE
5	LK	183	THR
6	LL	93	LEU
6	LL	104	LYS
6	LL	109	LEU
6	LL	112	GLN
6	LL	121	ASP
6	LL	125	LEU
6	LL	130	ASP
6	LL	143	ILE
6	LL	155	LEU
6	LL	172	VAL
6	LL	177	HIS
6	LL	190	MET
6	LL	193	LEU
6	LL	212	ASN
7	LM	129	LEU
7	LM	136	LEU
7	LM	146	LEU
7	LM	149	ASN
7	LM	152	LEU
7	LM	162	VAL
7	LM	176	VAL
7	LM	178	LYS
7	LM	182	LYS
7	LM	188	PHE

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Mol	Chain	Res	Type
7	LM	191	LEU
7	LM	192	ARG
7	LM	202	LEU
7	LM	203	SER
7	LM	207	ILE
7	LM	210	ASP
7	LM	212	LEU
7	LM	221	LYS
7	LM	259	SER
7	LM	275	ASP
7	LM	284	LEU
7	LM	298	VAL
7	LM	316	ASN
8	LN	39	ASP
8	LN	48	ILE
8	LN	51	CYS
8	LN	78	LEU
8	LN	81	LEU
8	LN	101	VAL
8	LN	102	VAL
8	LN	108	VAL
8	LN	114	LEU
2	Ld	27	LYS
2	Ld	30	ILE
2	Ld	41	LEU
2	Ld	53	LEU
2	Ld	61	VAL
2	Ld	63	THR
2	Ld	68	ASP
2	Ld	78	ASN
2	Ld	93	GLU
2	Ld	115	VAL
2	Ld	145	ILE
2	Ld	147	VAL
2	Ld	150	ASN
3	Lf	212	ILE
3	Lf	215	VAL
3	Lf	216	ILE
3	Lf	222	LEU
3	Lf	223	ILE
3	Lf	238	ILE
3	Lf	244	VAL

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Mol	Chain	Res	Type
3	Lf	250	LEU
3	Lf	260	GLN
3	Lf	261	VAL
3	Lf	262	ILE
5	AK	40	LYS
5	AK	41	LEU
5	AK	50	ASP
5	AK	70	VAL
5	AK	76	ILE
5	AK	92	ASN
5	AK	99	LEU
5	AK	109	PHE
5	AK	111	LYS
5	AK	112	ILE
5	AK	116	VAL
5	AK	125	SER
5	AK	126	VAL
5	AK	129	GLU
5	AK	132	LEU
5	AK	144	LEU
5	AK	156	THR
5	AK	163	LYS
5	AK	169	THR
5	AK	180	VAL
1	EG	865	THR
1	EG	869	MET
1	EG	874	ASP
1	EG	885	ILE
1	EG	890	VAL
1	EG	895	LYS
1	EG	898	LYS
1	EG	910	ASP
1	EG	911	LYS
1	EG	916	PHE
1	EG	919	MET
1	EG	930	ILE
1	EG	944	LEU
1	EG	953	LEU
1	EG	962	SER
1	EG	963	SER
1	EG	965	LEU
1	EG	972	PHE

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Mol	Chain	Res	Type
1	EG	1010	THR
1	EG	1017	GLN
1	EG	1028	THR
2	MD	30	ILE
2	MD	32	ASN
2	MD	38	THR
2	MD	41	LEU
2	MD	50	ASP
2	MD	61	VAL
2	MD	73	ILE
2	MD	86	ASP
2	MD	91	ILE
2	MD	92	GLU
2	MD	108	VAL
2	MD	109	LEU
2	MD	115	VAL
2	MD	118	LEU
2	MD	128	LEU
2	MD	131	ILE
2	MD	132	LEU
2	MD	138	GLN
2	MD	154	VAL
3	MF	209	ILE
3	MF	211	TYR
3	MF	215	VAL
3	MF	223	ILE
3	MF	231	THR
3	MF	233	ARG
3	MF	238	ILE
3	MF	250	LEU
3	MF	256	THR
1	Mg	795	GLN
1	Mg	809	VAL
1	Mg	810	GLN
1	Mg	811	ASP
1	Mg	815	VAL
4	MH	107	ILE
4	MH	108	ASP
4	MH	130	LEU
4	MH	147	THR
4	MH	175	PHE
4	MH	180	VAL

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Mol	Chain	Res	Type
4	MH	182	LEU
4	MH	203	ASN
4	MH	207	ASP
4	MH	214	MET
4	MH	218	THR
4	MH	226	LEU
4	MH	238	MET
4	MH	242	ILE
4	MH	250	TYR
4	MH	252	VAL
4	MH	268	THR
4	MH	280	LEU
4	MH	287	VAL
4	MH	296	VAL
4	MH	301	ASP
4	MH	313	VAL
4	MH	316	ASN
4	MH	317	LEU
4	MH	319	ILE
4	MH	329	THR
4	MH	353	VAL
5	MK	45	VAL
5	MK	46	ASP
5	MK	50	ASP
5	MK	58	THR
5	MK	62	LYS
5	MK	67	VAL
5	MK	70	VAL
5	MK	72	GLN
5	MK	76	ILE
5	MK	91	LEU
5	MK	92	ASN
5	MK	98	LEU
5	MK	99	LEU
5	MK	106	LEU
5	MK	112	ILE
5	MK	125	SER
5	MK	129	GLU
5	MK	144	LEU
5	MK	156	THR
5	MK	163	LYS
5	MK	180	VAL

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Mol	Chain	Res	Type
5	MK	182	ILE
6	ML	57	VAL
6	ML	93	LEU
6	ML	109	LEU
6	ML	113	ASP
6	ML	125	LEU
6	ML	130	ASP
6	ML	140	LEU
6	ML	143	ILE
6	ML	165	VAL
6	ML	172	VAL
6	ML	177	HIS
6	ML	185	GLN
6	ML	193	LEU
6	ML	210	ASP
6	ML	212	ASN
6	ML	216	ASP
6	ML	225	GLN
6	ML	230	GLU
7	MM	134	LEU
7	MM	146	LEU
7	MM	149	ASN
7	MM	152	LEU
7	MM	162	VAL
7	MM	173	LEU
7	MM	175	ILE
7	MM	180	ASP
7	MM	184	LEU
7	MM	203	SER
7	MM	208	LYS
7	MM	212	LEU
7	MM	222	ILE
7	MM	232	ASP
7	MM	242	LYS
7	MM	263	ILE
7	MM	308	ASP
8	MN	58	LEU
8	MN	65	TYR
8	MN	84	CYS
8	MN	92	TYR
8	MN	94	GLN
8	MN	100	LEU

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Mol	Chain	Res	Type
8	MN	108	VAL
8	MN	110	GLU
8	MN	115	GLN
2	Md	25	PHE
2	Md	41	LEU
2	Md	51	SER
2	Md	61	VAL
2	Md	63	THR
2	Md	73	ILE
2	Md	91	ILE
2	Md	92	GLU
2	Md	97	ARG
2	Md	108	VAL
2	Md	115	VAL
2	Md	126	GLU
2	Md	147	VAL
2	Md	150	ASN
2	Md	153	VAL
2	Md	155	GLU
3	Mf	212	ILE
3	Mf	216	ILE
3	Mf	238	ILE
3	Mf	255	LEU
3	Mf	260	GLN
3	Mf	261	VAL
3	VF	208	ILE
3	VF	215	VAL
3	VF	230	LEU
3	VF	231	THR
3	VF	238	ILE
3	VF	256	THR
1	VG	793	GLU
1	VG	800	ASP
1	VG	815	VAL
4	VH	105	GLU
4	VH	115	MET
4	VH	122	LEU
4	VH	138	GLU
4	VH	147	THR
4	VH	152	THR
4	VH	158	VAL
4	VH	160	LEU

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Mol	Chain	Res	Type
4	VH	180	VAL
4	VH	203	ASN
4	VH	204	ILE
4	VH	205	GLN
4	VH	218	THR
4	VH	225	ASN
4	VH	226	LEU
4	VH	231	ARG
4	VH	233	LEU
4	VH	234	ASN
4	VH	242	ILE
4	VH	249	ASP
4	VH	253	ASP
4	VH	281	LEU
4	VH	287	VAL
4	VH	296	VAL
4	VH	297	VAL
4	VH	313	VAL
4	VH	358	VAL
3	WF	208	ILE
3	WF	215	VAL
3	WF	223	ILE
3	WF	230	LEU
3	WF	232	VAL
3	WF	238	ILE
3	WF	261	VAL
1	WG	795	GLN
1	WG	800	ASP
1	WG	815	VAL
1	WG	816	GLU
1	WG	817	THR
1	WG	821	THR
4	WH	107	ILE
4	WH	134	TYR
4	WH	147	THR
4	WH	171	LEU
4	WH	180	VAL
4	WH	203	ASN
4	WH	218	THR
4	WH	220	LEU
4	WH	237	VAL
4	WH	239	LEU

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Mol	Chain	Res	Type
4	WH	240	THR
4	WH	241	LEU
4	WH	248	VAL
4	WH	249	ASP
4	WH	250	TYR
4	WH	253	ASP
4	WH	278	ASP
4	WH	297	VAL
4	WH	306	LEU
4	WH	311	MET
4	WH	312	TYR
4	WH	313	VAL
4	WH	315	THR
4	WH	317	LEU
4	WH	318	THR
4	WH	321	SER
4	WH	324	TRP
4	WH	329	THR
4	WH	340	GLN
4	WH	345	LEU
4	WH	358	VAL
3	XF	209	ILE
3	XF	215	VAL
3	XF	223	ILE
3	XF	230	LEU
3	XF	232	VAL
3	XF	238	ILE
1	XG	794	ILE
1	XG	796	GLN
1	XG	808	LEU
1	XG	815	VAL
1	XG	816	GLU
1	XG	819	VAL
4	XH	134	TYR
4	XH	147	THR
4	XH	168	VAL
4	XH	171	LEU
4	XH	175	PHE
4	XH	180	VAL
4	XH	195	ASP
4	XH	201	SER
4	XH	226	LEU

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Mol	Chain	Res	Type
4	XH	233	LEU
4	XH	237	VAL
4	XH	238	MET
4	XH	240	THR
4	XH	241	LEU
4	XH	242	ILE
4	XH	253	ASP
4	XH	256	VAL
4	XH	313	VAL
4	XH	319	ILE
4	XH	325	LEU
4	XH	354	MET
4	XH	357	LYS
3	YF	215	VAL
3	YF	223	ILE
3	YF	230	LEU
3	YF	231	THR
3	YF	238	ILE
3	YF	243	MET
3	YF	264	PHE
3	YF	267	GLU
6	AL	93	LEU
6	AL	100	ASP
6	AL	113	ASP
6	AL	129	THR
6	AL	130	ASP
6	AL	141	ASN
6	AL	148	LEU
6	AL	155	LEU
6	AL	172	VAL
6	AL	193	LEU
6	AL	203	LEU
6	AL	204	LYS
6	AL	217	ASN
1	FG	867	ASP
1	FG	873	LEU
1	FG	885	ILE
1	FG	900	ILE
1	FG	913	VAL
1	FG	930	ILE
1	FG	944	LEU
1	FG	946	SER

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Mol	Chain	Res	Type
1	FG	949	ASN
1	FG	953	LEU
1	FG	962	SER
1	FG	965	LEU
1	FG	972	PHE
1	FG	1010	THR
1	YG	795	GLN
1	YG	802	LEU
1	YG	808	LEU
1	YG	814	GLN
1	YG	817	THR
1	YG	819	VAL
4	YH	108	ASP
4	YH	116	THR
4	YH	117	ARG
4	YH	120	TYR
4	YH	122	LEU
4	YH	130	LEU
4	YH	147	THR
4	YH	152	THR
4	YH	154	THR
4	YH	176	VAL
4	YH	180	VAL
4	YH	195	ASP
4	YH	211	ASN
4	YH	225	ASN
4	YH	237	VAL
4	YH	241	LEU
4	YH	248	VAL
4	YH	249	ASP
4	YH	253	ASP
4	YH	256	VAL
4	YH	281	LEU
4	YH	283	VAL
4	YH	295	LEU
4	YH	318	THR
4	YH	321	SER
4	YH	358	VAL
11	DC	84	ASN
11	DC	97	ASN
11	DC	105	ILE
11	DC	112	GLU

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Mol	Chain	Res	Type
11	DC	116	THR
11	DC	119	LEU
11	DC	127	ILE
11	DC	146	THR
11	DC	148	ARG
11	DC	151	LEU
11	DC	153	MET
11	DC	157	LYS
11	DC	166	LEU
11	DC	184	TRP
11	DC	193	THR
11	DC	203	LYS
11	DC	204	GLU
11	DC	211	LEU
11	DC	228	HIS
11	DC	231	LEU
11	DC	233	VAL
11	DC	249	ILE
11	DC	266	VAL
3	ZF	208	ILE
3	ZF	211	TYR
3	ZF	230	LEU
3	ZF	231	THR
3	ZF	238	ILE
3	ZF	264	PHE
1	ZG	792	GLN
1	ZG	815	VAL
1	ZG	819	VAL
1	ZG	821	THR
4	ZH	105	GLU
4	ZH	107	ILE
4	ZH	108	ASP
4	ZH	130	LEU
4	ZH	147	THR
4	ZH	158	VAL
4	ZH	161	SER
4	ZH	168	VAL
4	ZH	179	LEU
4	ZH	180	VAL
4	ZH	196	LEU
4	ZH	203	ASN
4	ZH	221	TYR

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Mol	Chain	Res	Type
4	ZH	226	LEU
4	ZH	233	LEU
4	ZH	238	MET
4	ZH	240	THR
4	ZH	242	ILE
4	ZH	248	VAL
4	ZH	253	ASP
4	ZH	256	VAL
4	ZH	279	LEU
4	ZH	280	LEU
4	ZH	297	VAL
4	ZH	315	THR
4	ZH	328	MET
4	ZH	329	THR
4	ZH	358	VAL
7	AM	129	LEU
7	AM	134	LEU
7	AM	149	ASN
7	AM	150	ILE
7	AM	152	LEU
7	AM	171	ARG
7	AM	176	VAL
7	AM	177	LEU
7	AM	180	ASP
7	AM	191	LEU
7	AM	204	LEU
7	AM	205	TYR
7	AM	207	ILE
7	AM	212	LEU
7	AM	222	ILE
7	AM	234	GLU
7	AM	259	SER
7	AM	263	ILE
7	AM	269	GLN
7	AM	292	MET
7	AM	308	ASP
8	AN	51	CYS
8	AN	62	ASN
8	AN	69	TYR
8	AN	81	LEU
8	AN	84	CYS
8	AN	97	SER

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Mol	Chain	Res	Type
2	Ad	30	ILE
2	Ad	41	LEU
2	Ad	53	LEU
2	Ad	61	VAL
2	Ad	63	THR
2	Ad	68	ASP
2	Ad	73	ILE
2	Ad	85	VAL
2	Ad	94	LEU
2	Ad	115	VAL
2	Ad	118	LEU
2	Ad	123	THR
2	Ad	128	LEU
2	Ad	150	ASN
2	Ad	153	VAL
3	Af	216	ILE
3	Af	238	ILE
3	Af	247	ILE
3	Af	253	ARG
3	Af	255	LEU
3	Af	261	VAL
3	Af	263	LYS
3	Af	264	PHE
3	Af	266	GLN
2	BD	30	ILE
2	BD	35	ASP
2	BD	51	SER
2	BD	63	THR
2	BD	71	LEU
2	BD	85	VAL
2	BD	115	VAL
2	BD	153	VAL
2	BD	161	ILE
3	BF	207	ARG
3	BF	208	ILE
3	BF	215	VAL
3	BF	223	ILE
3	BF	230	LEU
3	BF	231	THR
3	BF	238	ILE
3	BF	250	LEU
3	BF	264	PHE

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Mol	Chain	Res	Type
4	BH	135	GLU
4	BH	147	THR
4	BH	160	LEU
4	BH	180	VAL
4	BH	185	THR
4	BH	204	ILE
4	BH	207	ASP
4	BH	240	THR
4	BH	248	VAL
4	BH	250	TYR
4	BH	257	GLN
4	BH	262	ASN
4	BH	269	GLU
4	BH	278	ASP
4	BH	287	VAL
4	BH	292	SER
4	BH	313	VAL
4	BH	317	LEU
4	BH	353	VAL
5	BK	45	VAL
5	BK	50	ASP
5	BK	62	LYS
5	BK	67	VAL
5	BK	70	VAL
5	BK	72	GLN
5	BK	73	ASN
5	BK	77	SER
5	BK	83	LEU
5	BK	98	LEU
5	BK	100	ASN
5	BK	111	LYS
5	BK	114	ILE
5	BK	126	VAL
5	BK	144	LEU
5	BK	149	VAL
5	BK	156	THR
5	BK	159	LEU
5	BK	162	ASP
5	BK	169	THR
5	BK	170	LEU
5	BK	180	VAL
6	BL	53	ASP

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Mol	Chain	Res	Type
6	BL	93	LEU
6	BL	109	LEU
6	BL	113	ASP
6	BL	123	ARG
6	BL	129	THR
6	BL	130	ASP
6	BL	148	LEU
6	BL	165	VAL
6	BL	172	VAL
6	BL	177	HIS
6	BL	183	GLN
6	BL	193	LEU
6	BL	210	ASP
6	BL	212	ASN
6	BL	216	ASP
7	BM	115	ARG
7	BM	127	ASN
7	BM	129	LEU
7	BM	134	LEU
7	BM	136	LEU
7	BM	146	LEU
7	BM	149	ASN
7	BM	150	ILE
7	BM	154	LYS
7	BM	155	LEU
7	BM	171	ARG
7	BM	175	ILE
7	BM	177	LEU
7	BM	180	ASP
7	BM	184	LEU
7	BM	199	LYS
7	BM	207	ILE
7	BM	212	LEU
7	BM	215	ARG
7	BM	222	ILE
7	BM	231	LEU
7	BM	242	LYS
7	BM	269	GLN
7	BM	271	SER
7	BM	290	ASP
7	BM	292	MET
7	BM	308	ASP

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Mol	Chain	Res	Type
8	BN	54	SER
8	BN	59	VAL
8	BN	70	CYS
8	BN	71	THR
8	BN	76	MET
8	BN	81	LEU
8	BN	86	LEU
8	BN	91	VAL
8	BN	94	GLN
8	BN	98	SER
8	BN	101	VAL
8	BN	102	VAL
2	Bd	26	LYS
2	Bd	41	LEU
2	Bd	51	SER
2	Bd	52	MET
2	Bd	61	VAL
2	Bd	63	THR
2	Bd	78	ASN
2	Bd	79	LEU
2	Bd	91	ILE
2	Bd	93	GLU
2	Bd	115	VAL
2	Bd	118	LEU
2	Bd	126	GLU
2	Bd	142	LYS
2	Bd	145	ILE
2	Bd	146	HIS
2	Bd	150	ASN
3	Bf	216	ILE
3	Bf	232	VAL
3	Bf	238	ILE
3	Bf	247	ILE
3	Bf	250	LEU
11	EC	80	ILE
11	EC	92	ASP
11	EC	100	LEU
11	EC	106	ILE
11	EC	117	THR
11	EC	118	LEU
11	EC	128	ILE
11	EC	147	THR

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Mol	Chain	Res	Type
11	EC	149	ARG
11	EC	152	LEU
11	EC	164	VAL
11	EC	167	LEU
11	EC	190	ASP
11	EC	205	GLU
11	EC	222	VAL
11	EC	227	VAL
11	EC	231	ASP
11	EC	259	ASN
11	EC	267	VAL
1	GG	865	THR
1	GG	869	MET
1	GG	885	ILE
1	GG	886	LEU
1	GG	895	LYS
1	GG	898	LYS
1	GG	900	ILE
1	GG	910	ASP
1	GG	913	VAL
1	GG	918	THR
1	GG	930	ILE
1	GG	944	LEU
1	GG	956	TYR
1	GG	962	SER
1	GG	963	SER
1	GG	965	LEU
1	GG	966	GLN
1	GG	972	PHE
1	GG	1010	THR
1	GG	1017	GLN
1	GG	1028	THR
1	GG	1037	LEU
11	FC	28	THR
11	FC	31	LEU
11	FC	35	GLN
11	FC	56	GLU
11	FC	105	ILE
11	FC	111	LEU
11	FC	116	THR
11	FC	119	LEU
11	FC	125	ILE

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Mol	Chain	Res	Type
11	FC	146	THR
11	FC	163	VAL
11	FC	169	THR
11	FC	174	GLU
11	FC	195	LEU
11	FC	221	VAL
11	FC	225	TYR
11	FC	226	VAL
11	FC	230	ASP
11	FC	234	THR
11	FC	255	LEU
11	HC	64	LEU
11	HC	97	ASN
11	HC	99	LEU
11	HC	105	ILE
11	HC	111	LEU
11	HC	118	ASN
11	HC	119	LEU
11	HC	127	ILE
11	HC	133	LYS
11	HC	143	THR
11	HC	151	LEU
11	HC	157	LYS
11	HC	169	THR
11	HC	195	LEU
11	HC	196	GLU
11	HC	226	VAL
11	HC	233	VAL
11	HC	241	HIS
11	HC	256	ASN
11	HC	263	ARG
11	HC	266	VAL
11	IC	65	SER
11	IC	81	GLU
11	IC	89	ASN
11	IC	91	ASP
11	IC	97	ASN
11	IC	105	ILE
11	IC	111	LEU
11	IC	112	GLU
11	IC	116	THR
11	IC	123	GLN

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Mol	Chain	Res	Type
11	IC	125	ILE
11	IC	127	ILE
11	IC	143	THR
11	IC	146	THR
11	IC	151	LEU
11	IC	157	LYS
11	IC	163	VAL
11	IC	165	LEU
11	IC	166	LEU
11	IC	174	GLU
11	IC	176	TRP
11	IC	180	THR
11	IC	184	TRP
11	IC	195	LEU
11	IC	204	GLU
11	IC	211	LEU
11	IC	221	VAL
11	IC	226	VAL
11	IC	249	ILE
11	IC	256	ASN
11	IC	258	ASN
11	IC	266	VAL
11	JC	65	LEU
11	JC	84	LEU
11	JC	91	LEU
11	JC	101	VAL
11	JC	106	ILE
11	JC	113	GLU
11	JC	120	LEU
11	JC	143	THR
11	JC	152	LEU
11	JC	163	ASN
11	JC	166	LEU
11	JC	167	LEU
11	JC	170	THR
11	JC	196	LEU
11	JC	205	GLU
11	JC	207	PHE
11	JC	227	VAL
11	JC	234	VAL
11	JC	235	THR
11	JC	259	ASN

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Mol	Chain	Res	Type
11	LC	64	LEU
11	LC	95	ASP
11	LC	97	ASN
11	LC	102	GLU
11	LC	105	ILE
11	LC	109	VAL
11	LC	119	LEU
11	LC	127	ILE
11	LC	140	PHE
11	LC	143	THR
11	LC	146	THR
11	LC	149	GLN
11	LC	153	MET
11	LC	162	ASN
11	LC	163	VAL
11	LC	195	LEU
11	LC	215	LEU
11	LC	226	VAL
11	LC	228	HIS
11	LC	234	THR
11	LC	243	ASP
11	LC	245	ARG
11	MC	83	LEU
11	MC	91	ASP
11	MC	97	ASN
11	MC	99	LEU
11	MC	100	VAL
11	MC	105	ILE
11	MC	109	VAL
11	MC	111	LEU
11	MC	116	THR
11	MC	119	LEU
11	MC	127	ILE
11	MC	133	LYS
11	MC	143	THR
11	MC	148	ARG
11	MC	151	LEU
11	MC	156	VAL
11	MC	159	GLU
11	MC	169	THR
11	MC	170	LYS
11	MC	181	GLU

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Mol	Chain	Res	Type
11	MC	211	LEU
11	MC	215	LEU
11	MC	226	VAL
11	MC	234	THR
11	MC	241	HIS
11	MC	256	ASN
11	MC	258	ASN
11	MC	266	VAL
2	CD	26	LYS
2	CD	30	ILE
2	CD	31	ASN
2	CD	35	ASP
2	CD	41	LEU
2	CD	50	ASP
2	CD	55	MET
2	CD	78	ASN
2	CD	84	SER
2	CD	85	VAL
2	CD	92	GLU
2	CD	105	ARG
2	CD	108	VAL
2	CD	111	LYS
2	CD	115	VAL
2	CD	123	THR
2	CD	131	ILE
2	CD	154	VAL
2	CD	156	LEU
2	CD	161	ILE
3	CF	208	ILE
3	CF	215	VAL
3	CF	230	LEU
3	CF	231	THR
3	CF	238	ILE
1	Cg	802	LEU
1	Cg	808	LEU
1	Cg	809	VAL
1	Cg	811	ASP
1	Cg	812	TRP
1	Cg	815	VAL
4	CH	105	GLU
4	CH	107	ILE
4	CH	109	LYS

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Mol	Chain	Res	Type
4	CH	115	MET
4	CH	130	LEU
4	CH	147	THR
4	CH	156	GLN
4	CH	179	LEU
4	CH	204	ILE
4	CH	221	TYR
4	CH	229	ARG
4	CH	235	THR
4	CH	238	MET
4	CH	241	LEU
4	CH	245	GLN
4	CH	248	VAL
4	CH	252	VAL
4	CH	256	VAL
4	CH	257	GLN
4	CH	269	GLU
4	CH	278	ASP
4	CH	306	LEU
4	CH	313	VAL
4	CH	314	ARG
4	CH	353	VAL
4	CH	361	LEU
5	CK	38	VAL
5	CK	50	ASP
5	CK	62	LYS
5	CK	65	ILE
5	CK	70	VAL
5	CK	76	ILE
5	CK	83	LEU
5	CK	92	ASN
5	CK	99	LEU
5	CK	126	VAL
5	CK	134	LEU
5	CK	144	LEU
5	CK	149	VAL
5	CK	156	THR
5	CK	162	ASP
5	CK	165	ILE
5	CK	180	VAL
5	CK	183	THR
6	CL	51	GLN

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Mol	Chain	Res	Type
6	CL	57	VAL
6	CL	93	LEU
6	CL	109	LEU
6	CL	121	ASP
6	CL	125	LEU
6	CL	129	THR
6	CL	143	ILE
6	CL	163	ILE
6	CL	172	VAL
6	CL	174	SER
6	CL	177	HIS
6	CL	182	SER
6	CL	203	LEU
6	CL	212	ASN
6	CL	216	ASP
6	CL	225	GLN
7	CM	124	VAL
7	CM	129	LEU
7	CM	134	LEU
7	CM	141	GLU
7	CM	149	ASN
7	CM	152	LEU
7	CM	155	LEU
7	CM	173	LEU
7	CM	174	GLN
7	CM	175	ILE
7	CM	176	VAL
7	CM	180	ASP
7	CM	184	LEU
7	CM	191	LEU
7	CM	192	ARG
7	CM	212	LEU
7	CM	222	ILE
7	CM	233	VAL
7	CM	245	TYR
7	CM	257	ASP
7	CM	263	ILE
7	CM	271	SER
7	CM	275	ASP
7	CM	290	ASP
7	CM	292	MET
7	CM	299	LEU

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Mol	Chain	Res	Type
7	CM	308	ASP
7	CM	316	ASN
8	CN	82	MET
8	CN	86	LEU
8	CN	95	LEU
8	CN	100	LEU
8	CN	101	VAL
8	CN	114	LEU
2	Cd	30	ILE
2	Cd	41	LEU
2	Cd	51	SER
2	Cd	59	GLU
2	Cd	61	VAL
2	Cd	62	ILE
2	Cd	91	ILE
2	Cd	108	VAL
2	Cd	115	VAL
2	Cd	126	GLU
2	Cd	131	ILE
2	Cd	147	VAL
2	Cd	150	ASN
3	Cf	209	ILE
3	Cf	212	ILE
3	Cf	216	ILE
3	Cf	230	LEU
3	Cf	233	ARG
3	Cf	236	SER
3	Cf	250	LEU
3	Cf	254	ILE
2	DD	30	ILE
2	DD	41	LEU
2	DD	51	SER
2	DD	63	THR
2	DD	73	ILE
2	DD	108	VAL
2	DD	115	VAL
2	DD	118	LEU
2	DD	154	VAL
2	DD	161	ILE
3	DF	208	ILE
3	DF	209	ILE
3	DF	215	VAL

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Mol	Chain	Res	Type
3	DF	223	ILE
3	DF	230	LEU
3	DF	238	ILE
3	DF	250	LEU
3	DF	256	THR
3	DF	263	LYS
1	Dg	793	GLU
1	Dg	808	LEU
1	Dg	809	VAL
1	Dg	814	GLN
1	Dg	815	VAL
1	Dg	816	GLU
1	Dg	819	VAL
4	DH	107	ILE
4	DH	108	ASP
4	DH	115	MET
4	DH	120	TYR
4	DH	130	LEU
4	DH	138	GLU
4	DH	147	THR
4	DH	168	VAL
4	DH	180	VAL
4	DH	196	LEU
4	DH	203	ASN
4	DH	207	ASP
4	DH	225	ASN
4	DH	226	LEU
4	DH	231	ARG
4	DH	240	THR
4	DH	241	LEU
4	DH	242	ILE
4	DH	248	VAL
4	DH	254	LEU
4	DH	256	VAL
4	DH	262	ASN
4	DH	278	ASP
4	DH	285	GLU
4	DH	314	ARG
4	DH	325	LEU
4	DH	332	ASP
4	DH	344	VAL
4	DH	345	LEU

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Mol	Chain	Res	Type
4	DH	356	LEU
4	DH	361	LEU
5	DK	45	VAL
5	DK	83	LEU
5	DK	107	LYS
5	DK	111	LYS
5	DK	116	VAL
5	DK	144	LEU
5	DK	149	VAL
5	DK	156	THR
5	DK	159	LEU
5	DK	166	THR
5	DK	180	VAL
1	HG	865	THR
1	HG	898	LYS
1	HG	910	ASP
1	HG	913	VAL
1	HG	916	PHE
1	HG	919	MET
1	HG	930	ILE
1	HG	939	THR
1	HG	944	LEU
1	HG	947	ARG
1	HG	953	LEU
1	HG	962	SER
1	HG	963	SER
1	HG	965	LEU
1	HG	972	PHE
1	HG	1010	THR
1	HG	1017	GLN
1	IG	865	THR
1	IG	869	MET
1	IG	886	LEU
1	IG	893	LYS
1	IG	895	LYS
1	IG	898	LYS
1	IG	913	VAL
1	IG	916	PHE
1	IG	930	ILE
1	IG	933	TYR
1	IG	939	THR
1	IG	944	LEU

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Mol	Chain	Res	Type
1	IG	947	ARG
1	IG	953	LEU
1	IG	962	SER
1	IG	963	SER
1	IG	965	LEU
1	IG	966	GLN
1	IG	972	PHE
1	IG	1010	THR
1	JG	865	THR
1	JG	867	ASP
1	JG	880	ASP
1	JG	885	ILE
1	JG	895	LYS
1	JG	898	LYS
1	JG	900	ILE
1	JG	913	VAL
1	JG	916	PHE
1	JG	917	ASN
1	JG	930	ILE
1	JG	944	LEU
1	JG	953	LEU
1	JG	962	SER
1	JG	965	LEU
1	JG	972	PHE
1	JG	1010	THR
1	JG	1028	THR
1	KG	864	LYS
1	KG	868	ILE
1	KG	873	LEU
1	KG	874	ASP
1	KG	885	ILE
1	KG	886	LEU
1	KG	889	ILE
1	KG	900	ILE
1	KG	913	VAL
1	KG	925	GLU
1	KG	930	ILE
1	KG	944	LEU
1	KG	953	LEU
1	KG	956	TYR
1	KG	962	SER
1	KG	963	SER

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Mol	Chain	Res	Type
1	KG	965	LEU
1	KG	966	GLN
1	KG	972	PHE
1	KG	1010	THR
1	KG	1045	VAL
1	LG	864	LYS
1	LG	869	MET
1	LG	881	GLU
1	LG	886	LEU
1	LG	898	LYS
1	LG	911	LYS
1	LG	913	VAL
1	LG	930	ILE
1	LG	944	LEU
1	LG	953	LEU
1	LG	956	TYR
1	LG	962	SER
1	LG	963	SER
1	LG	965	LEU
1	LG	972	PHE
1	LG	1010	THR
1	LG	1017	GLN
1	LG	1027	THR
1	LG	1037	LEU
1	LG	1044	ASP
1	MG	864	LYS
1	MG	869	MET
1	MG	886	LEU
1	MG	898	LYS
1	MG	911	LYS
1	MG	913	VAL
1	MG	916	PHE
1	MG	930	ILE
1	MG	944	LEU
1	MG	953	LEU
1	MG	956	TYR
1	MG	962	SER
1	MG	963	SER
1	MG	965	LEU
1	MG	1010	THR
1	MG	1017	GLN
1	NG	869	MET

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Mol	Chain	Res	Type
1	NG	895	LYS
1	NG	911	LYS
1	NG	916	PHE
1	NG	930	ILE
1	NG	944	LEU
1	NG	962	SER
1	NG	965	LEU
1	NG	972	PHE
1	NG	1010	THR
1	NG	1017	GLN
1	OG	867	ASP
1	OG	869	MET
1	OG	873	LEU
1	OG	886	LEU
1	OG	904	ASN
1	OG	913	VAL
1	OG	916	PHE
1	OG	930	ILE
1	OG	933	TYR
1	OG	944	LEU
1	OG	947	ARG
1	OG	956	TYR
1	OG	962	SER
1	OG	963	SER
1	OG	965	LEU
1	OG	966	GLN
1	OG	1010	THR
1	OG	1017	GLN
1	OG	1045	VAL
1	PG	867	ASP
1	PG	869	MET
1	PG	886	LEU
1	PG	898	LYS
1	PG	899	LEU
1	PG	900	ILE
1	PG	910	ASP
1	PG	911	LYS
1	PG	913	VAL
1	PG	916	PHE
1	PG	919	MET
1	PG	930	ILE
1	PG	944	LEU

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Mol	Chain	Res	Type
1	PG	947	ARG
1	PG	956	TYR
1	PG	962	SER
1	PG	965	LEU
1	PG	972	PHE
1	PG	1010	THR
1	PG	1017	GLN
1	PG	1044	ASP
11	AC	87	GLN
11	AC	90	ASN
11	AC	91	LEU
11	AC	100	LEU
11	AC	106	ILE
11	AC	111	LEU
11	AC	118	LEU
11	AC	124	GLN
11	AC	144	THR
11	AC	152	LEU
11	AC	155	ASP
11	AC	164	VAL
11	AC	167	LEU
11	AC	170	THR
11	AC	171	LYS
11	AC	196	LEU
11	AC	219	MET
11	AC	222	VAL
11	AC	227	VAL
11	AC	234	VAL
11	AC	235	THR
6	DL	57	VAL
6	DL	93	LEU
6	DL	109	LEU
6	DL	113	ASP
6	DL	130	ASP
6	DL	133	PHE
6	DL	143	ILE
6	DL	154	LEU
6	DL	172	VAL
6	DL	193	LEU
6	DL	212	ASN
6	DL	217	ASN
7	DM	124	VAL

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Mol	Chain	Res	Type
7	DM	134	LEU
7	DM	146	LEU
7	DM	149	ASN
7	DM	152	LEU
7	DM	175	ILE
7	DM	176	VAL
7	DM	178	LYS
7	DM	180	ASP
7	DM	183	VAL
7	DM	184	LEU
7	DM	194	LEU
7	DM	201	THR
7	DM	205	TYR
7	DM	207	ILE
7	DM	212	LEU
7	DM	246	LEU
7	DM	255	THR
7	DM	259	SER
7	DM	263	ILE
7	DM	274	THR
7	DM	292	MET
7	DM	299	LEU
7	DM	317	LYS
8	DN	57	ARG
8	DN	62	ASN
8	DN	76	MET
8	DN	78	LEU
8	DN	82	MET
8	DN	84	CYS
8	DN	86	LEU
8	DN	101	VAL
8	DN	102	VAL
8	DN	108	VAL
8	DN	115	GLN
2	Dd	30	ILE
2	Dd	41	LEU
2	Dd	52	MET
2	Dd	54	GLU
2	Dd	61	VAL
2	Dd	78	ASN
2	Dd	108	VAL
2	Dd	115	VAL

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Mol	Chain	Res	Type
2	Dd	118	LEU
2	Dd	126	GLU
2	Dd	142	LYS
2	Dd	145	ILE
2	Dd	147	VAL
2	Dd	153	VAL
2	Dd	154	VAL
1	Ag	793	GLU
1	Ag	794	ILE
1	Ag	801	MET
1	Ag	808	LEU
1	Ag	811	ASP
1	Ag	814	GLN
1	Ag	815	VAL
1	Ag	819	VAL
3	Df	216	ILE
3	Df	230	LEU
3	Df	232	VAL
3	Df	238	ILE
3	Df	246	LEU
3	Df	250	LEU
3	Df	262	ILE
2	AD	24	LYS
2	AD	32	ASN
2	AD	51	SER
2	AD	54	GLU
2	AD	70	THR
2	AD	71	LEU
2	AD	85	VAL
2	AD	115	VAL
2	AD	117	VAL
2	AD	118	LEU
2	AD	124	LYS
2	AD	132	LEU
2	AD	138	GLN
2	AD	147	VAL
2	AD	154	VAL
2	AD	155	GLU
2	AD	156	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (259) such sidechains are listed below:

Mol	Chain	Res	Type
1	AG	951	HIS
1	AG	1020	GLN
2	ED	80	GLN
1	Eg	810	GLN
4	EH	132	GLN
4	EH	156	GLN
5	EK	108	GLN
6	EL	112	GLN
6	EL	141	ASN
6	EL	196	ASN
2	Ed	152	GLN
3	FF	213	GLN
3	FF	260	GLN
1	Fg	791	GLN
1	Fg	796	GLN
11	CC	118	ASN
11	CC	190	GLN
11	CC	192	ASN
4	FH	126	GLN
4	FH	173	GLN
4	FH	245	GLN
8	FN	79	GLN
8	FN	104	ASN
3	Ff	266	GLN
11	BC	49	GLN
11	BC	69	GLN
11	BC	162	ASN
11	BC	198	ASN
1	BG	878	ASN
1	BG	908	ASN
1	BG	951	HIS
1	BG	1017	GLN
2	GD	75	ASN
2	GD	80	GLN
4	GH	118	ASN
4	GH	308	ASN
4	GH	340	GLN
6	GL	112	GLN
6	GL	115	GLN
6	GL	149	ASN
7	GM	153	GLN
8	GN	61	ASN
8	GN	79	GLN

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Mol	Chain	Res	Type
2	Gd	75	ASN
2	HD	31	ASN
2	HD	80	GLN
2	HD	152	GLN
11	GC	84	ASN
11	GC	149	GLN
11	GC	162	ASN
3	HF	266	GLN
4	HH	118	ASN
5	HK	100	ASN
5	HK	147	GLN
6	HL	49	ASN
6	HL	112	GLN
6	HL	177	HIS
6	HL	196	ASN
7	HM	164	GLN
7	HM	174	GLN
7	HM	267	ASN
7	HM	306	GLN
8	HN	61	ASN
2	Hd	75	ASN
1	Bg	810	GLN
3	IF	260	GLN
3	IF	266	GLN
1	Ig	810	GLN
4	IH	132	GLN
4	IH	156	GLN
6	IL	112	GLN
6	IL	217	ASN
6	IL	226	ASN
7	IM	269	GLN
7	IM	295	ASN
8	IN	61	ASN
8	IN	79	GLN
8	IN	94	GLN
8	IN	104	ASN
2	Id	69	ASN
11	KC	35	GLN
11	KC	69	GLN
11	KC	97	ASN
11	KC	123	GLN
11	KC	162	ASN

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Mol	Chain	Res	Type
11	KC	198	ASN
2	JD	78	ASN
4	JH	173	GLN
5	JK	87	GLN
6	JL	44	HIS
6	JL	49	ASN
6	JL	112	GLN
7	JM	249	GLN
7	JM	267	ASN
8	JN	61	ASN
3	Jf	266	GLN
1	DG	1017	GLN
1	DG	1020	GLN
2	KD	152	GLN
3	KF	266	GLN
1	Kg	818	GLN
4	KH	118	ASN
4	KH	132	GLN
4	KH	222	ASN
4	KH	262	ASN
6	KL	44	HIS
6	KL	49	ASN
6	KL	51	GLN
7	KM	114	ASN
7	KM	269	GLN
7	KM	295	ASN
8	KN	96	ASN
8	KN	104	ASN
2	Kd	32	ASN
2	Kd	75	ASN
2	LD	152	GLN
1	Lg	818	GLN
4	LH	203	ASN
4	LH	222	ASN
4	LH	234	ASN
6	LL	225	GLN
8	LN	61	ASN
2	Ld	69	ASN
2	Ld	75	ASN
2	Ld	146	HIS
3	Lf	260	GLN
3	Lf	266	GLN

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Mol	Chain	Res	Type
1	EG	878	ASN
1	EG	1020	GLN
2	MD	78	ASN
1	Mg	795	GLN
4	MH	211	ASN
4	MH	245	GLN
4	MH	308	ASN
7	MM	174	GLN
7	MM	190	ASN
7	MM	229	ASN
7	MM	249	GLN
7	MM	267	ASN
7	MM	295	ASN
2	Md	31	ASN
2	Md	78	ASN
1	VG	791	GLN
1	VG	818	GLN
4	VH	222	ASN
4	WH	118	ASN
4	WH	123	ASN
4	WH	132	GLN
4	WH	205	GLN
4	WH	211	ASN
4	WH	222	ASN
4	WH	245	GLN
4	WH	340	GLN
4	WH	355	GLN
3	XF	260	GLN
4	XH	173	GLN
4	XH	245	GLN
3	YF	260	GLN
6	AL	156	ASN
6	AL	196	ASN
1	YG	818	GLN
4	YH	118	ASN
4	YH	203	ASN
4	YH	205	GLN
4	YH	262	ASN
11	DC	104	ASN
11	DC	115	ASN
11	DC	118	ASN
1	ZG	791	GLN

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Mol	Chain	Res	Type
1	ZG	818	GLN
4	ZH	118	ASN
4	ZH	203	ASN
4	ZH	225	ASN
7	AM	160	ASN
7	AM	269	GLN
7	AM	295	ASN
2	Ad	32	ASN
2	BD	32	ASN
2	BD	78	ASN
3	BF	260	GLN
4	BH	132	GLN
4	BH	222	ASN
6	BL	141	ASN
6	BL	226	ASN
6	BL	232	GLN
7	BM	153	GLN
7	BM	267	ASN
11	EC	83	GLN
11	EC	85	ASN
11	EC	119	ASN
11	EC	163	ASN
1	GG	878	ASN
11	FC	69	GLN
11	FC	104	ASN
11	FC	123	GLN
11	FC	192	ASN
11	HC	123	GLN
11	IC	84	ASN
11	LC	118	ASN
11	MC	89	ASN
11	MC	219	ASN
4	CH	225	ASN
4	CH	234	ASN
4	CH	262	ASN
5	CK	61	ASN
5	CK	72	GLN
5	CK	108	GLN
6	CL	115	GLN
6	CL	141	ASN
6	CL	217	ASN
6	CL	225	GLN

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Mol	Chain	Res	Type
7	CM	267	ASN
7	CM	295	ASN
7	CM	306	GLN
8	CN	79	GLN
2	Cd	31	ASN
2	Cd	69	ASN
2	Cd	152	GLN
3	Cf	251	GLN
3	Cf	266	GLN
2	DD	31	ASN
2	DD	80	GLN
4	DH	118	ASN
4	DH	222	ASN
4	DH	245	GLN
5	DK	100	ASN
5	DK	147	GLN
1	HG	878	ASN
1	HG	973	GLN
1	IG	1017	GLN
1	IG	1020	GLN
1	IG	1043	GLN
1	LG	1020	GLN
1	MG	878	ASN
1	MG	938	ASN
1	MG	1017	GLN
1	MG	1020	GLN
1	OG	970	ASN
1	OG	976	ASN
1	OG	1017	GLN
1	PG	976	ASN
1	PG	1020	GLN
1	PG	1043	GLN
11	AC	85	ASN
11	AC	87	GLN
11	AC	193	ASN
6	DL	112	GLN
6	DL	141	ASN
6	DL	183	GLN
6	DL	217	ASN
6	DL	226	ASN
7	DM	160	ASN
7	DM	249	GLN

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Mol	Chain	Res	Type
8	DN	79	GLN
2	Dd	80	GLN
1	Ag	818	GLN
3	Df	266	GLN
2	AD	31	ASN
2	AD	152	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 [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
10	JX	1
10	WX	1
10	YX	1
10	XX	1
10	GX	1
10	CX	1

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Mol	Chain	Number of breaks
10	MX	1
10	ZX	1
10	KX	1
10	HX	1
10	FX	1
10	EX	1
10	IX	1
10	DX	1
10	BX	1
10	AX	1
10	VX	1
10	LX	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	JX	38:UNK	C	70:UNK	N	25.78
1	WX	38:UNK	C	70:UNK	N	25.34
1	YX	38:UNK	C	70:UNK	N	25.23
1	XX	38:UNK	C	70:UNK	N	25.08
1	GX	38:UNK	C	70:UNK	N	24.81
1	CX	38:UNK	C	70:UNK	N	24.61
1	MX	38:UNK	C	70:UNK	N	24.45
1	ZX	38:UNK	C	70:UNK	N	24.28
1	KX	38:UNK	C	70:UNK	N	23.87
1	HX	38:UNK	C	70:UNK	N	23.68
1	FX	38:UNK	C	70:UNK	N	23.65
1	EX	38:UNK	C	70:UNK	N	23.35
1	IX	38:UNK	C	70:UNK	N	23.30
1	DX	38:UNK	C	70:UNK	N	23.06
1	BX	38:UNK	C	70:UNK	N	22.80
1	AX	38:UNK	C	70:UNK	N	22.26
1	VX	38:UNK	C	70:UNK	N	22.09
1	LX	38:UNK	C	70:UNK	N	21.21

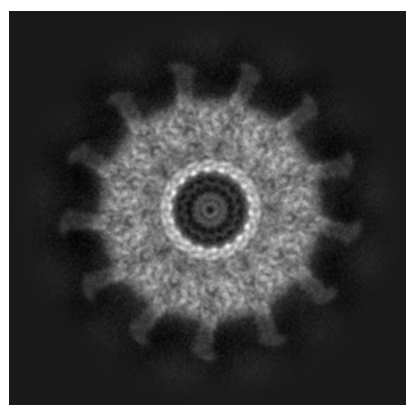
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24026. These allow visual inspection of the internal detail of the map and identification of artifacts.

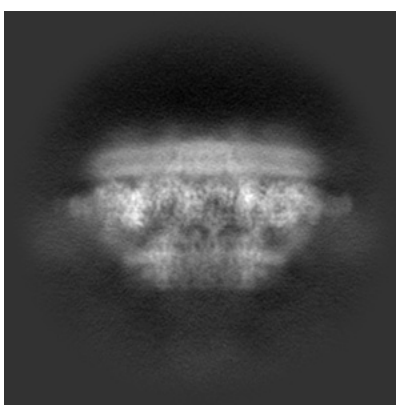
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

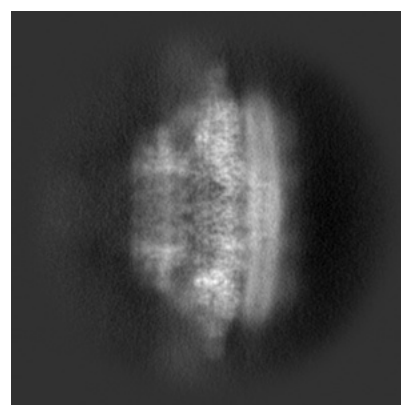
6.1.1 Primary map



X



Y

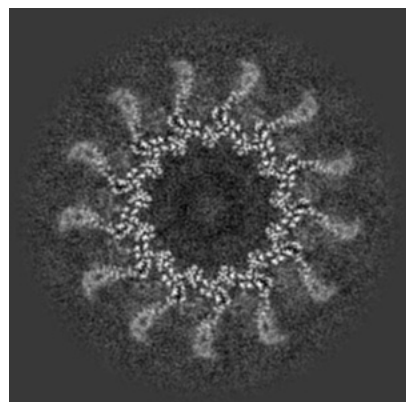


Z

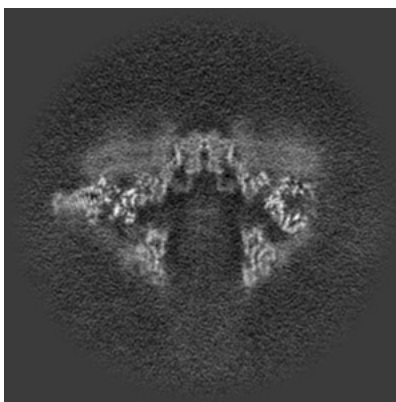
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

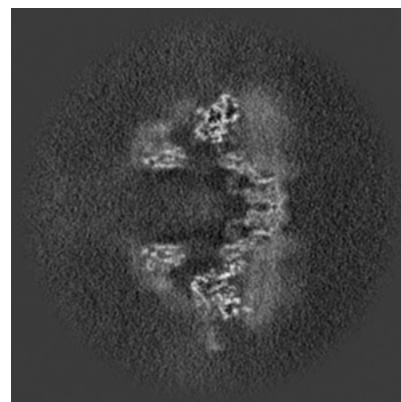
6.2.1 Primary map



X Index: 125



Y Index: 125

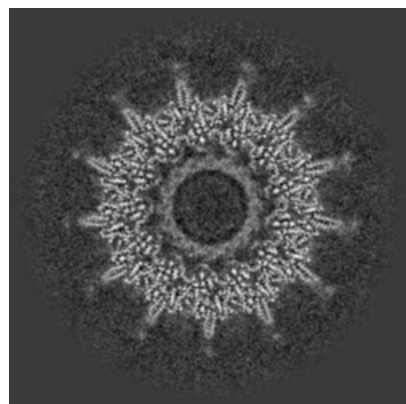


Z Index: 125

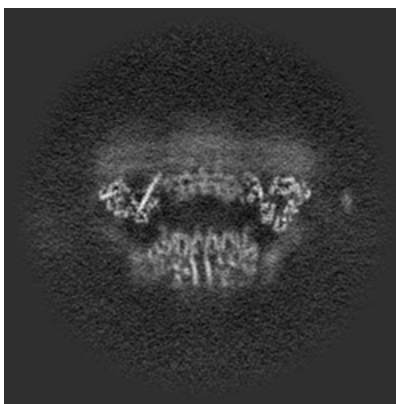
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

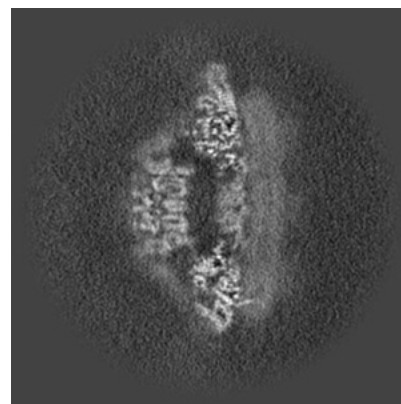
6.3.1 Primary map



X Index: 134



Y Index: 101

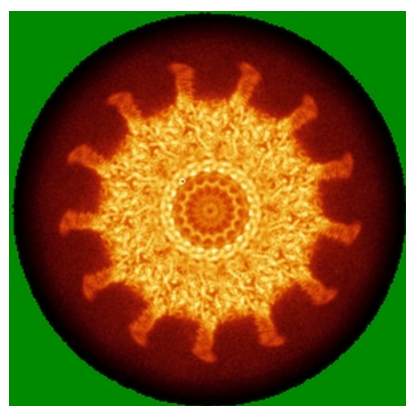


Z Index: 152

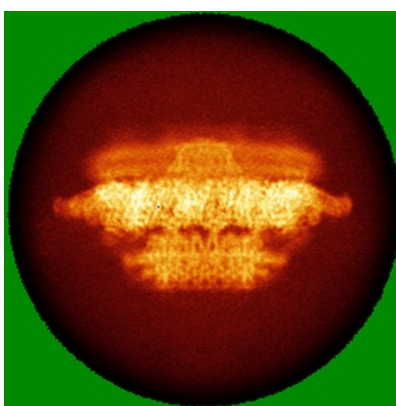
The images above show the largest variance slices of the map in three orthogonal directions.

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

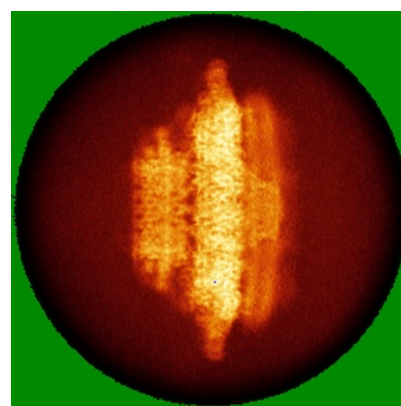
6.4.1 Primary map



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

This section was not generated.

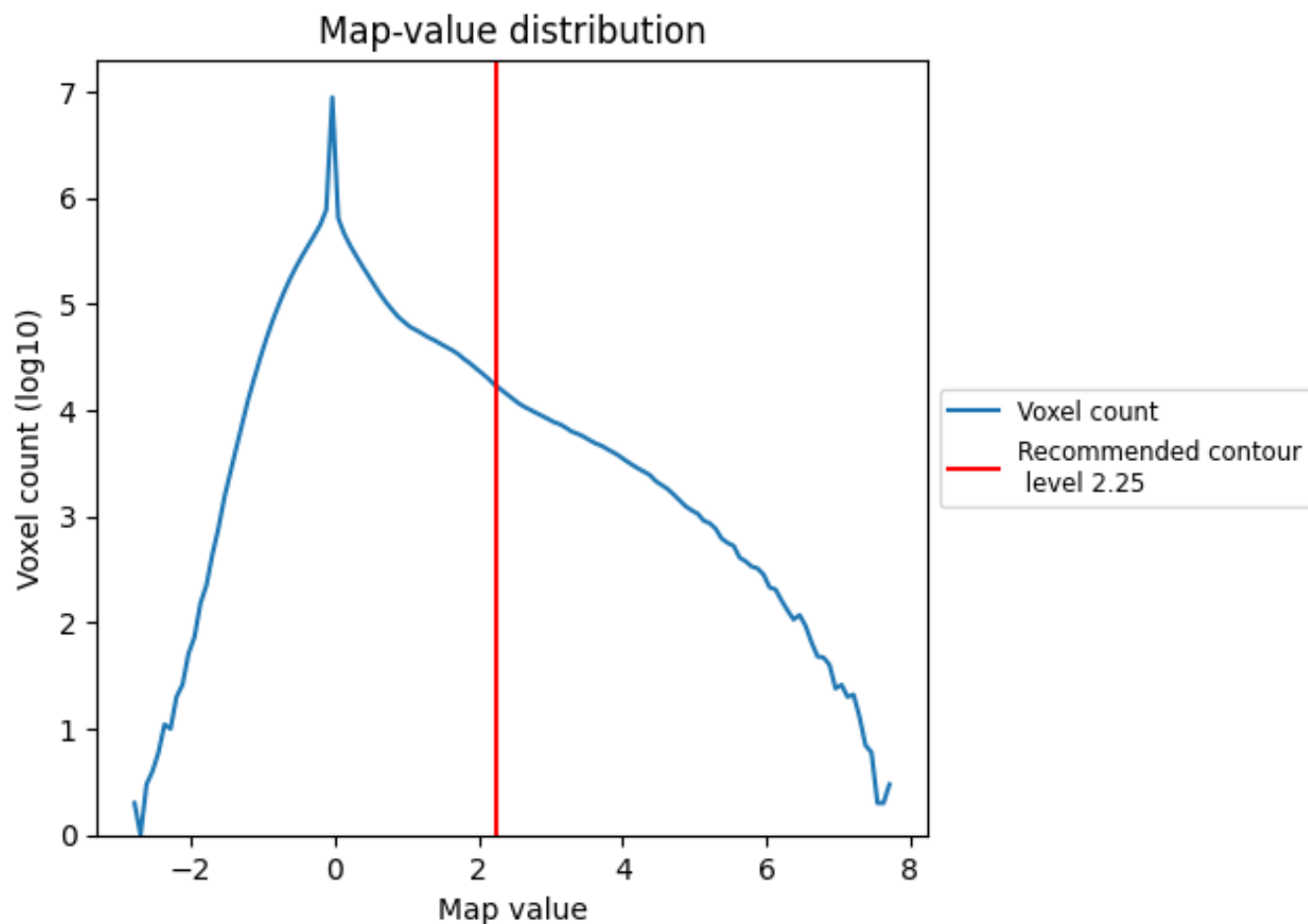
6.6 Mask visualisation

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

7 Map analysis [i](#)

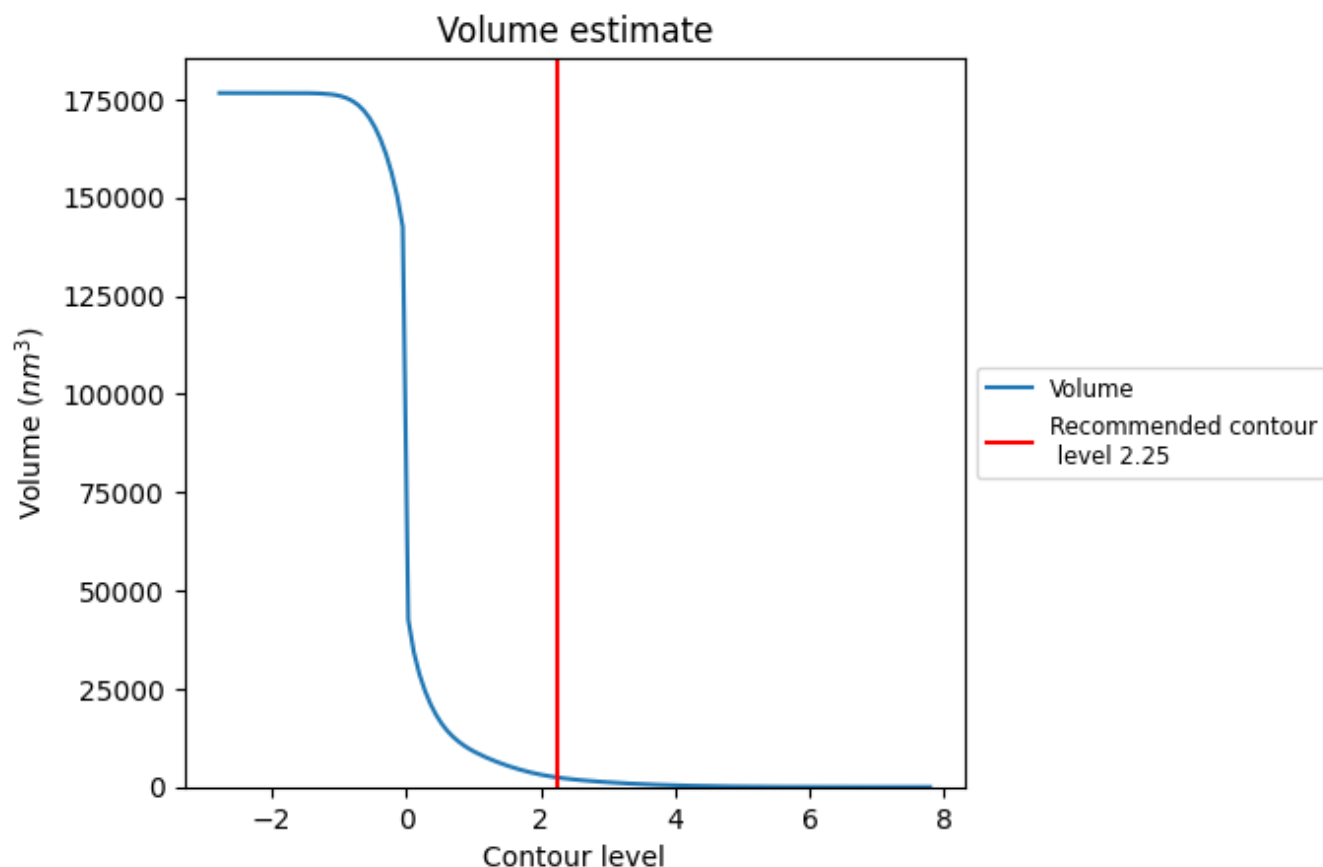
This section contains the results of statistical analysis of the map.

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.

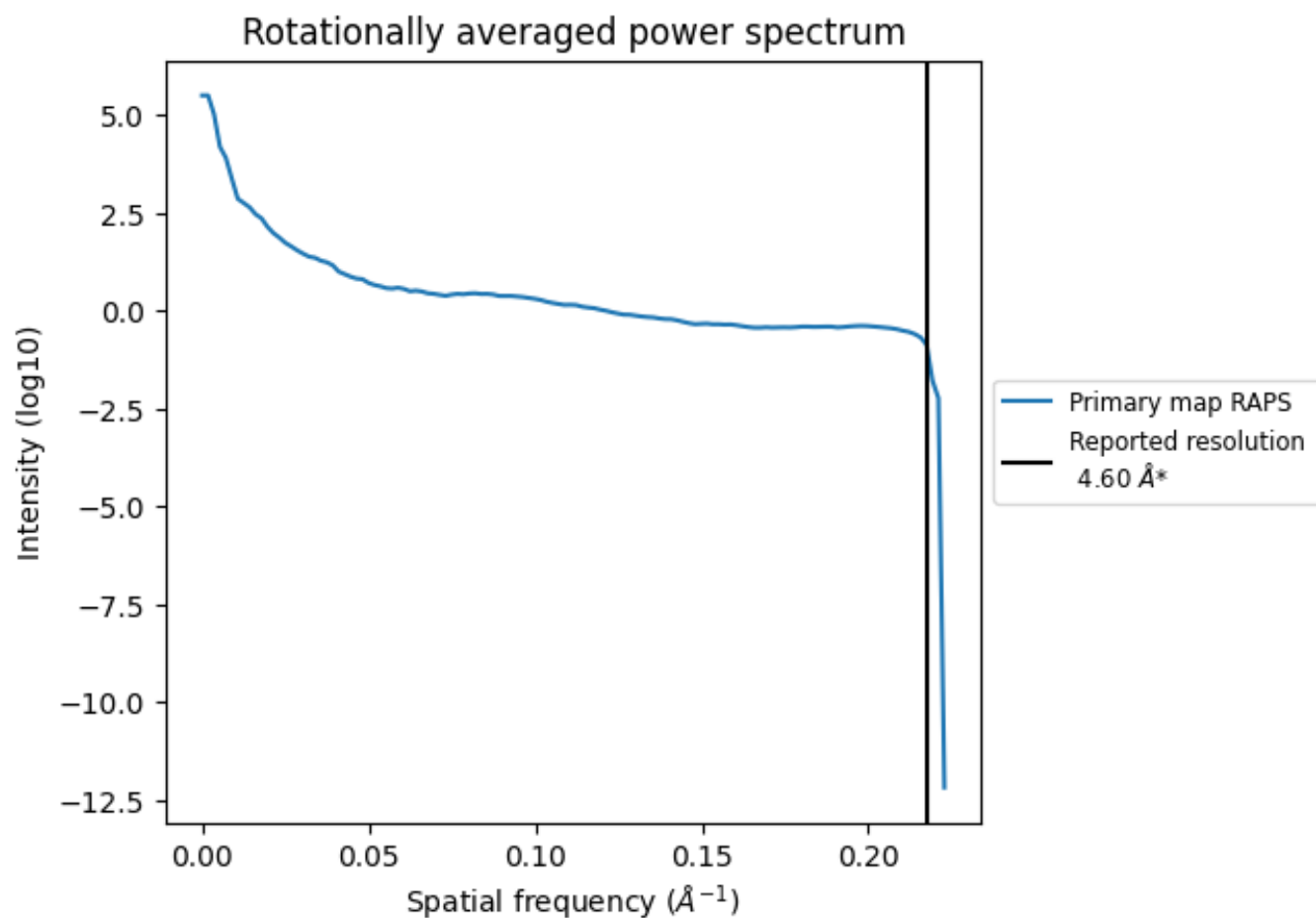
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2412 nm^3 ; this corresponds to an approximate mass of 2179 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 Å⁻¹

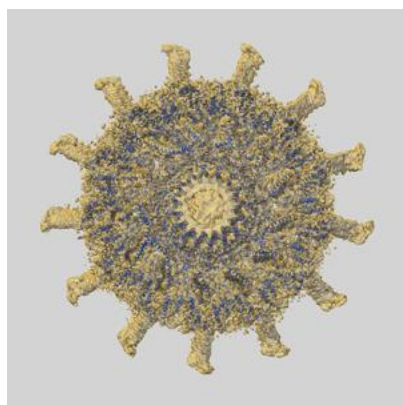
8 Fourier-Shell correlation

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

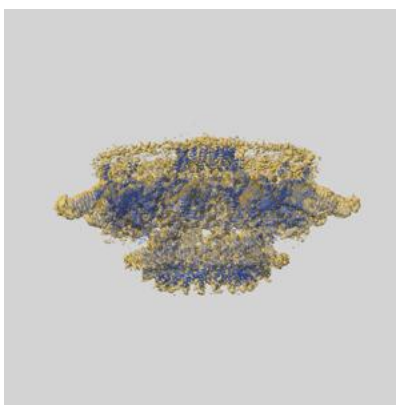
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24026 and PDB model 7MUY. Per-residue inclusion information can be found in section [3](#) on page [23](#).

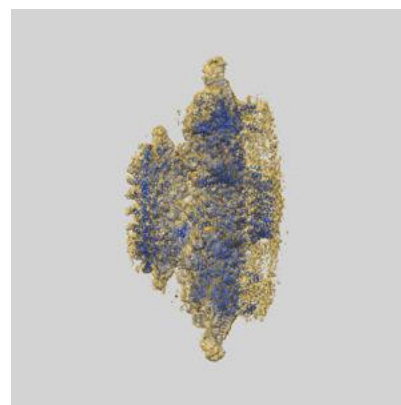
9.1 Map-model overlay [i](#)



X



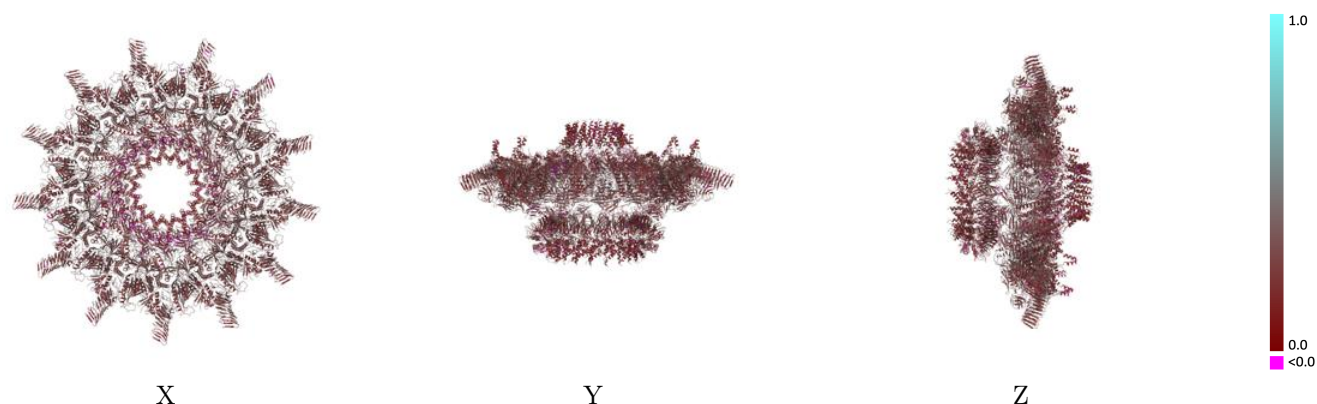
Y



Z

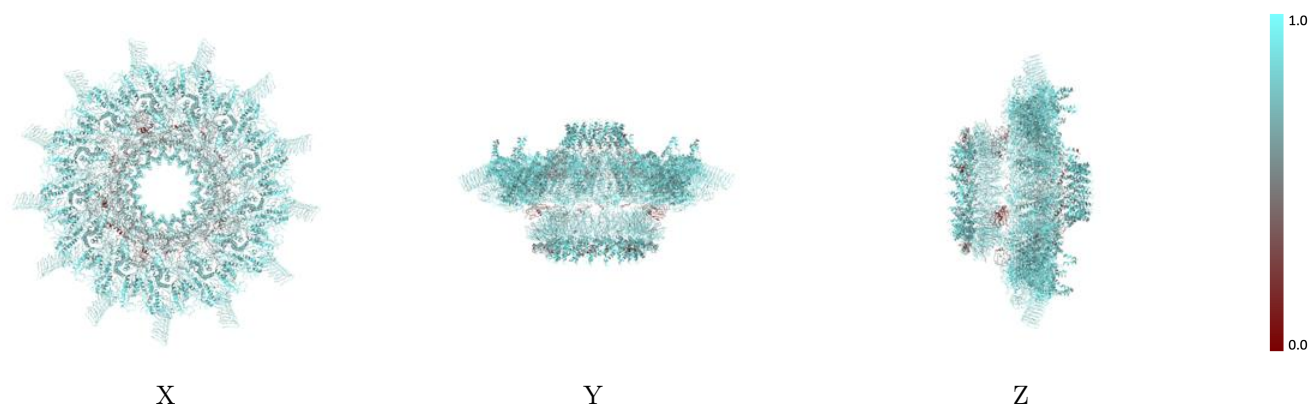
The images above show the 3D surface view of the map at the recommended contour level 2.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



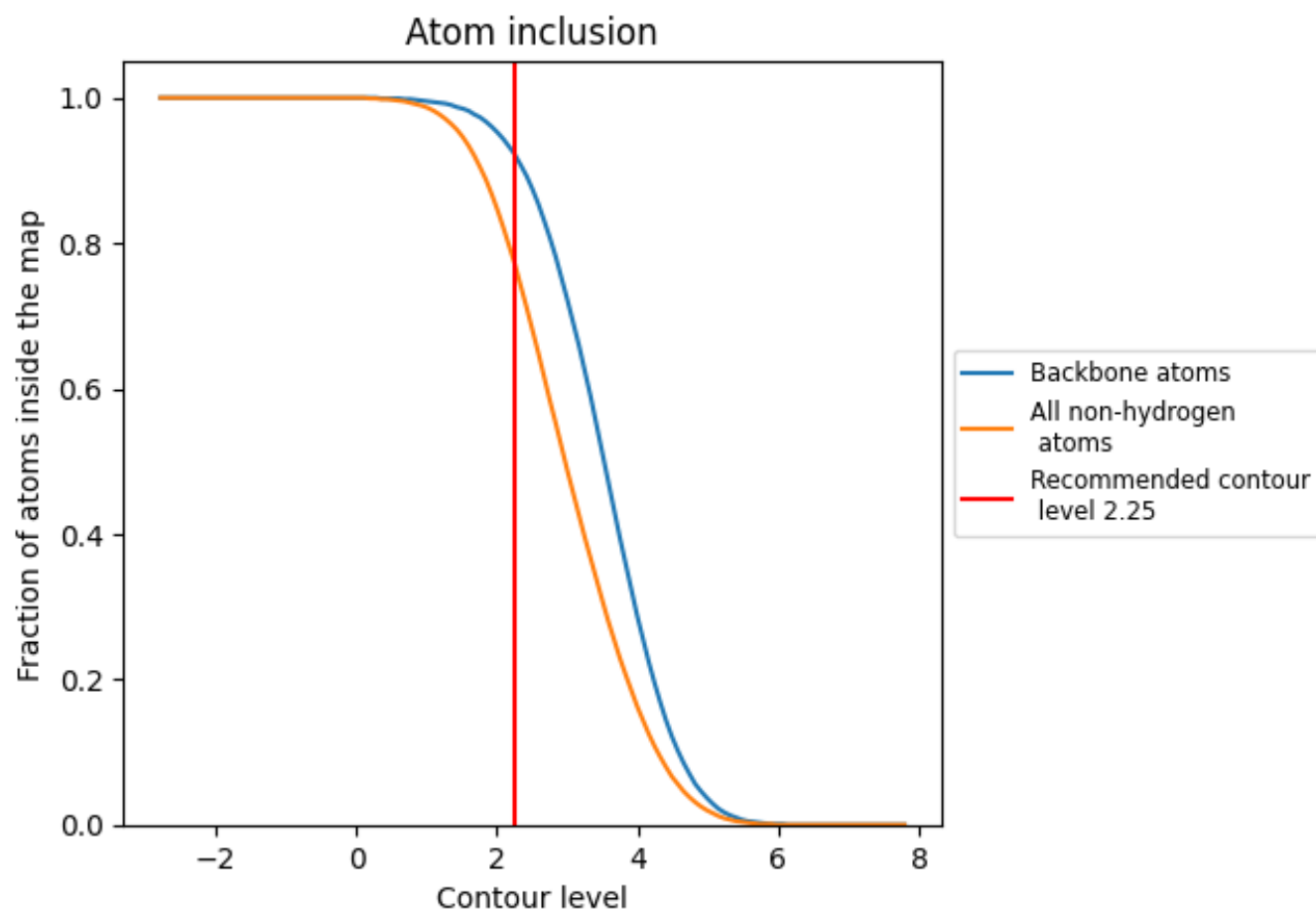
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 77% 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	 0.7730	 0.2760
AC	 0.8090	 0.3010
AD	 0.8300	 0.3070
AF	 0.8070	 0.2390
AG	 0.6780	 0.1990
AH	 0.7930	 0.2780
AK	 0.8240	 0.3060
AL	 0.8320	 0.2870
AM	 0.8110	 0.2930
AN	 0.8060	 0.3290
AU	 0.9780	 0.4800
AX	 0.5620	 0.1910
Ad	 0.8360	 0.3050
Af	 0.8410	 0.2840
Ag	 0.8680	 0.2400
BC	 0.7680	 0.3000
BD	 0.8110	 0.3100
BF	 0.8000	 0.2210
BG	 0.5760	 0.1780
BH	 0.8040	 0.2840
BK	 0.8440	 0.3160
BL	 0.8480	 0.2920
BM	 0.8370	 0.2960
BN	 0.7730	 0.3370
BU	 1.0000	 0.4440
BX	 0.5170	 0.1940
Bd	 0.8270	 0.3040
Bf	 0.7950	 0.2670
Bg	 0.8420	 0.2520
CC	 0.7450	 0.2840
CD	 0.8220	 0.3190
CF	 0.7370	 0.2400
CG	 0.5850	 0.1750
CH	 0.8050	 0.2760
CK	 0.8270	 0.3190



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Chain	Atom inclusion	Q-score
CL	 0.8290	 0.2950
CM	 0.8100	 0.2900
CN	 0.7410	 0.3380
CU	 0.9780	 0.4570
CX	 0.6040	 0.2160
Cd	 0.8280	 0.2950
Cf	 0.8020	 0.2600
Cg	 0.8600	 0.2560
DC	 0.8220	 0.2960
DD	 0.8010	 0.3120
DF	 0.8000	 0.2370
DG	 0.5670	 0.1720
DH	 0.7900	 0.2790
DK	 0.8100	 0.3170
DL	 0.8220	 0.2850
DM	 0.8230	 0.2840
DN	 0.8110	 0.3340
DU	 0.8670	 0.4170
DX	 0.6920	 0.2460
Dd	 0.8110	 0.3070
Df	 0.7680	 0.2910
Dg	 0.8420	 0.2580
EC	 0.8140	 0.3010
ED	 0.8030	 0.3060
EF	 0.7660	 0.2310
EG	 0.5670	 0.1690
EH	 0.7830	 0.2780
EK	 0.8360	 0.3140
EL	 0.8290	 0.2990
EM	 0.8360	 0.2900
EN	 0.8080	 0.3250
EU	 1.0000	 0.4630
EX	 0.5000	 0.2210
Ed	 0.8310	 0.3090
Ef	 0.8060	 0.2840
Eg	 0.8090	 0.2370
FC	 0.7650	 0.2860
FD	 0.8060	 0.3090
FF	 0.7790	 0.2250
FG	 0.5720	 0.1640
FH	 0.7880	 0.2810
FK	 0.8230	 0.3110

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Chain	Atom inclusion	Q-score
FL	 0.8180	 0.2830
FM	 0.8110	 0.2900
FN	 0.7920	 0.3320
FU	 0.8890	 0.4460
FX	 0.6830	 0.2640
Fd	 0.8220	 0.3010
Ff	 0.7630	 0.2770
Fg	 0.8200	 0.2510
GC	 0.7540	 0.2760
GD	 0.8070	 0.3110
GF	 0.7940	 0.2330
GG	 0.5490	 0.1540
GH	 0.7890	 0.2720
GK	 0.8290	 0.3170
GL	 0.8460	 0.2970
GM	 0.8060	 0.2900
GN	 0.7600	 0.3230
GU	 0.9780	 0.4930
GX	 0.7540	 0.2280
Gd	 0.8160	 0.3040
Gf	 0.7810	 0.2770
Gg	 0.8120	 0.2400
HC	 0.8190	 0.2870
HD	 0.7990	 0.3110
HF	 0.7560	 0.2290
HG	 0.5740	 0.1470
HH	 0.7900	 0.2830
HK	 0.8130	 0.3070
HL	 0.8350	 0.2900
HM	 0.8270	 0.2810
HN	 0.7430	 0.3150
HU	 0.9780	 0.4660
HX	 0.6330	 0.2130
Hd	 0.8340	 0.3130
Hf	 0.8090	 0.2770
Hg	 0.8240	 0.2530
IC	 0.8120	 0.3000
ID	 0.8130	 0.3190
IF	 0.7920	 0.2090
IG	 0.5890	 0.1470
IH	 0.7770	 0.2780
IK	 0.8200	 0.3100

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Chain	Atom inclusion	Q-score
IL	 0.8190	 0.2860
IM	 0.8040	 0.2980
IN	 0.8200	 0.3340
IU	 0.9330	 0.4130
IX	 0.5330	 0.2020
Id	 0.8360	 0.3110
If	 0.7770	 0.2870
Ig	 0.8380	 0.2560
JC	 0.8140	 0.3040
JD	 0.8010	 0.3240
JF	 0.7920	 0.2260
JG	 0.5470	 0.1340
JH	 0.7970	 0.2810
JK	 0.8020	 0.3110
JL	 0.8260	 0.2990
JM	 0.8160	 0.2980
JN	 0.7760	 0.3380
JU	 0.9560	 0.4960
JX	 0.5920	 0.1790
Jd	 0.8250	 0.3120
Jf	 0.7860	 0.2530
Jg	 0.8380	 0.2630
KC	 0.7720	 0.2850
KD	 0.8220	 0.3120
KF	 0.7560	 0.2180
KG	 0.5580	 0.1490
KH	 0.8070	 0.2800
KK	 0.8140	 0.3140
KL	 0.8070	 0.2920
KM	 0.8060	 0.2860
KN	 0.7500	 0.3350
KU	 0.9560	 0.4320
KX	 0.6000	 0.2380
Kd	 0.8400	 0.3020
Kf	 0.8220	 0.2720
Kg	 0.8420	 0.2560
LC	 0.8150	 0.2930
LD	 0.8180	 0.3060
LF	 0.8090	 0.2360
LG	 0.6230	 0.1850
LH	 0.7910	 0.2780
LK	 0.8290	 0.3050

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Chain	Atom inclusion	Q-score
LL	 0.8360	 0.2980
LM	 0.8290	 0.2920
LN	 0.7920	 0.3200
LU	 0.9780	 0.4390
LX	 0.5710	 0.2220
Ld	 0.8140	 0.2990
Lf	 0.8180	 0.2670
Lg	 0.8380	 0.2540
MC	 0.8260	 0.3020
MD	 0.8240	 0.3130
MF	 0.7620	 0.2100
MG	 0.6430	 0.2100
MH	 0.7800	 0.2660
MK	 0.8150	 0.3140
ML	 0.8480	 0.2960
MM	 0.8180	 0.2790
MN	 0.8040	 0.3250
MU	 0.9560	 0.4300
MX	 0.7210	 0.2410
Md	 0.8450	 0.3040
Mf	 0.7520	 0.2790
Mg	 0.8090	 0.2380
NG	 0.6150	 0.1880
OG	 0.6430	 0.2060
PG	 0.6460	 0.1920
VF	 0.7880	 0.2260
VG	 0.8270	 0.2320
VH	 0.6910	 0.2720
VX	 0.5580	 0.2250
WF	 0.7580	 0.2210
WG	 0.7940	 0.2310
WH	 0.6340	 0.2520
WX	 0.6040	 0.2630
XF	 0.7330	 0.2210
XG	 0.8380	 0.2520
XH	 0.5360	 0.2570
XX	 0.7580	 0.2450
YF	 0.7880	 0.2220
YG	 0.8120	 0.2310
YH	 0.6780	 0.2530
YX	 0.6880	 0.2570
ZF	 0.7450	 0.2220

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Chain	Atom inclusion	Q-score
ZG	 0.8310	 0.2490
ZH	 0.5510	 0.2250
ZX	 0.6000	 0.2180