



Full wwPDB EM Validation Report ⓘ

Mar 25, 2026 – 08:15 PM UTC

PDB ID : 7MUS / pdb_00007mus
EMDB ID : EMD-24020
Title : Reconstruction of the Legionella pneumophila Dot/Icm T4SS 3DVA Map 2
Authors : Sheedlo, M.J.; Durie, C.L.; Swanson, M.; Lacy, D.B.; Ohi, M.D.
Deposited on : 2021-05-14
Resolution : 4.60 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

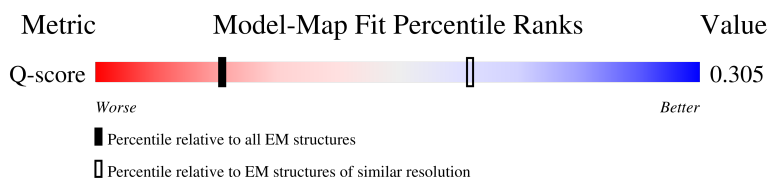
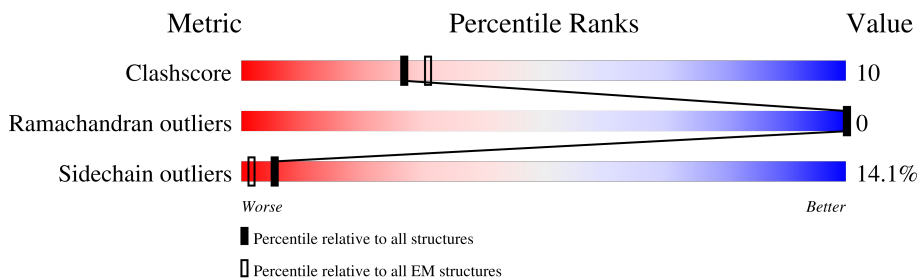
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

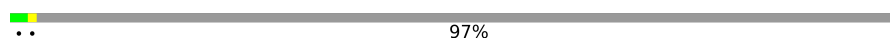
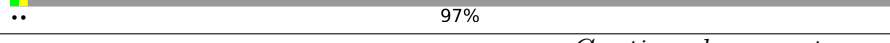
The reported resolution of this entry is 4.60 Å.

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



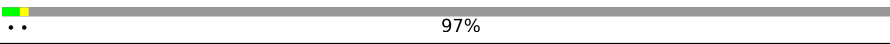
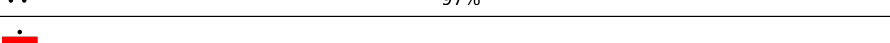
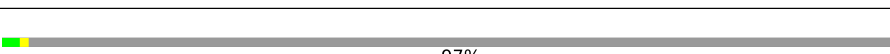
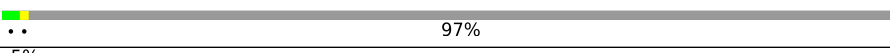
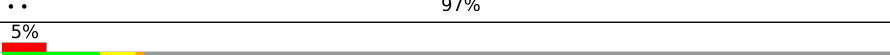
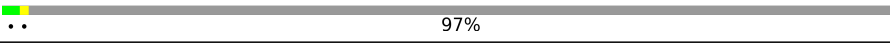
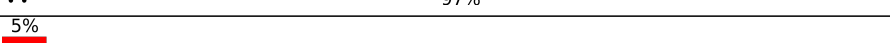
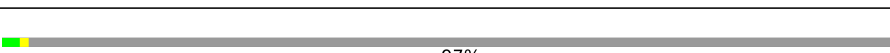
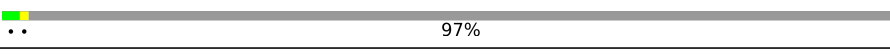
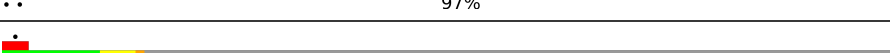
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2407 (4.10 - 5.10)

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

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

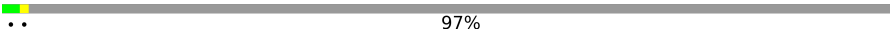
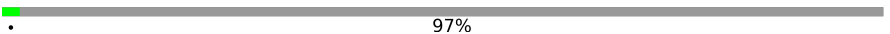
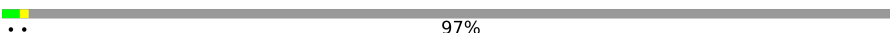
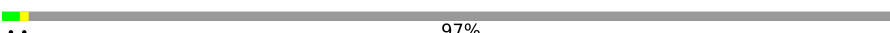
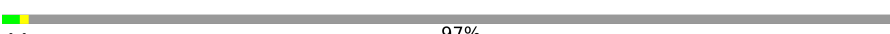
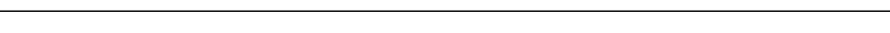
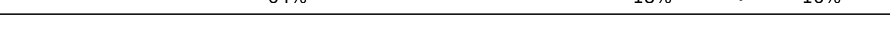
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Mol	Chain	Length	Quality of chain
1	CG	1048	 11% 84%
1	Cg	1048	 97%
1	DG	1048	 10% 5% 84%
1	Dg	1048	 97%
1	EG	1048	 10% 5% 84%
1	Eg	1048	 97%
1	FG	1048	 5% 10% 5% 84%
1	Fg	1048	 97%
1	GG	1048	 5% 10% 84%
1	Gg	1048	 97%
1	HG	1048	 5% 11% 84%
1	Hg	1048	 97%
1	IG	1048	 5% 11% 84%
1	Ig	1048	 97%
1	JG	1048	 5% 11% 84%
1	Jg	1048	 97%
1	KG	1048	 5% 11% 84%
1	Kg	1048	 97%
1	LG	1048	 11% 84%
1	Lg	1048	 97%
1	MG	1048	 11% 84%
1	Mg	1048	 97%
1	NG	1048	 11% 84%
1	OG	1048	 10% 84%
1	PG	1048	11% 84%

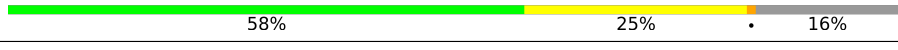
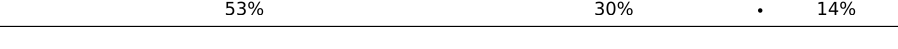
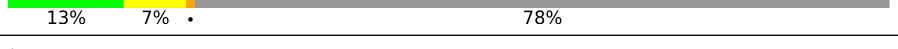
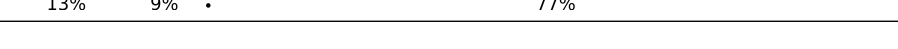
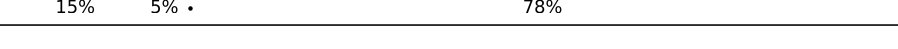
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Mol	Chain	Length	Quality of chain
1	VG	1048	 97%
1	WG	1048	 97%
1	XG	1048	 97%
1	YG	1048	 97%
1	ZG	1048	 97%
2	AD	163	 52% 31% 14%
2	Ad	163	 58% 21% 5% 16%
2	BD	163	 62% 20% 14%
2	Bd	163	 64% 17% 16%
2	CD	163	 54% 28% 14%
2	Cd	163	 67% 15% 16%
2	DD	163	 55% 27% 14%
2	Dd	163	 57% 23% 16%
2	ED	163	 60% 21% 5% 14%
2	Ed	163	 64% 18% 16%
2	FD	163	 60% 25% 14%
2	Fd	163	 57% 24% 16%
2	GD	163	 56% 26% 14%
2	Gd	163	 56% 23% 5% 16%
2	HD	163	 66% 18% 14%
2	Hd	163	 64% 17% 16%
2	ID	163	 66% 17% 14%
2	Id	163	 60% 20% 16%
2	JD	163	 61% 23% 14%
2	Jd	163	 61% 19% 16%

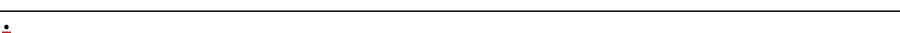
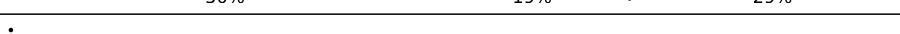
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Mol	Chain	Length	Quality of chain
2	KD	163	
2	Kd	163	
2	LD	163	
2	Ld	163	
2	MD	163	
2	Md	163	
3	AF	269	
3	Af	269	
3	BF	269	
3	Bf	269	
3	CF	269	
3	Cf	269	
3	DF	269	
3	Df	269	
3	EF	269	
3	Ef	269	
3	FF	269	
3	Ff	269	
3	GF	269	
3	Gf	269	
3	HF	269	
3	Hf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

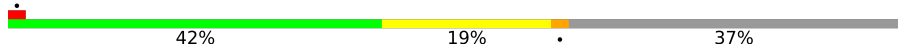
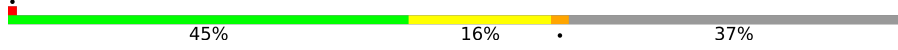
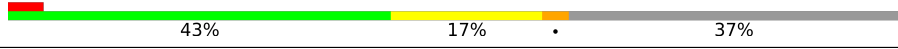
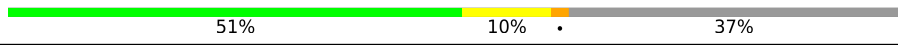
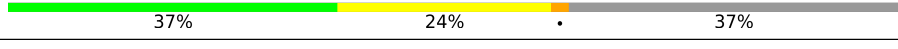
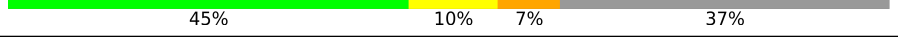
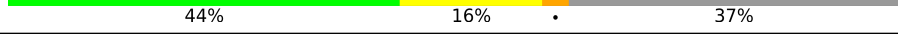
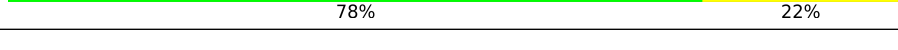
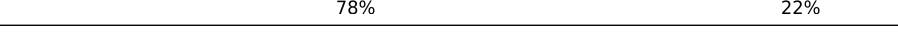
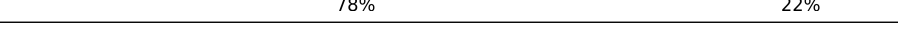
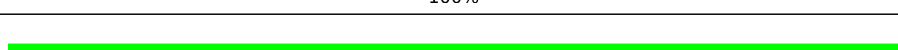
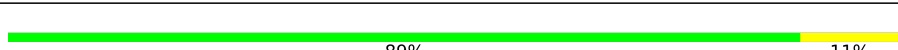
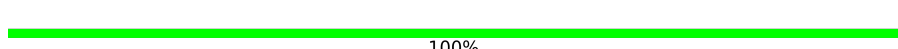
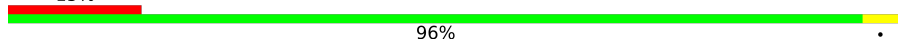
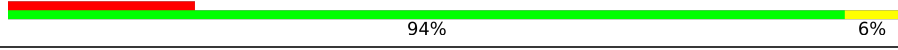
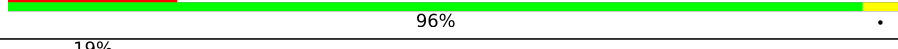
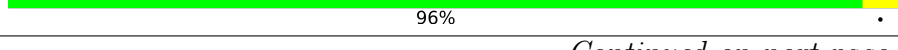
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Mol	Chain	Length	Quality of chain
6	HL	249	
6	IL	249	
6	JL	249	
6	KL	249	
6	LL	249	
6	ML	249	
7	AM	320	
7	BM	320	
7	CM	320	
7	DM	320	
7	EM	320	
7	FM	320	
7	GM	320	
7	HM	320	
7	IM	320	
7	JM	320	
7	KM	320	
7	LM	320	
7	MM	320	
8	AN	124	
8	BN	124	
8	CN	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	54%24%20%

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 1229	C 780	N 203	O 242	S 4	0	0
1	Gg	34	Total 276	C 168	N 47	O 60	S 1	0	0
1	Hg	34	Total 276	C 168	N 47	O 60	S 1	0	0
1	Bg	34	Total 276	C 168	N 47	O 60	S 1	0	0
1	BG	165	Total 1229	C 780	N 203	O 242	S 4	0	0
1	Ig	34	Total 276	C 168	N 47	O 60	S 1	0	0
1	Jg	34	Total 276	C 168	N 47	O 60	S 1	0	0
1	CG	165	Total 1229	C 780	N 203	O 242	S 4	0	0
1	Kg	34	Total 276	C 168	N 47	O 60	S 1	0	0
1	Ag	34	Total 276	C 168	N 47	O 60	S 1	0	0
1	Lg	34	Total 276	C 168	N 47	O 60	S 1	0	0
1	DG	165	Total 1229	C 780	N 203	O 242	S 4	0	0
1	Cg	34	Total 276	C 168	N 47	O 60	S 1	0	0
1	Mg	34	Total 276	C 168	N 47	O 60	S 1	0	0
1	VG	34	Total 276	C 168	N 47	O 60	S 1	0	0
1	WG	34	Total 276	C 168	N 47	O 60	S 1	0	0
1	XG	34	Total 276	C 168	N 47	O 60	S 1	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	EG	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	FG	165	Total	C	N	O	S	0	0
			1229	780	203	242	4		
1	Dg	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
1	GG	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	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		

- Molecule 2 is a protein called DotD.

Mol	Chain	Residues	Atoms					AltConf	Trace
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		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	HD	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	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	CD	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	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
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	ED	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		
2	DD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ed	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
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		

- Molecule 3 is a protein called DotF.

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

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Mol	Chain	Residues	Atoms					AltConf	Trace
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	CF	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	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	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		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
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		
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		

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Mol	Chain	Residues	Atoms					AltConf	Trace
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		
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		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
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		
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		

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Mol	Chain	Residues	Atoms					AltConf	Trace
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		
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		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
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		
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		

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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		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
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		
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		

- Molecule 8 is a protein called Neurogenic locus notch.

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		

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Mol	Chain	Residues	Atoms					AltConf	Trace
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		
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		

- Molecule 9 is a protein called Unknown protein fragment.

Mol	Chain	Residues	Atoms				AltConf	Trace
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		
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		

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Mol	Chain	Residues	Atoms				AltConf	Trace
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		
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		

- Molecule 10 is a protein called Unknown protein fragment.

Mol	Chain	Residues	Atoms				AltConf	Trace
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		
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		

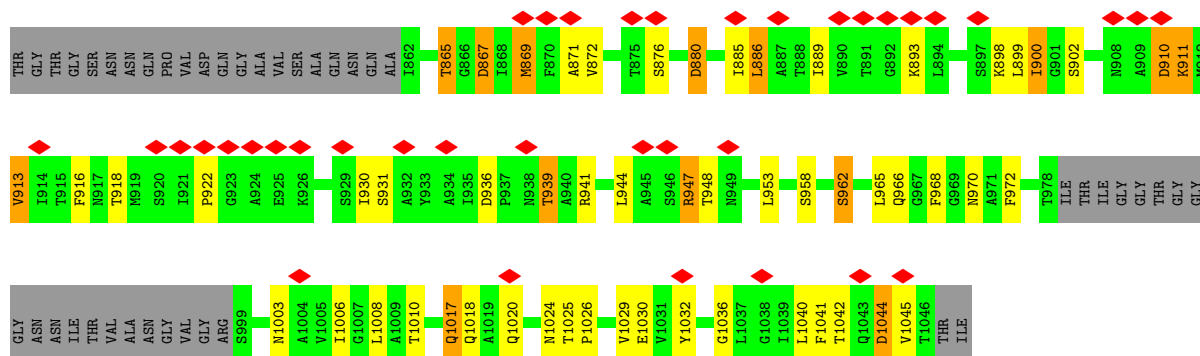
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Mol	Chain	Residues	Atoms				AltConf	Trace
10	CX	48	Total	C	N	O	0	0
			240	144	48	48		
10	DX	48	Total	C	N	O	0	0
			240	144	48	48		
10	EX	48	Total	C	N	O	0	0
			240	144	48	48		
10	FX	48	Total	C	N	O	0	0
			240	144	48	48		

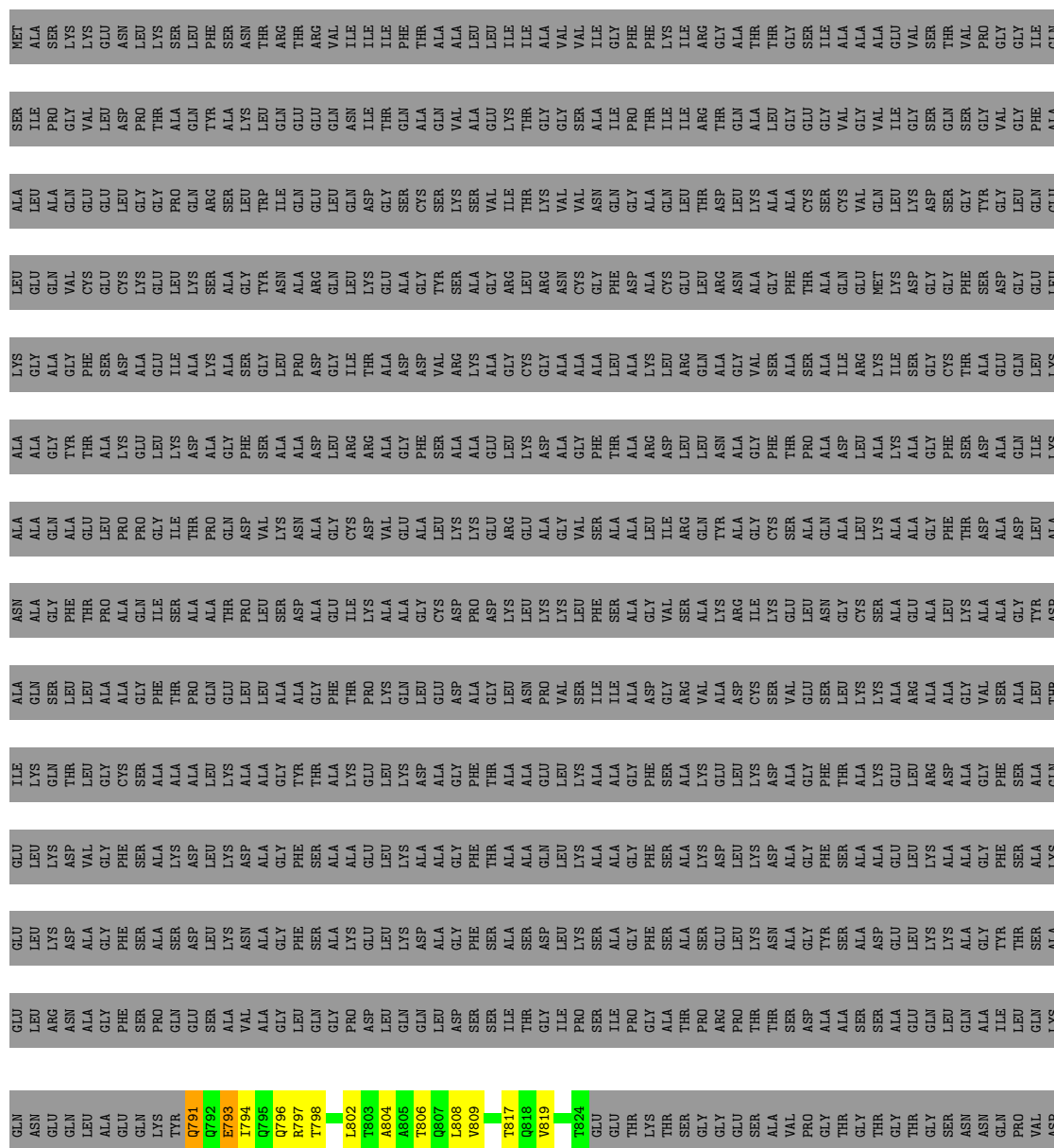
- Molecule 11 is a protein called DotC.

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



• Molecule 1: IcmE protein

Chain Gg: .. 97%



[illegible]

- Molecule 1: IcmE protein

Chain Hg: 97%

[illegible]

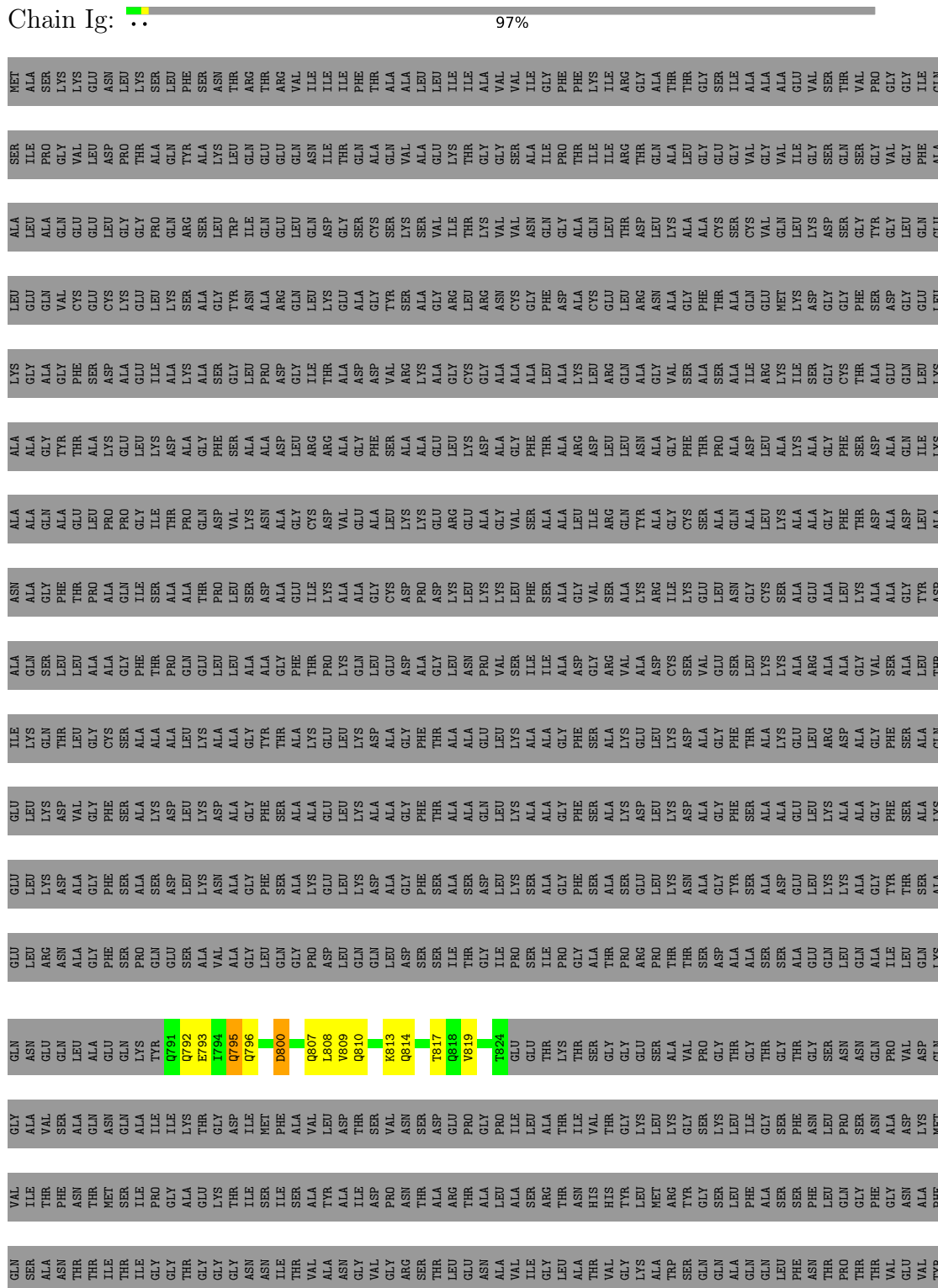
ILE
LEU
PHE
THR
GLN
ASP
VAL
THR
THR
ILE

- Molecule 1: IcmE protein

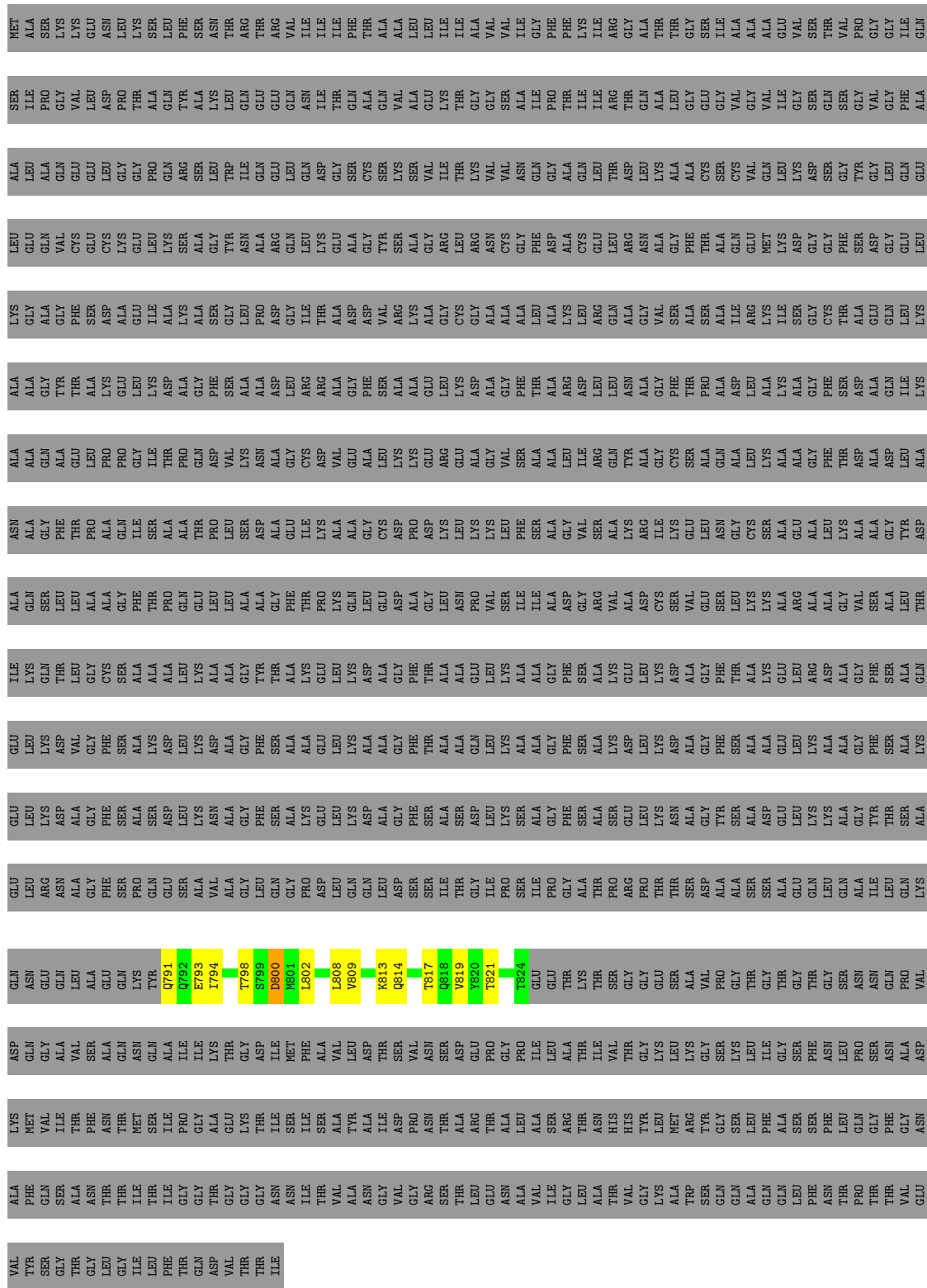
Chain Bg: 97%

[illegible]

- Molecule 1: IcmE protein

Chain Ig:  ..

Chain Jg: .. 97%



Chain CG: 11% . . 84%



97%

- Molecule 1: IcmE protein

97%

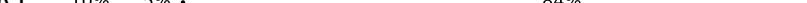


[illegible]

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

[illegible]

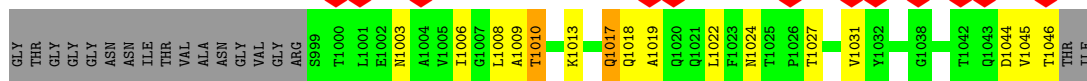
- Molecule 1: IcmE protein

Chain EG:  10% 5% 84%

[illegible]



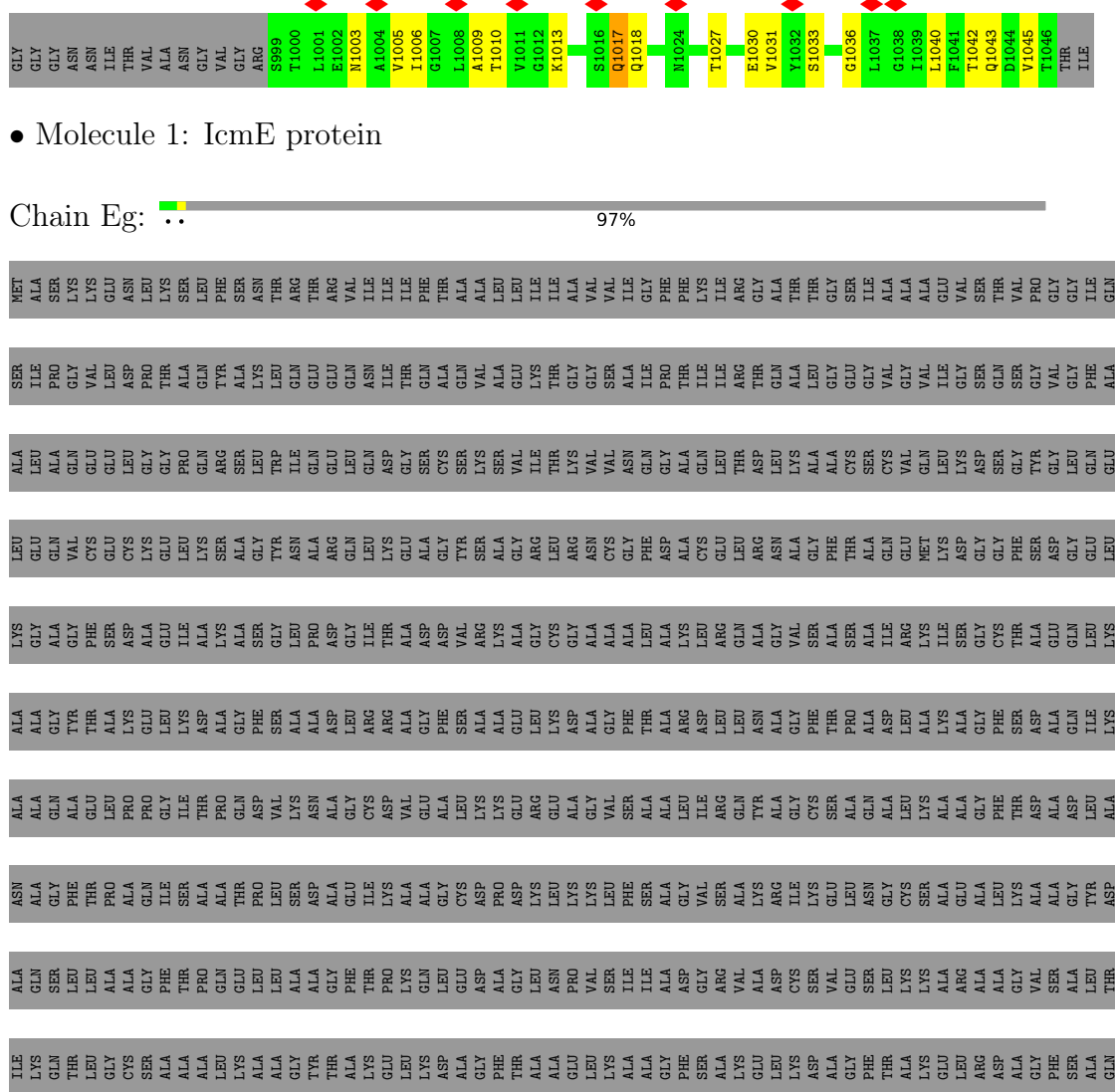
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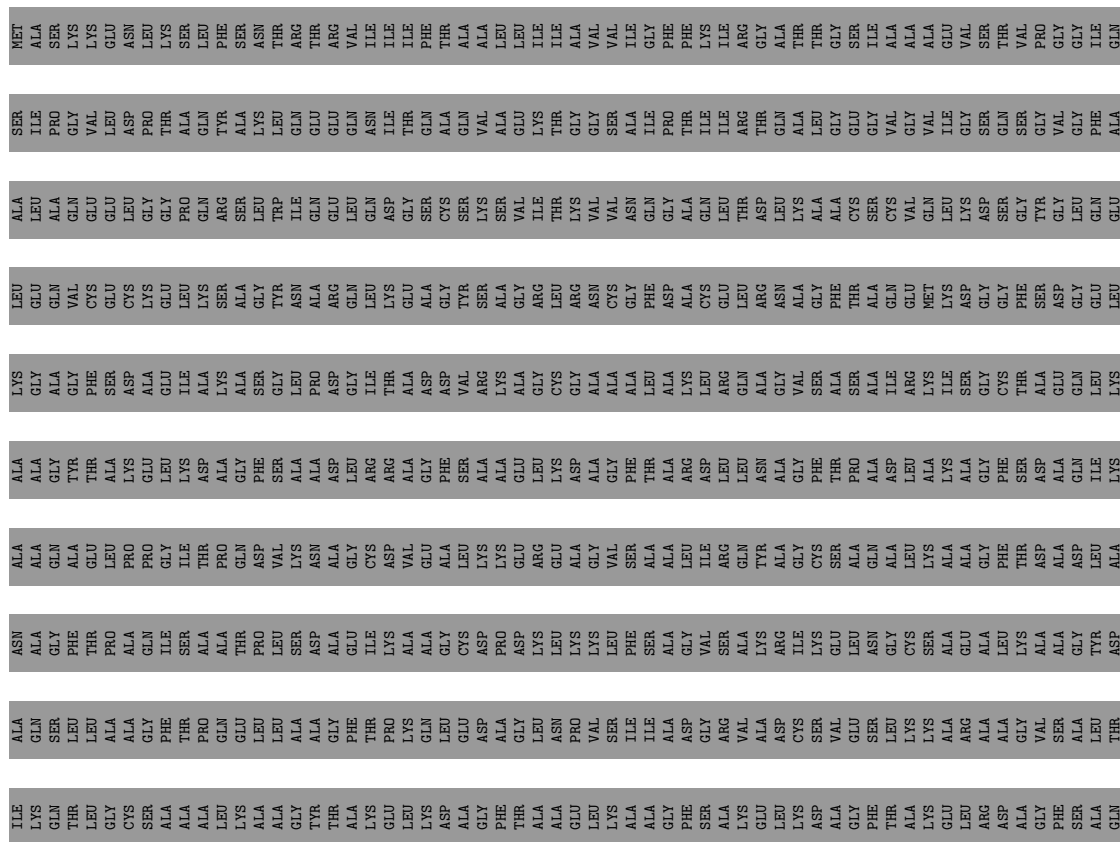
Chain Dg: .. 97%



[illegible]



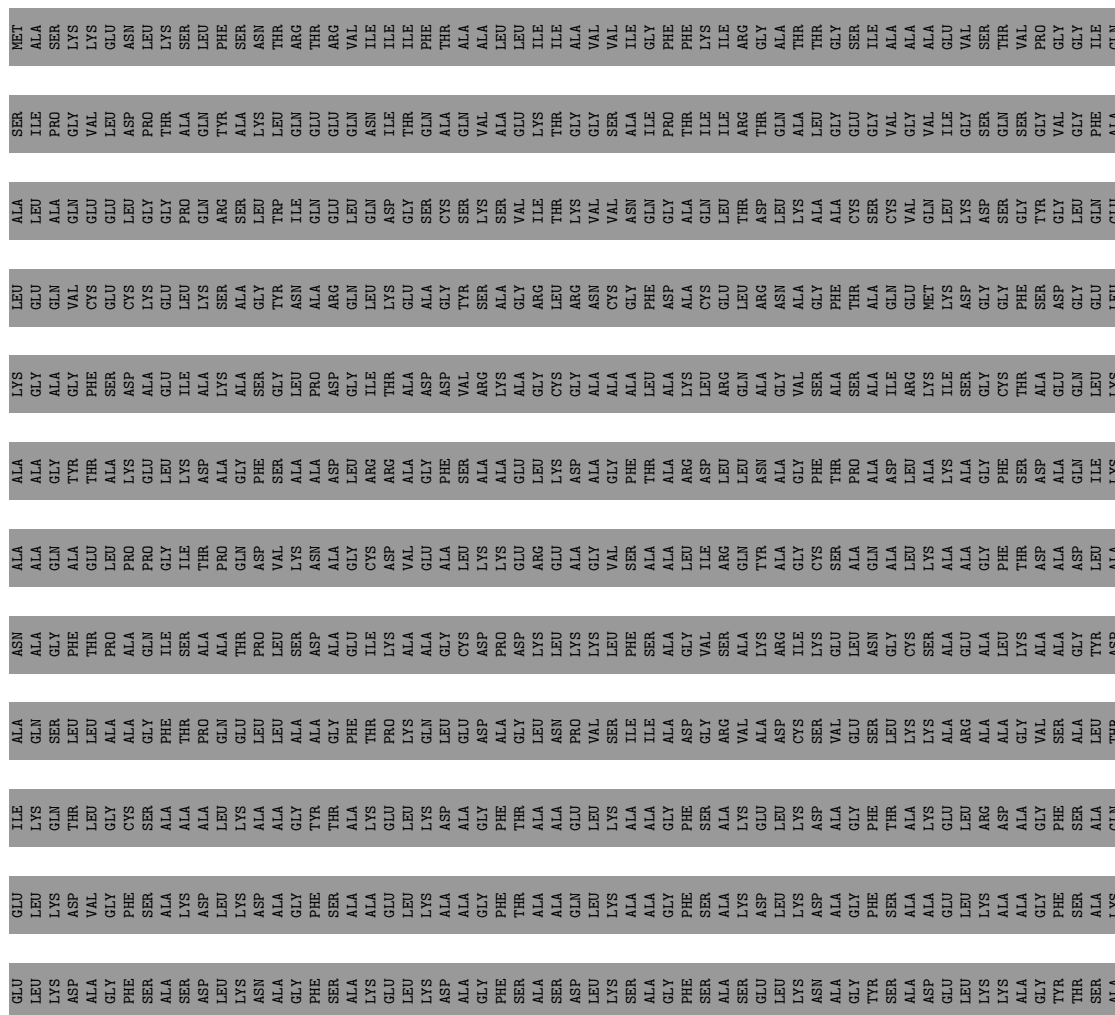
Chain Eg: .. 97%



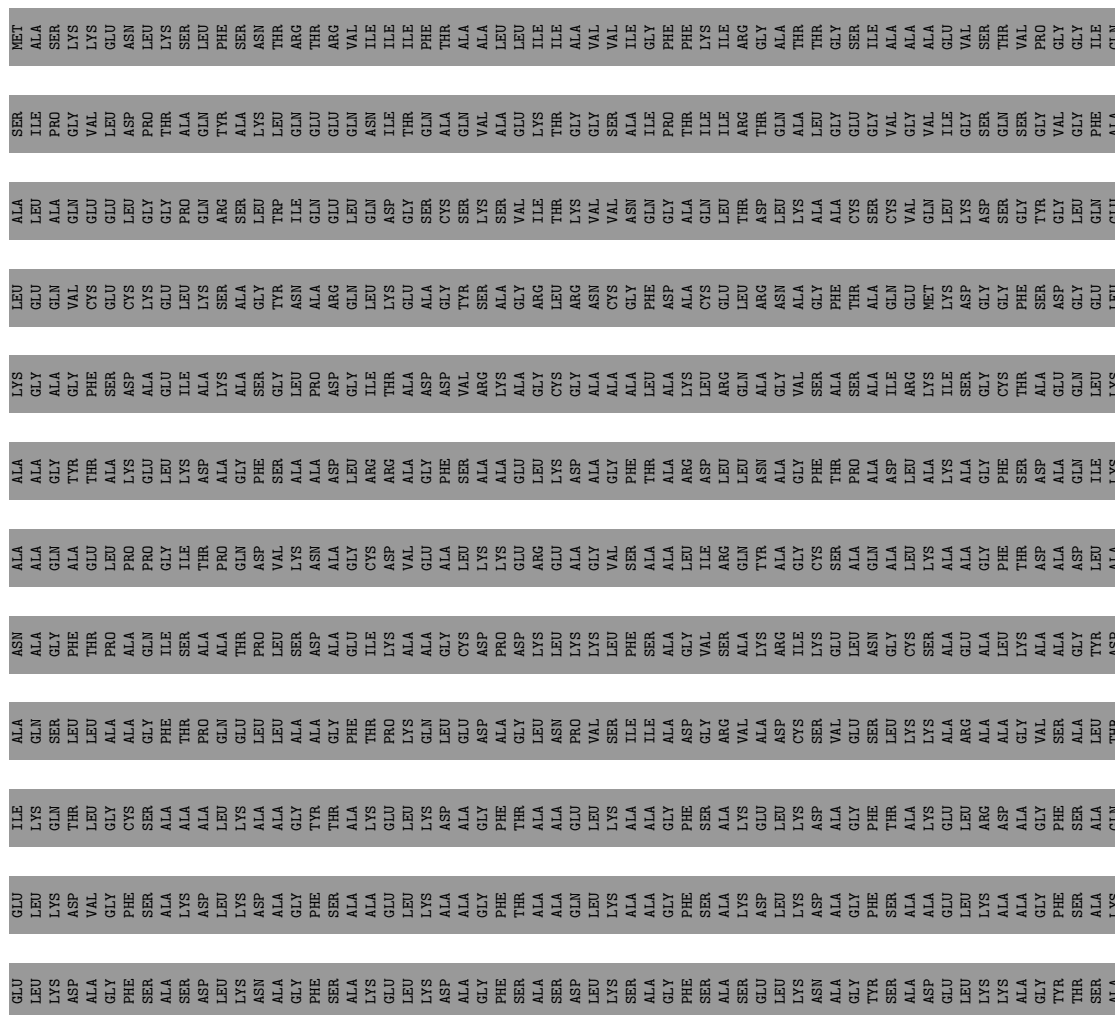


[illegible]

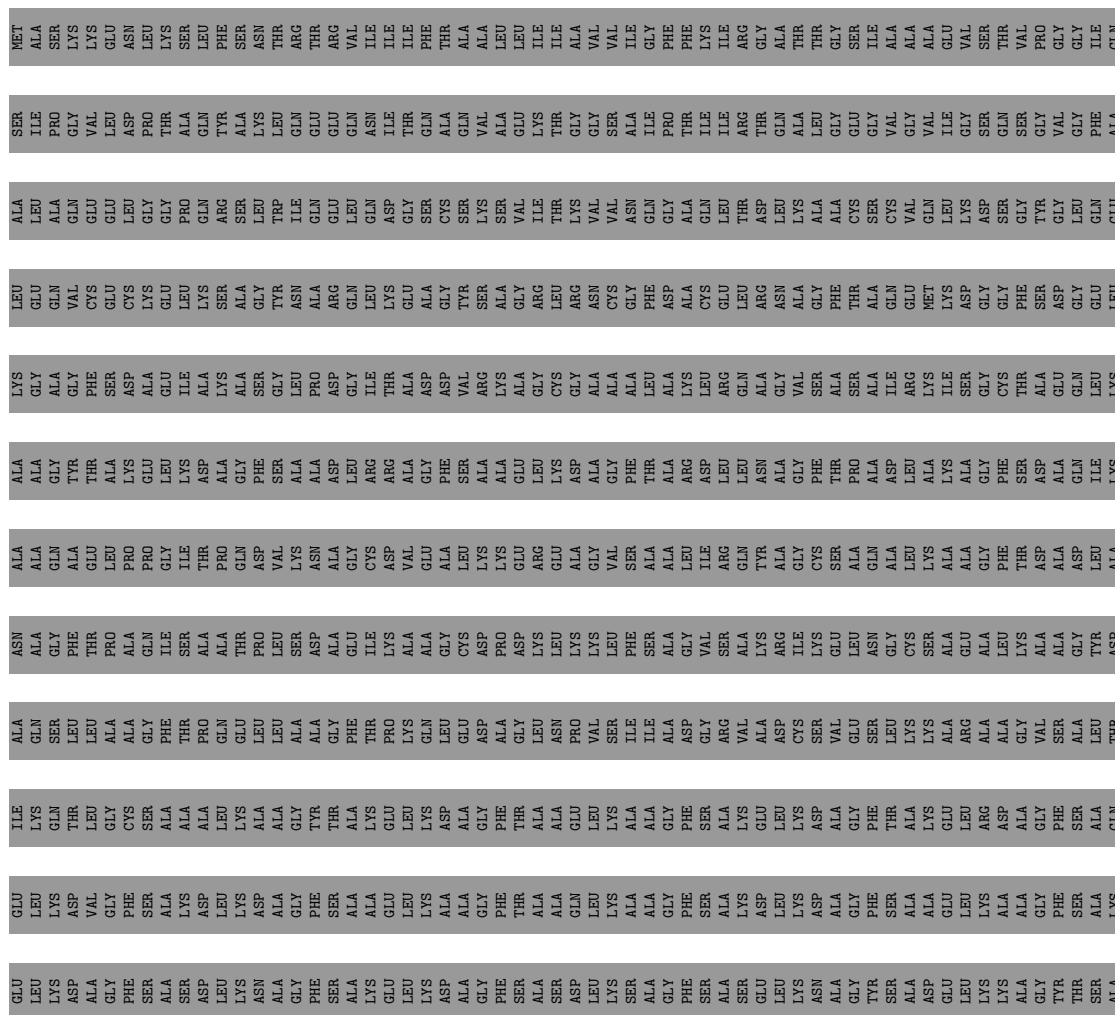
- Molecule 1: IcmE protein



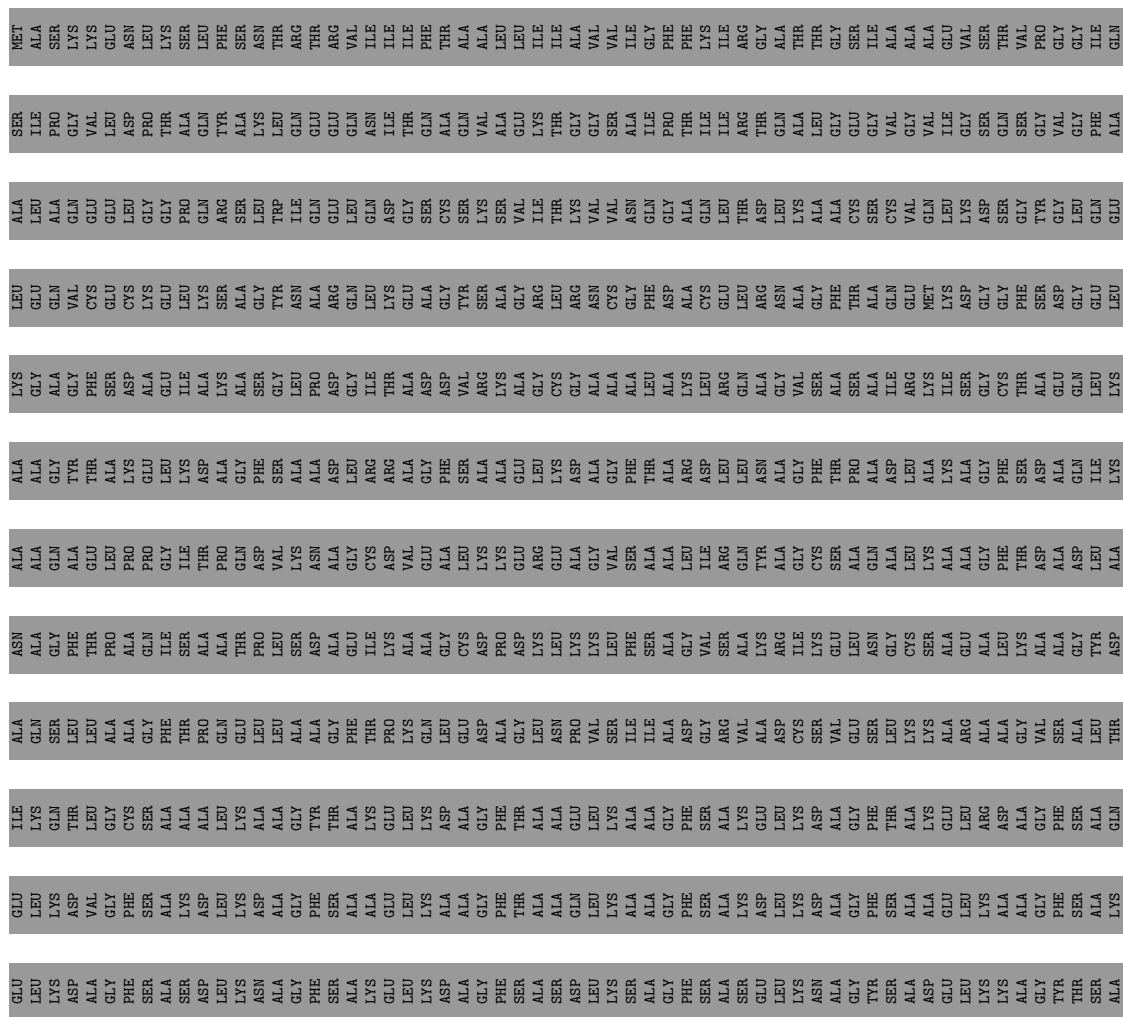
- Molecule 1: IcmE protein

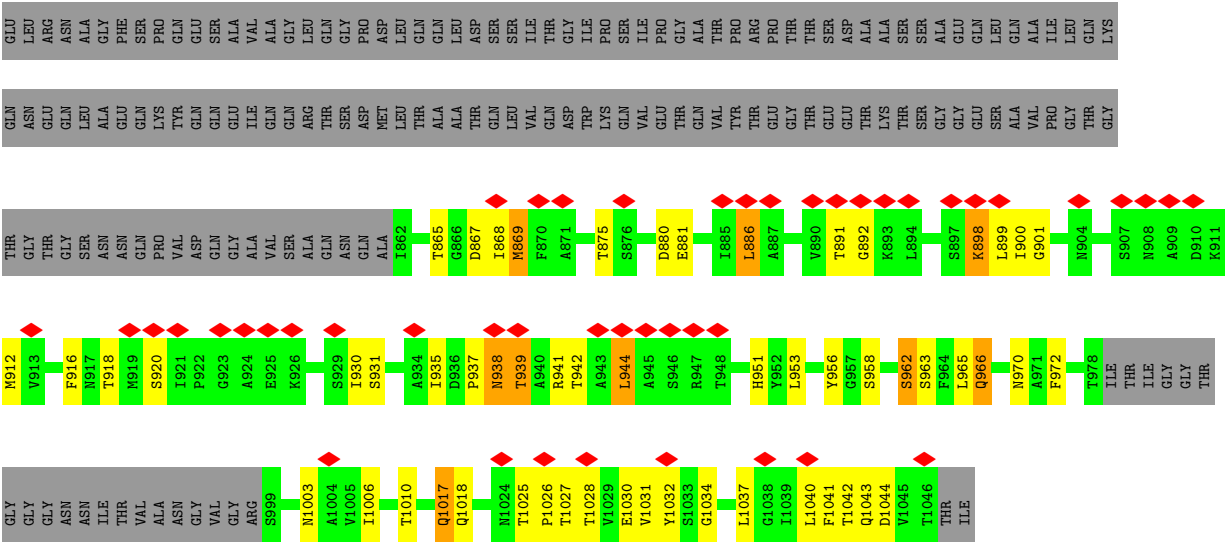


- Molecule 1: IcmE protein

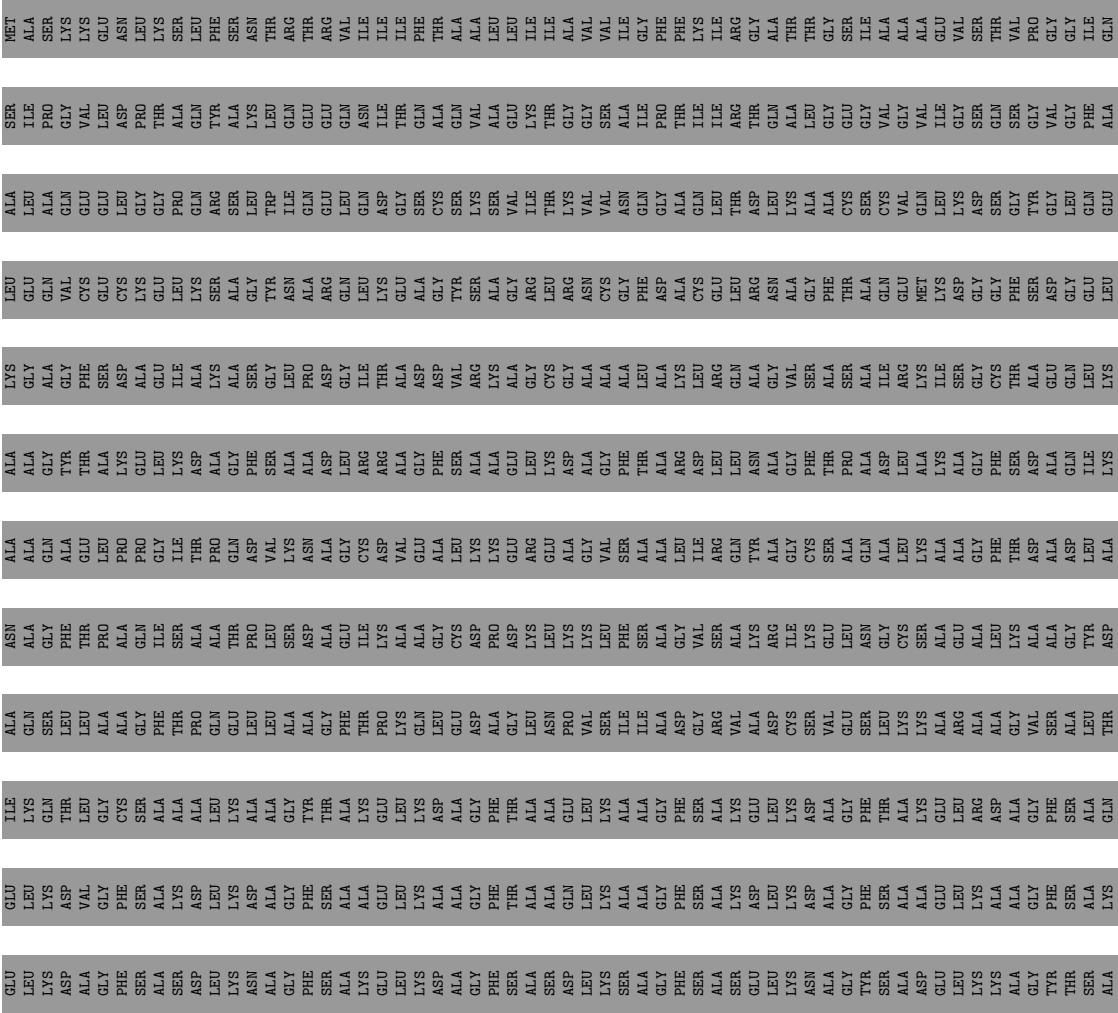


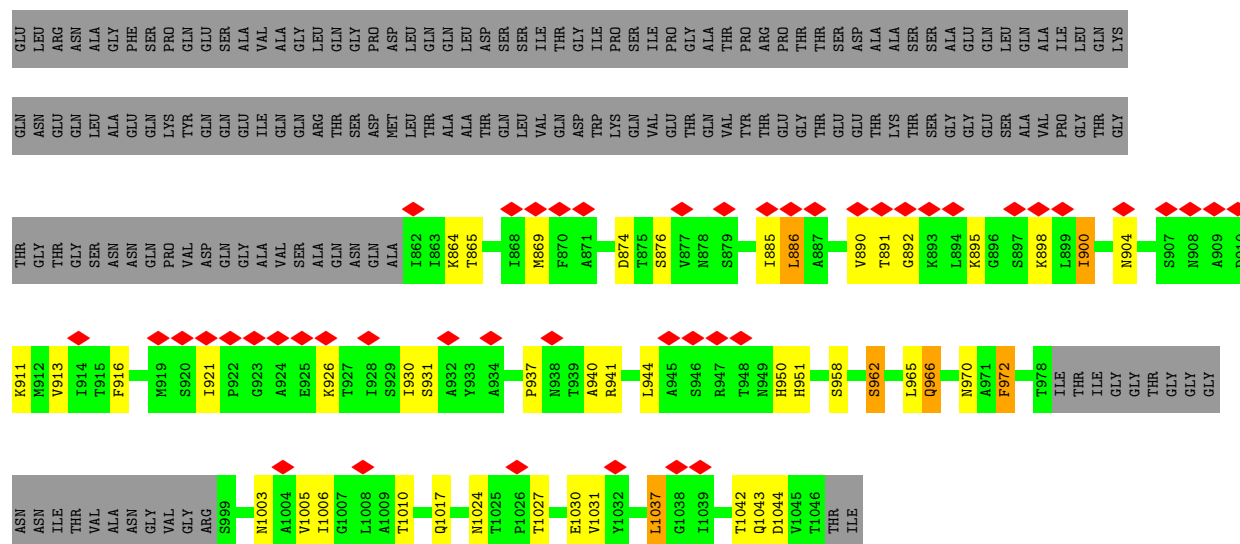
- Molecule 1: IcmE protein



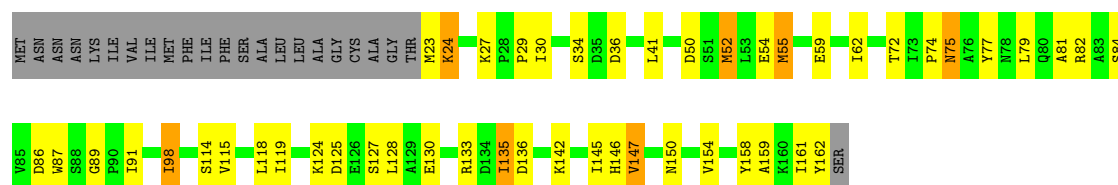


● Molecule 1: IcmE protein

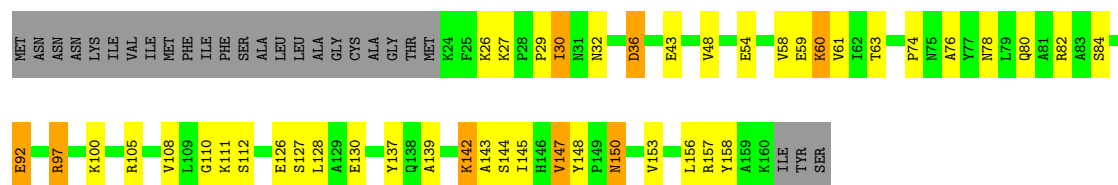




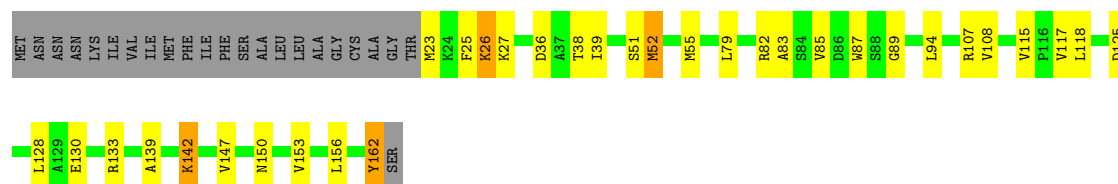
• Molecule 2: DotD



• Molecule 2: DotD

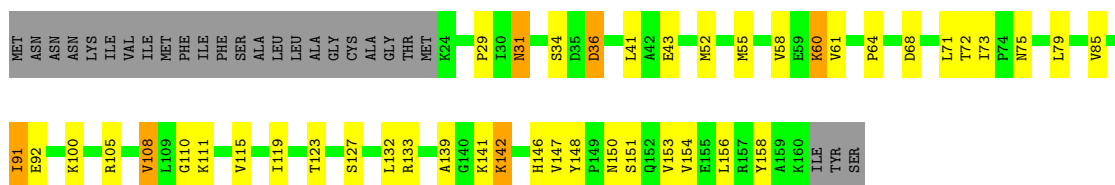


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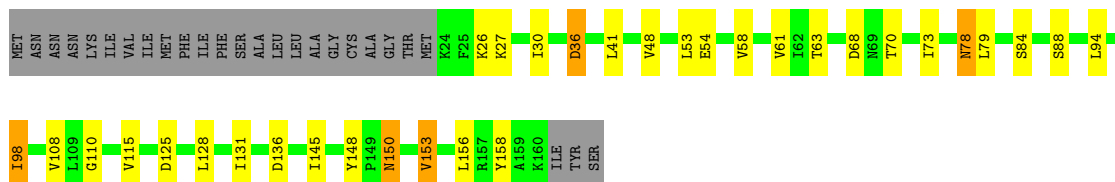


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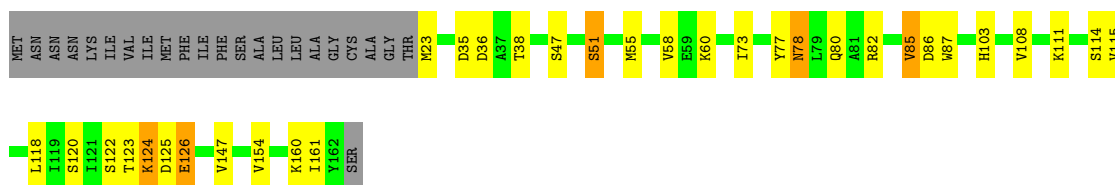




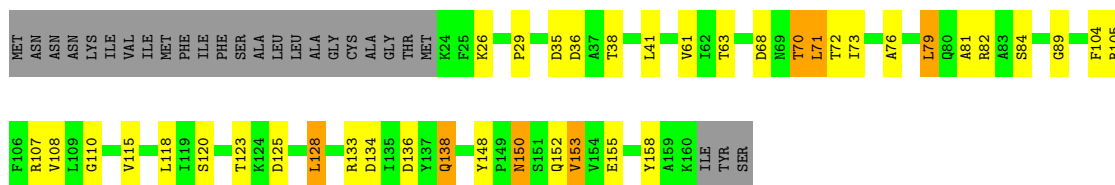
• Molecule 2: DotD



• Molecule 2: DotD



• Molecule 2: DotD

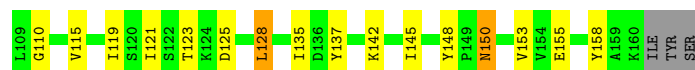
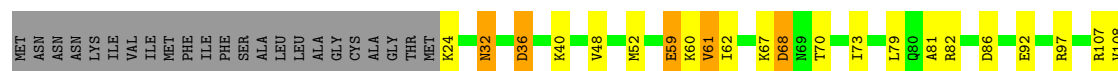


• Molecule 2: DotD



• Molecule 2: DotD





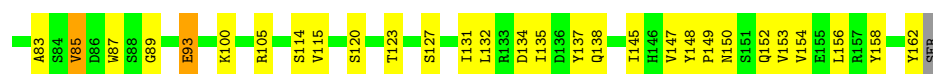
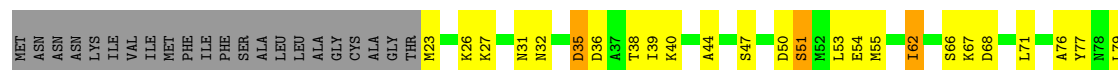
• Molecule 2: DotD



• Molecule 2: DotD



• Molecule 2: DotD

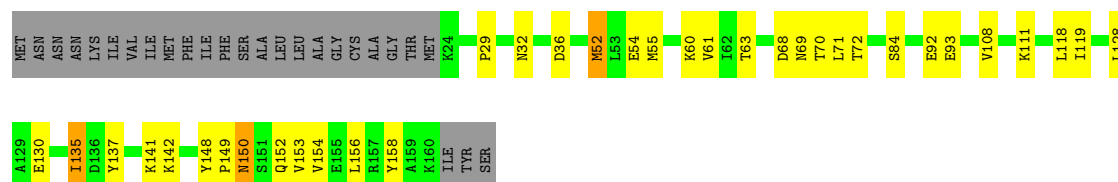


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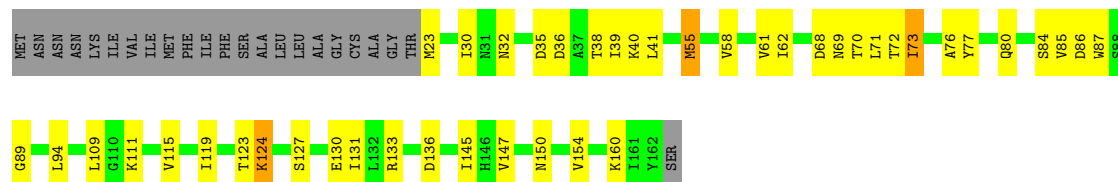


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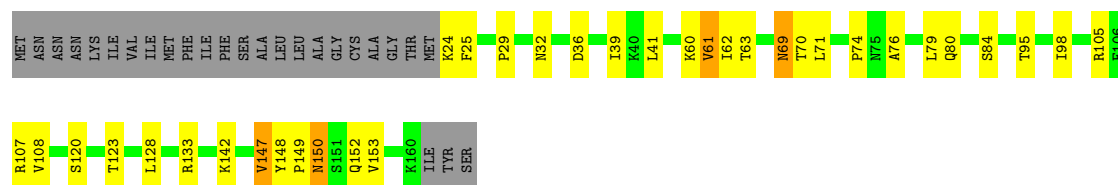




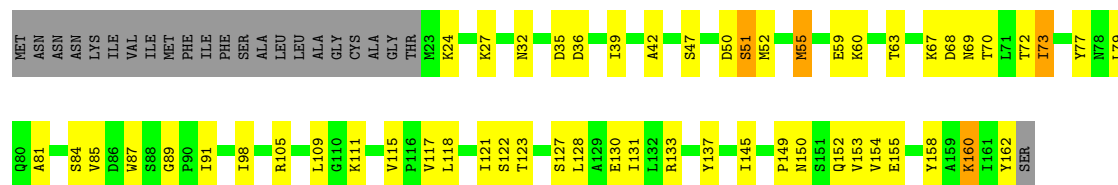
- Molecule 2: DotD



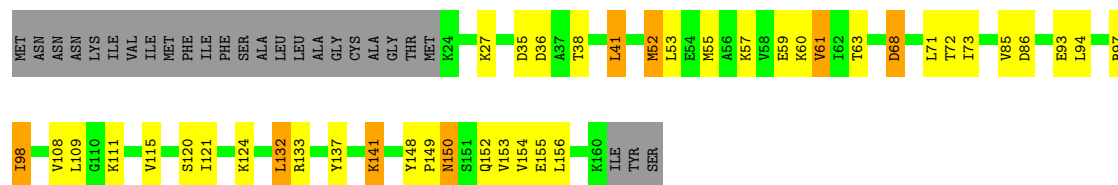
- Molecule 2: DotD



- Molecule 2: DotD

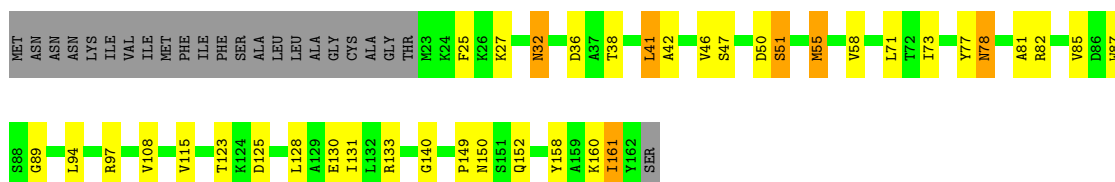


- Molecule 2: DotD

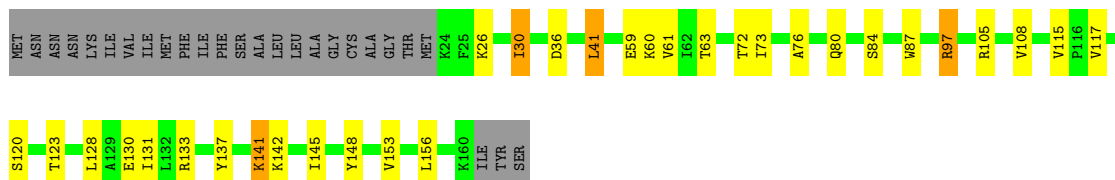


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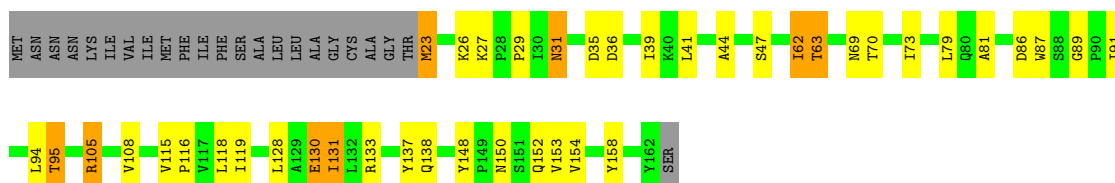




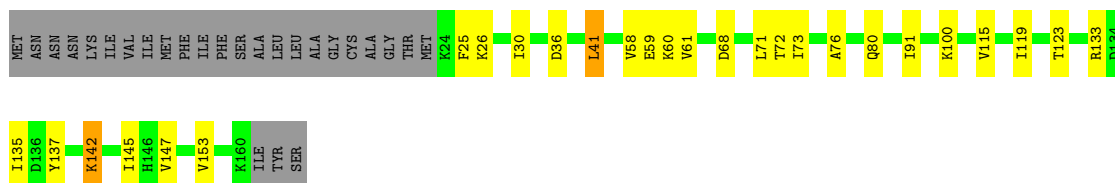
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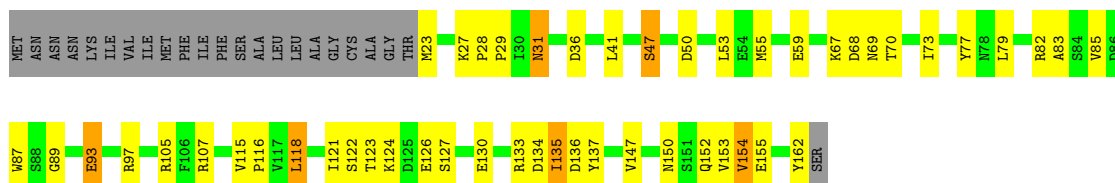
- Molecule 2: DotD



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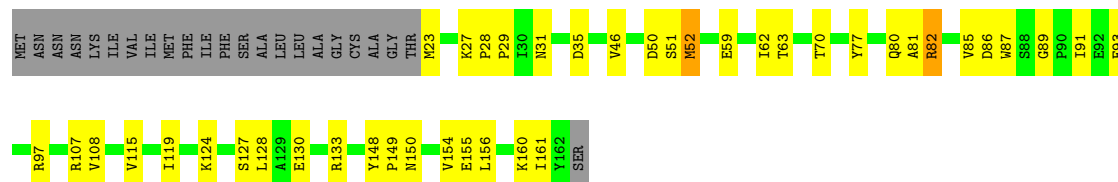
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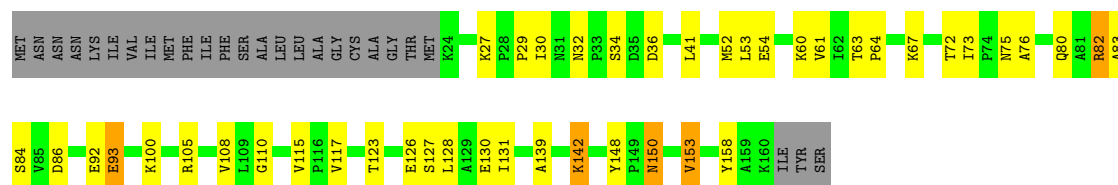
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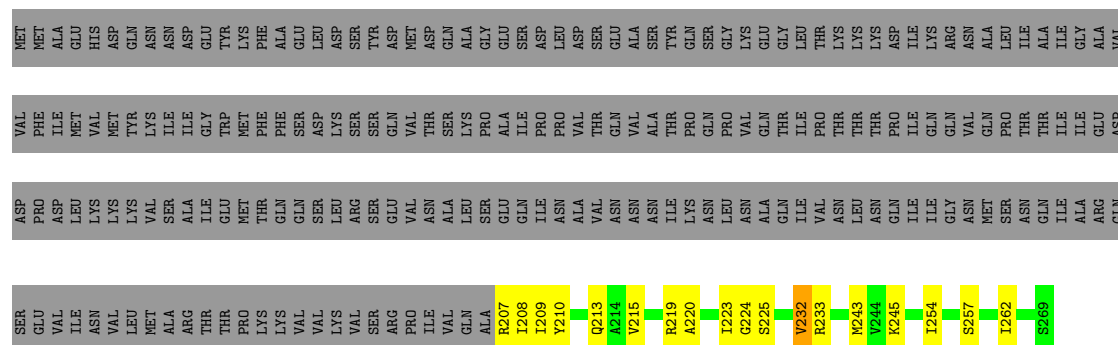
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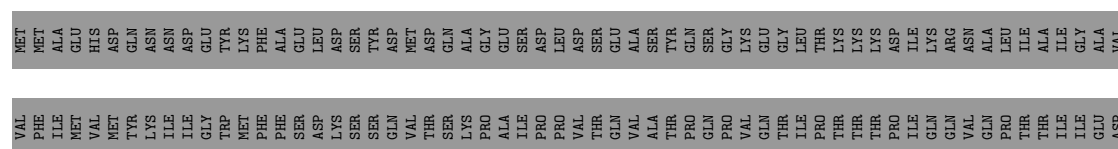
- Molecule 2: DotD



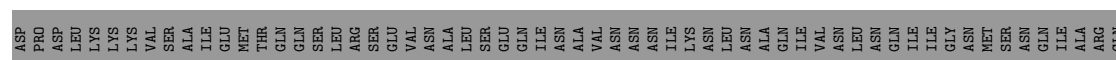
- Molecule 3: DotF

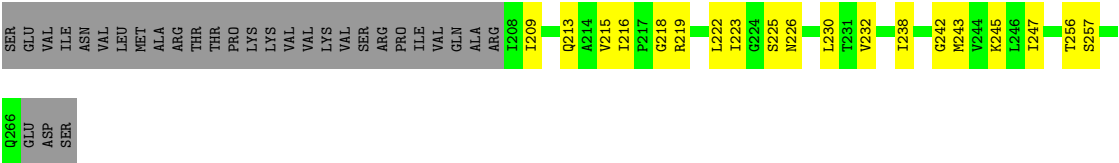


- Molecule 3: DotF

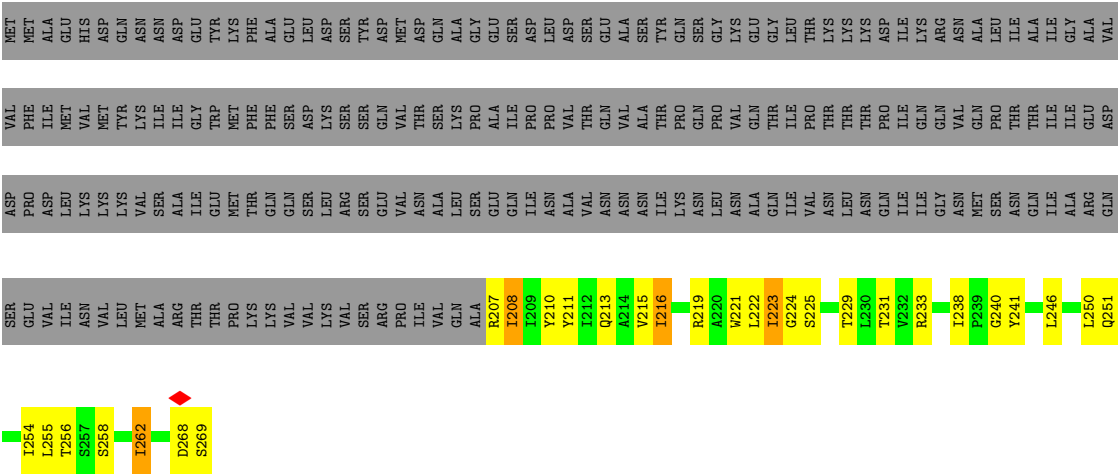




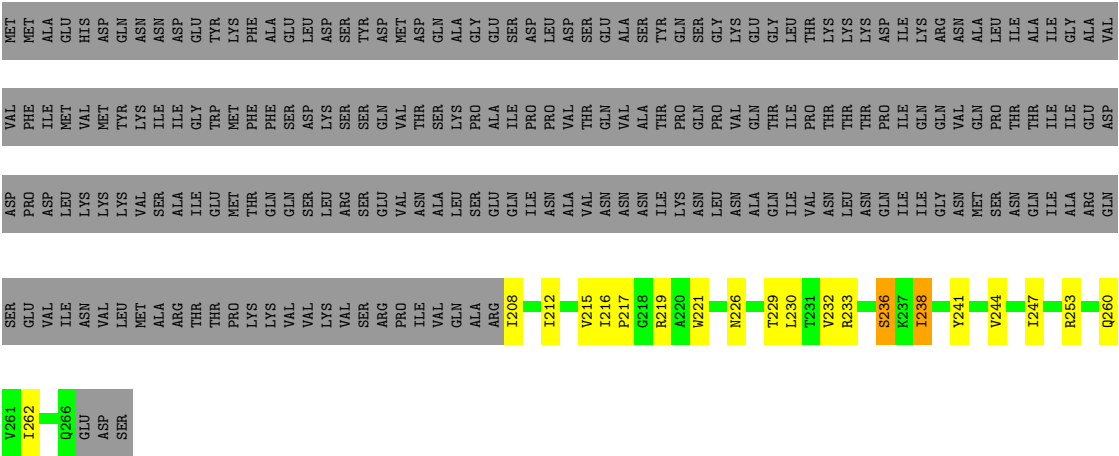




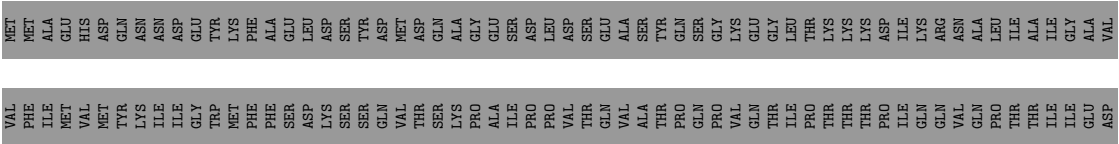
• Molecule 3: DotF



• Molecule 3: DotF

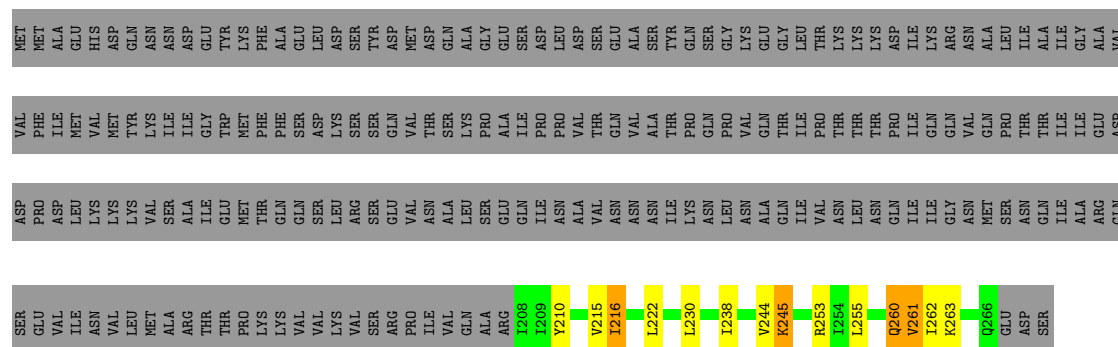


• Molecule 3: DotF



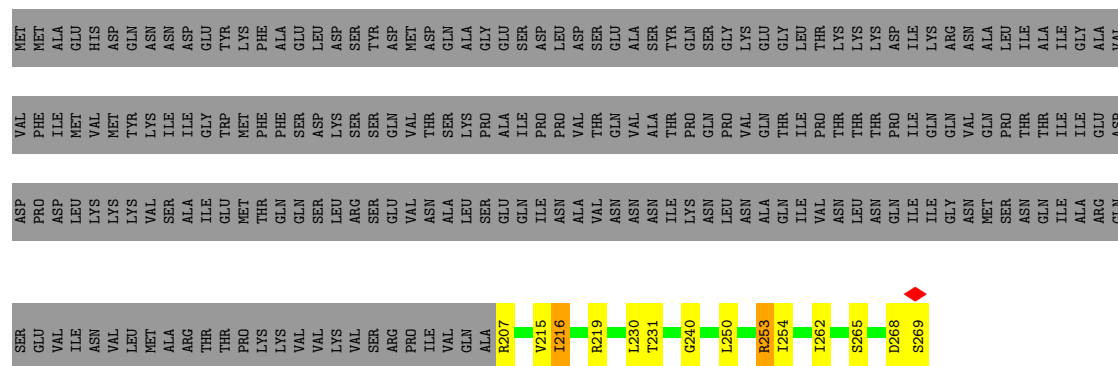
- Molecule 3: DotF

Chain Lf: 17% 2% 2% 78%

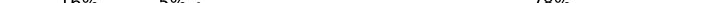


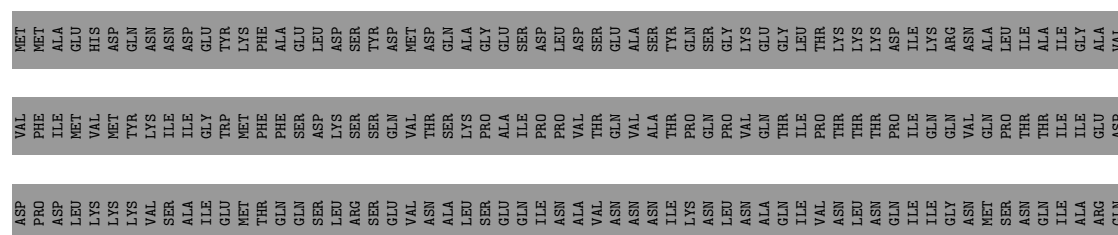
- Molecule 3: DotF

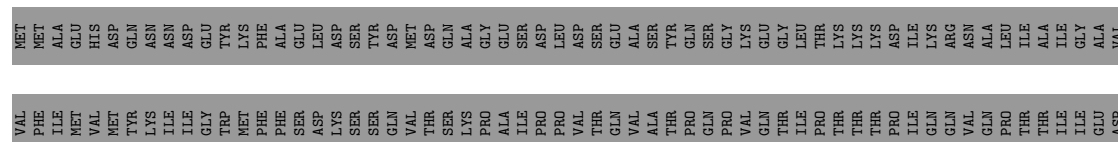
Chain MF: 18% 77%

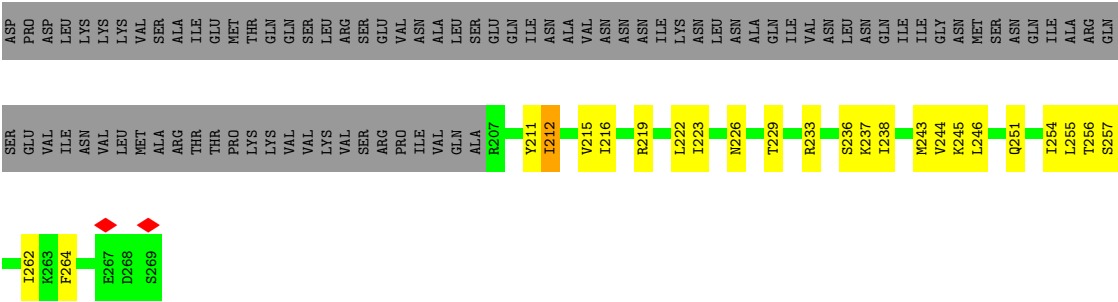


- Molecule 3: DotF

Chain Df: 



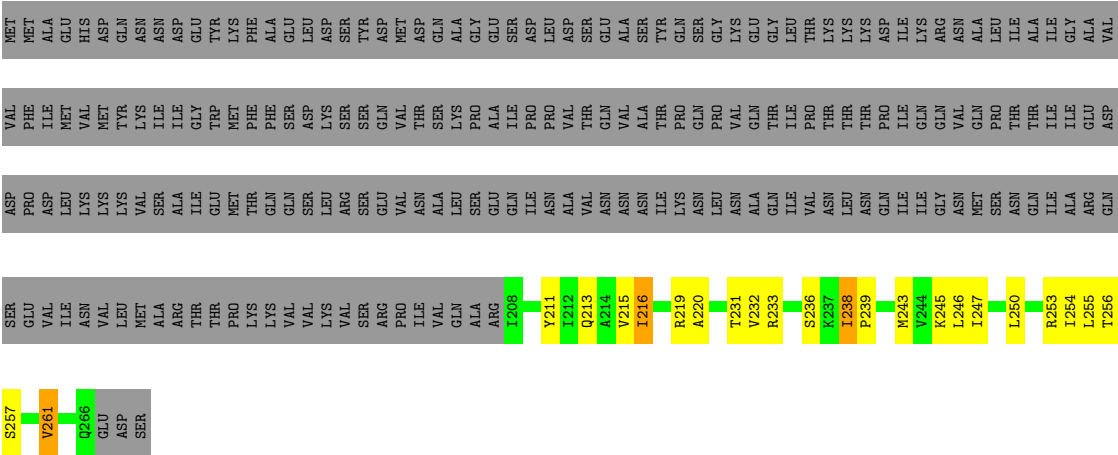




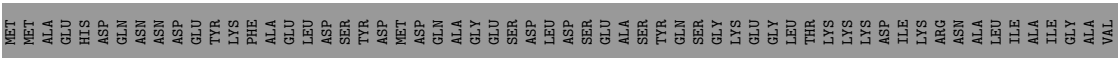
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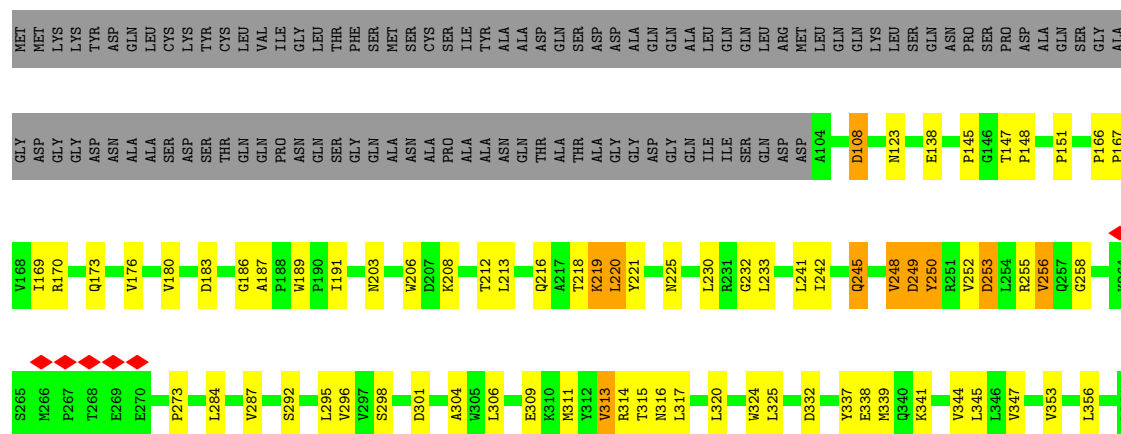
• Molecule 3: DotF



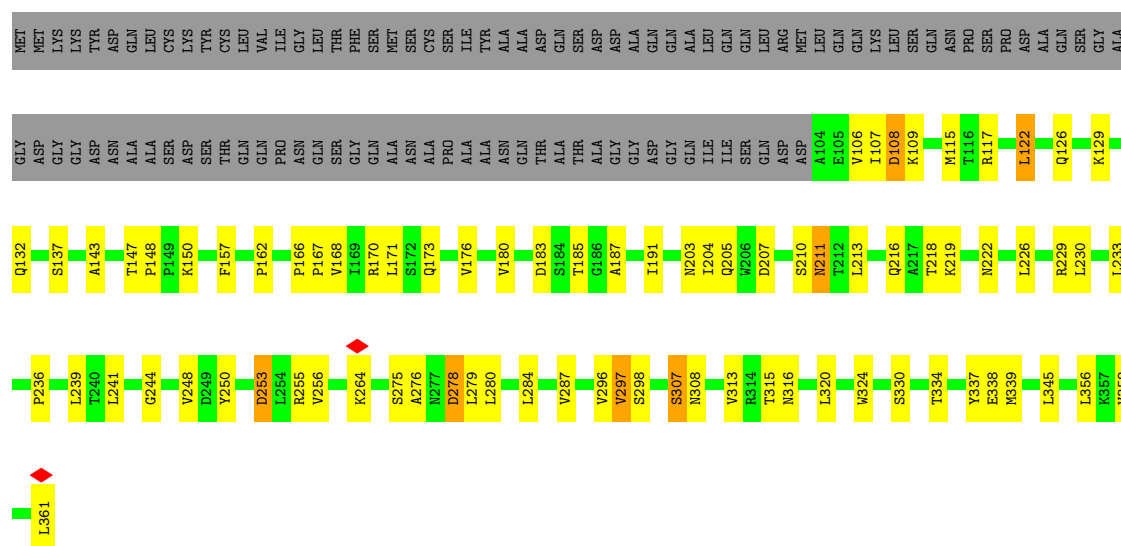
• Molecule 3: DotF



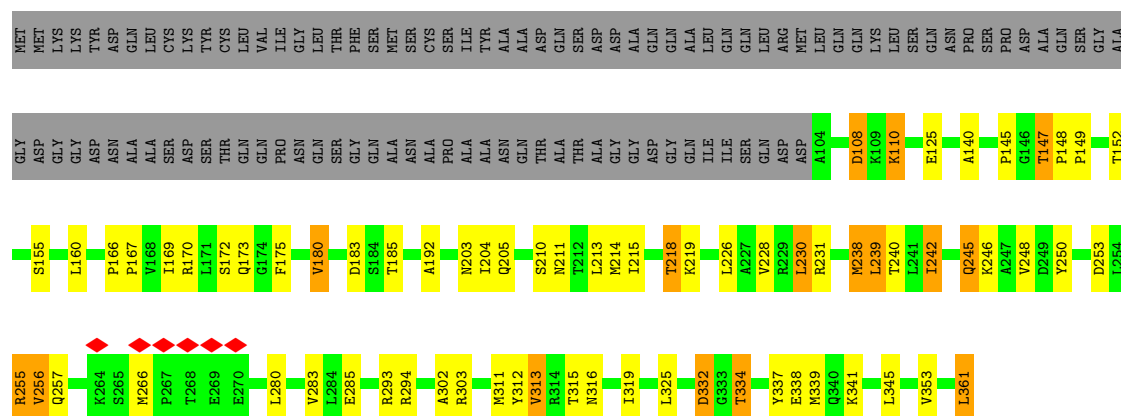




• Molecule 4: Type IV secretion protein IcmK

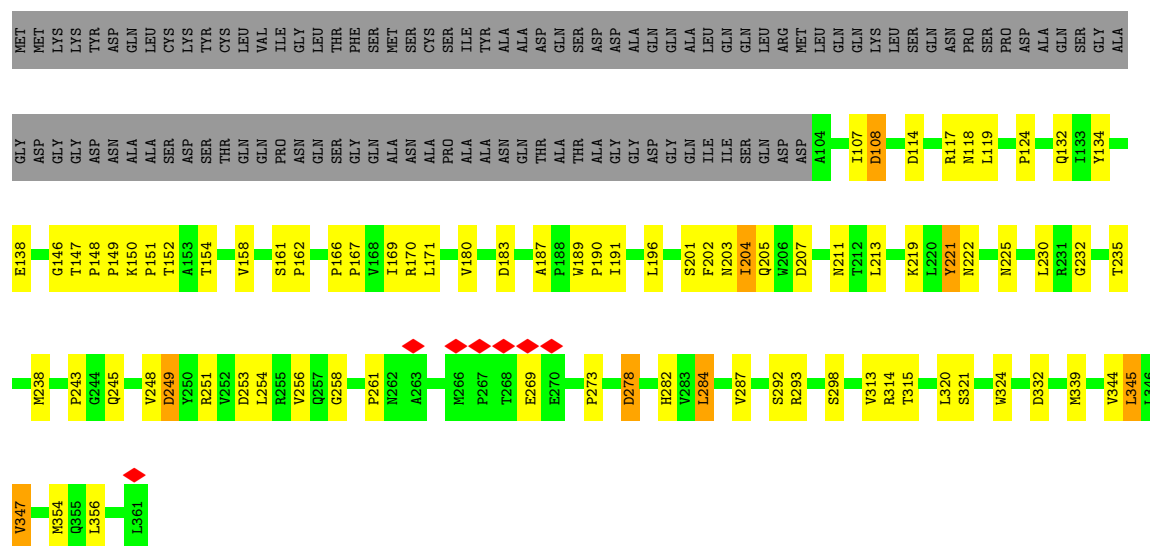


• Molecule 4: Type IV secretion protein IcmK



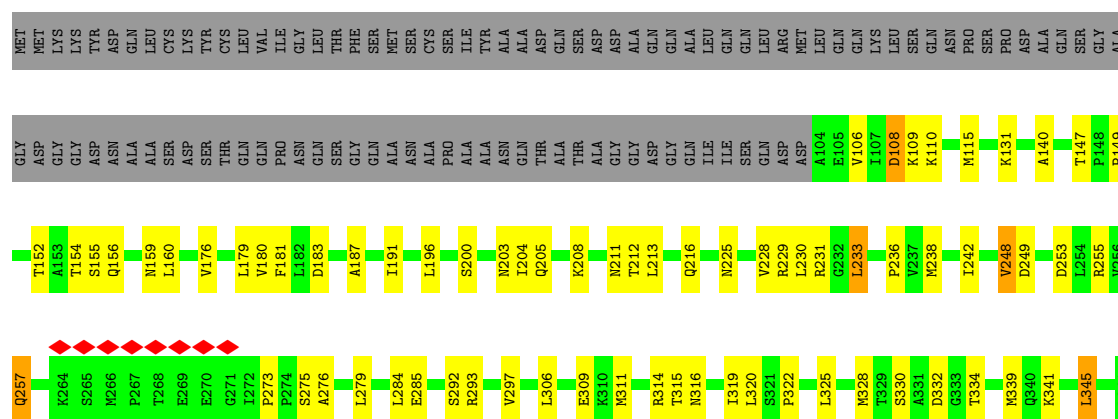
• Molecule 4: Type IV secretion protein IcmK

Chain JH: 



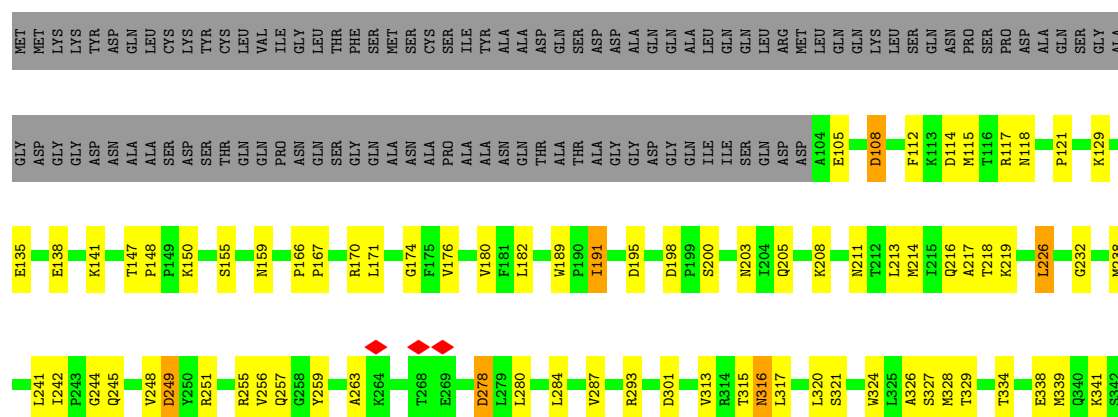
- Molecule 4: Type IV secretion protein IcmK

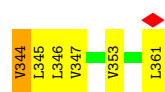
Chain AH: 



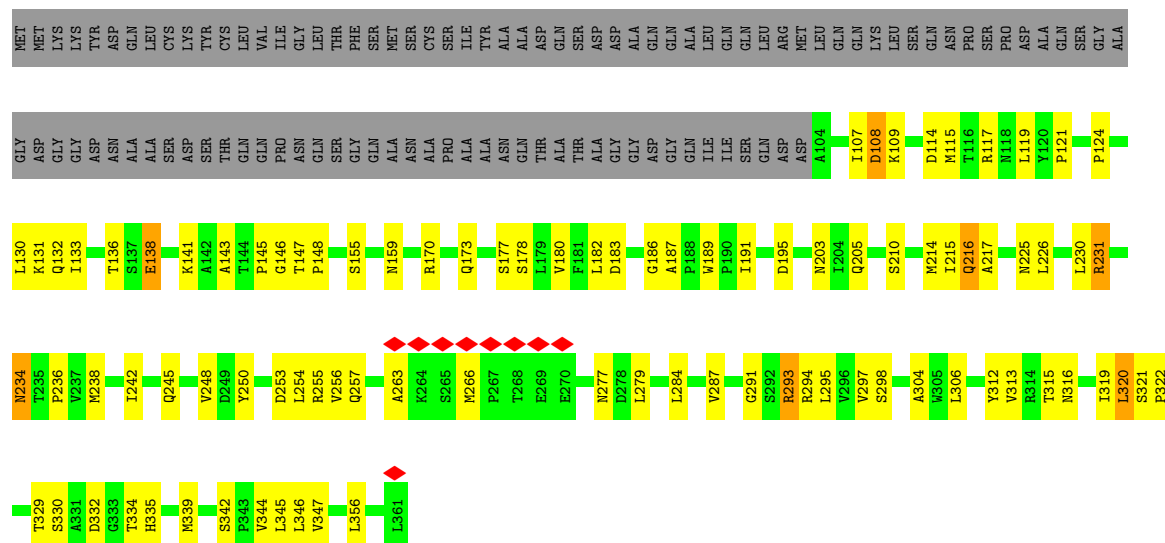
- Molecule 4: Type IV secretion protein IcmK

Chain KH: 

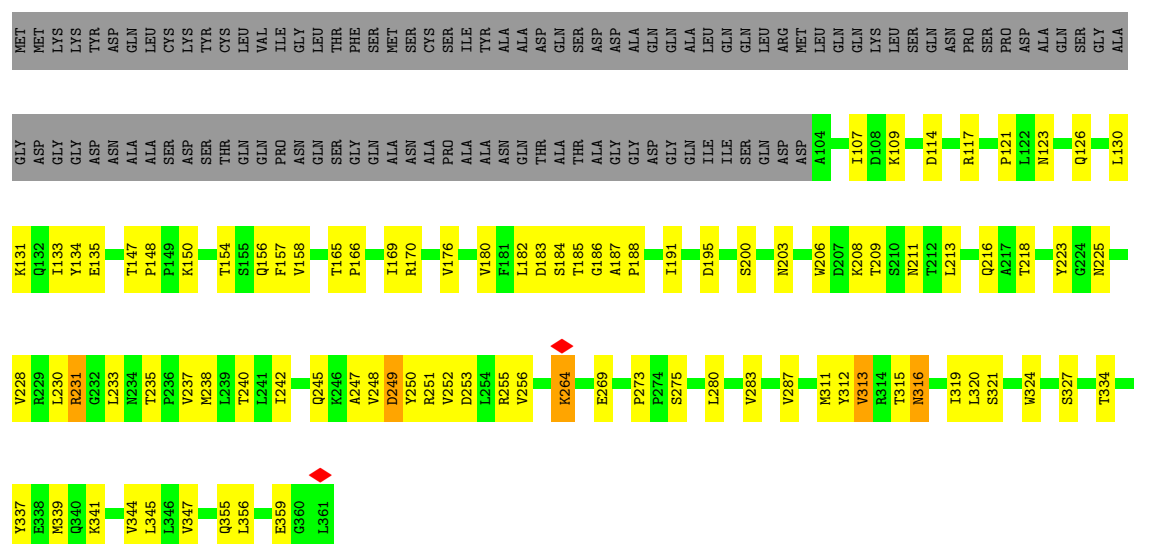




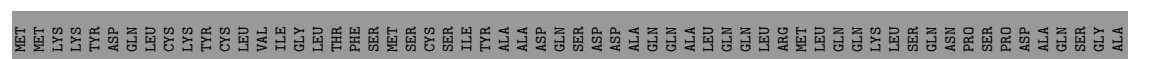
• Molecule 4: Type IV secretion protein IcmK



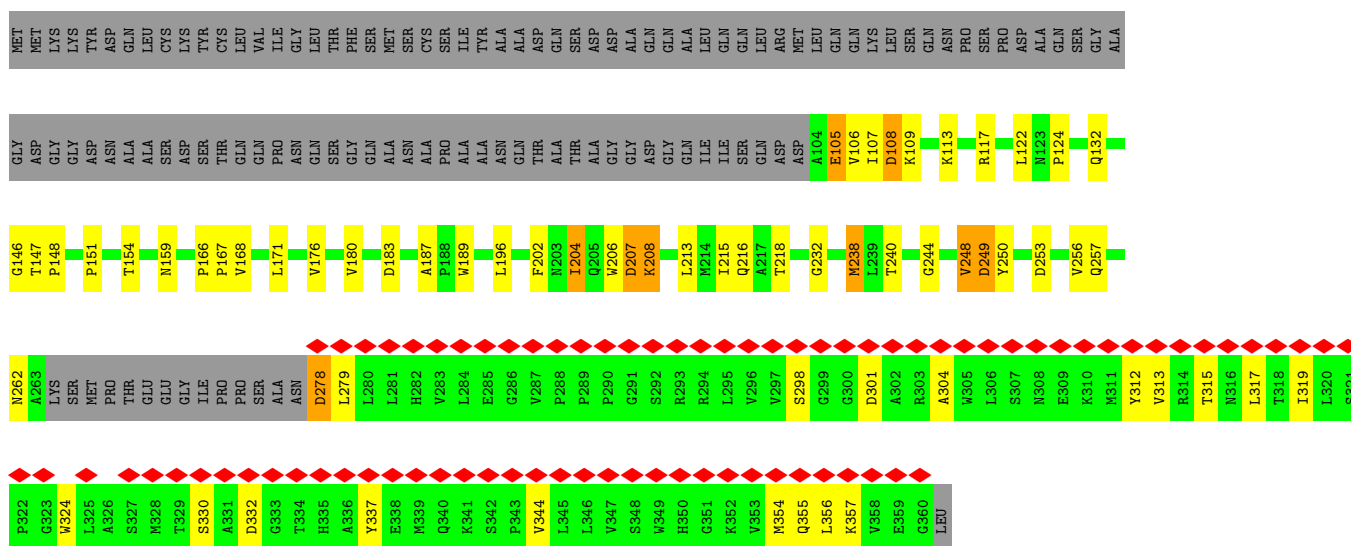
• Molecule 4: Type IV secretion protein IcmK



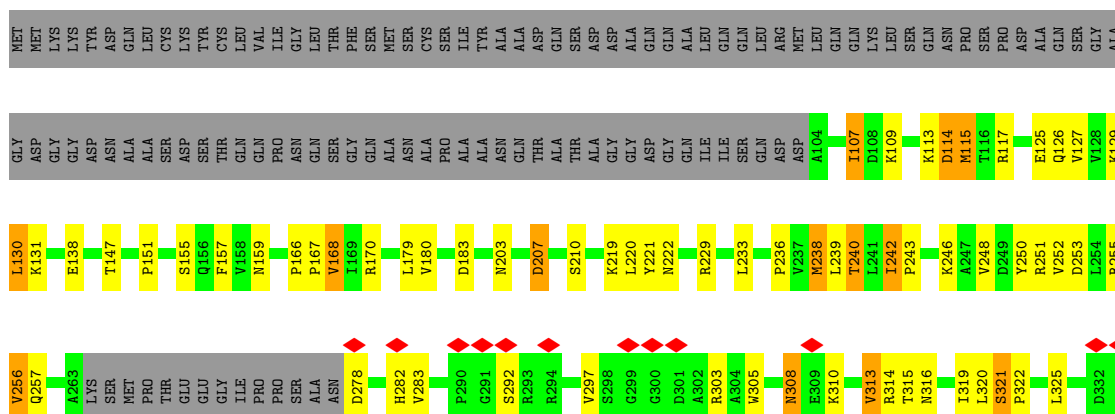
• Molecule 4: Type IV secretion protein IcmK

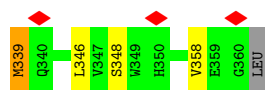


- Molecule 4: Type IV secretion protein IcmK

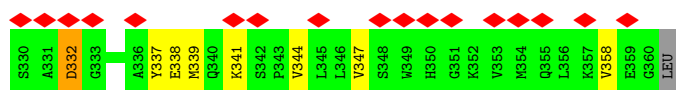
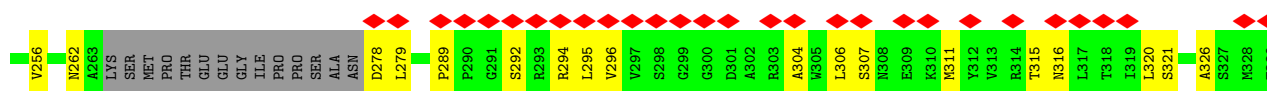
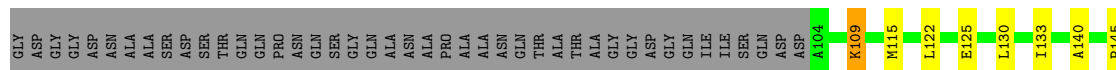
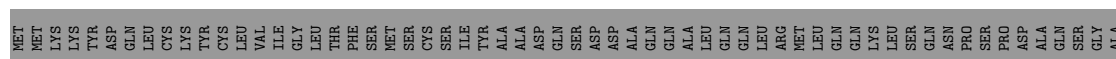


- Molecule 4: Type IV secretion protein IcmK

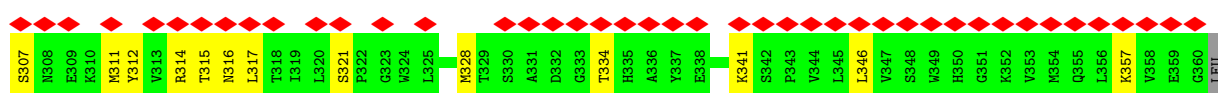
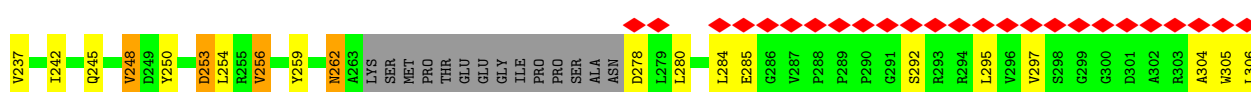
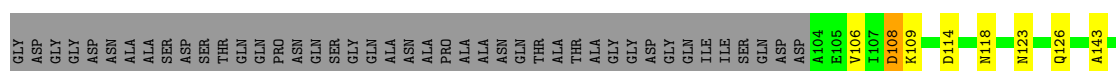




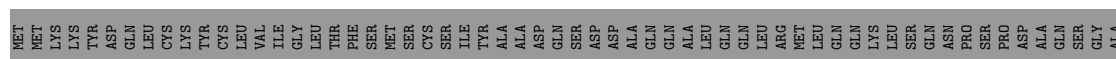
• Molecule 4: Type IV secretion protein IcmK

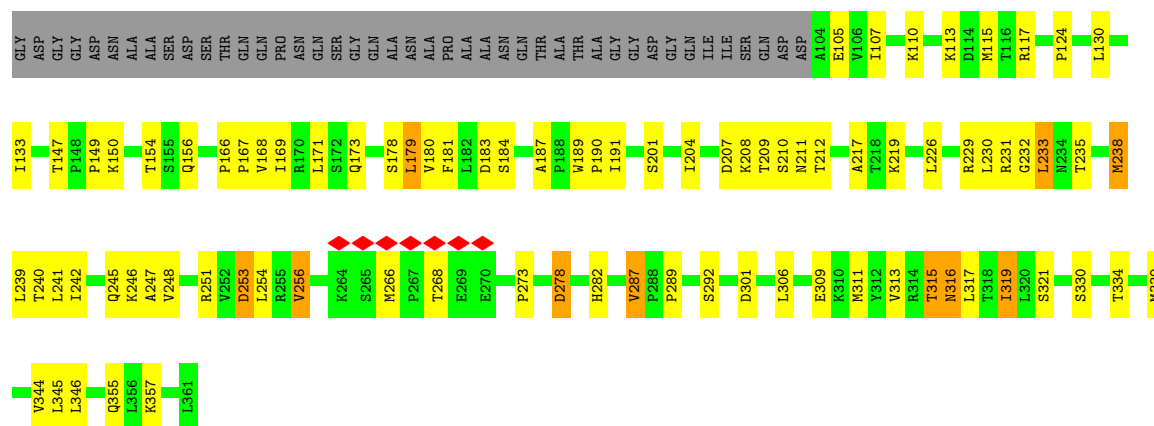


• Molecule 4: Type IV secretion protein IcmK

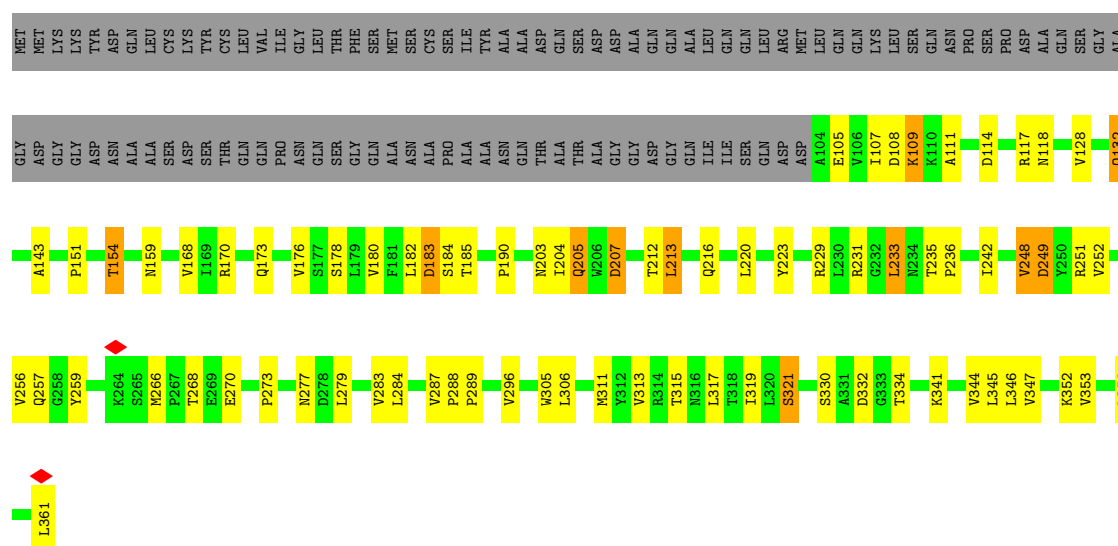


• Molecule 4: Type IV secretion protein IcmK

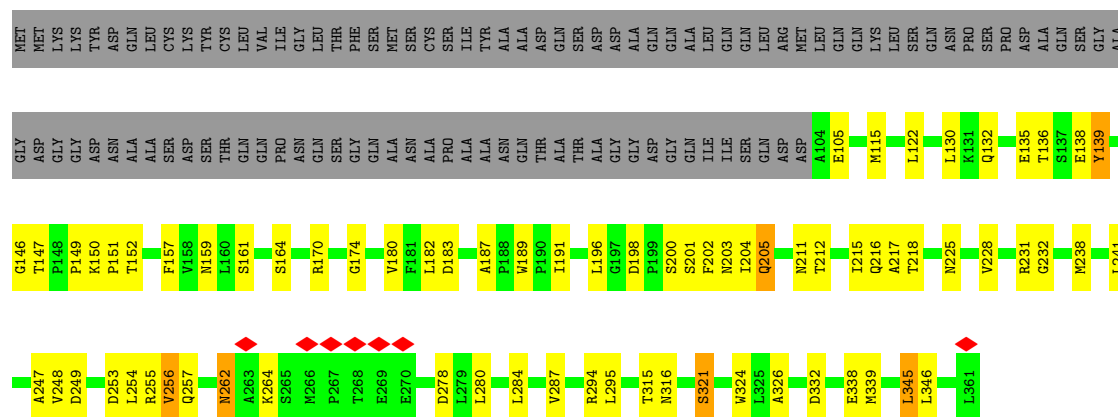




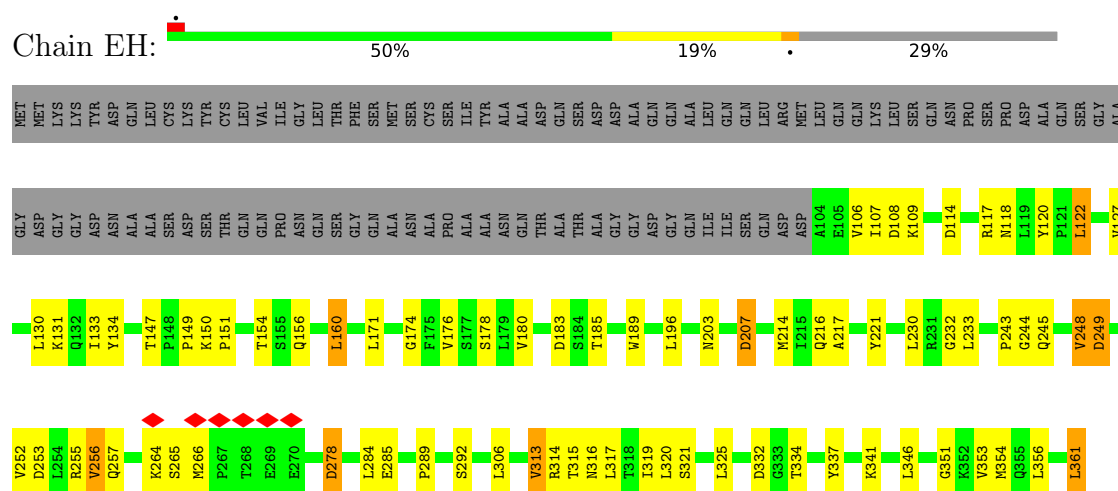
• Molecule 4: Type IV secretion protein IcmK



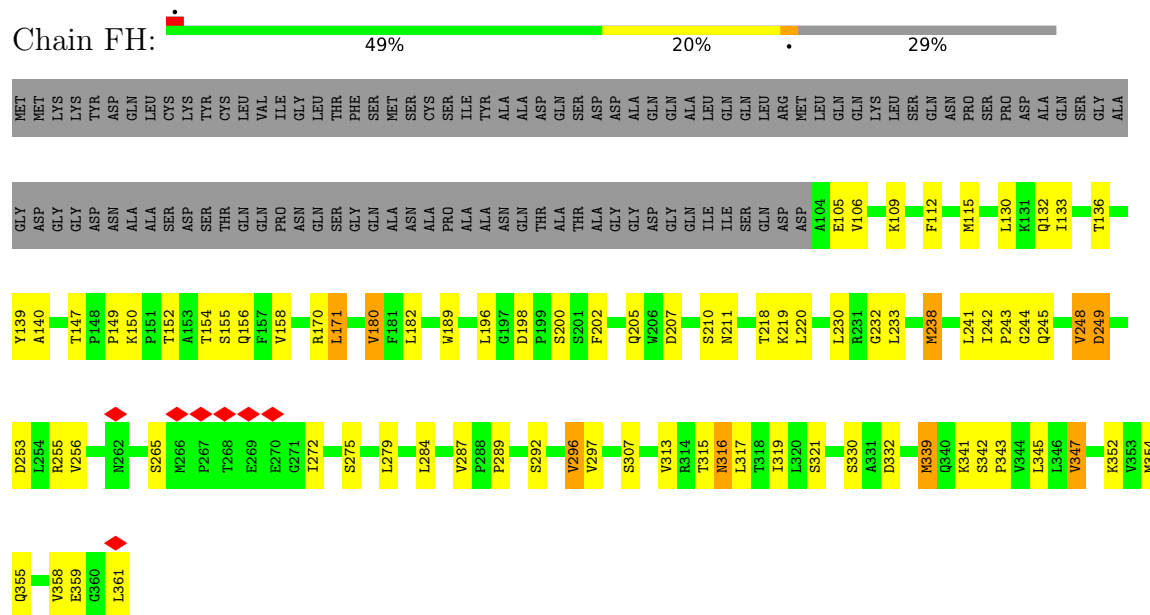
• Molecule 4: Type IV secretion protein IcmK



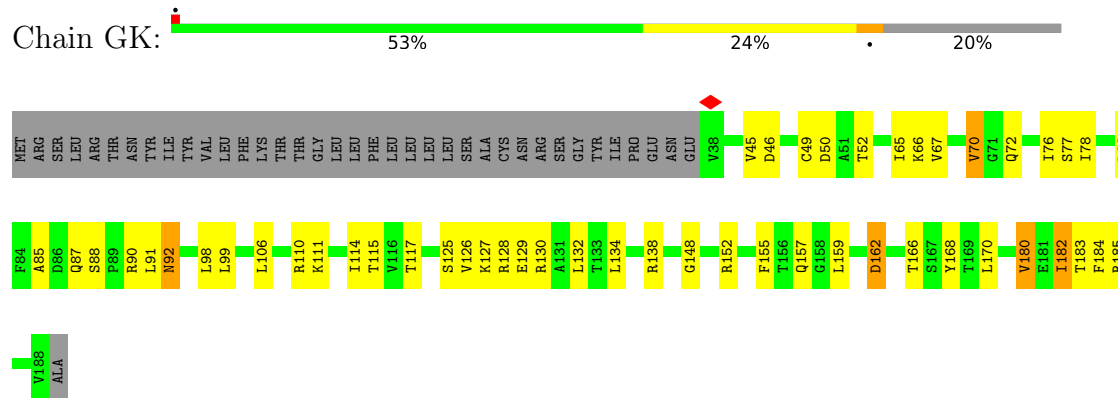
• Molecule 4: Type IV secretion protein IcmK



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• Molecule 5: Inner membrane lipoprotein YiaD

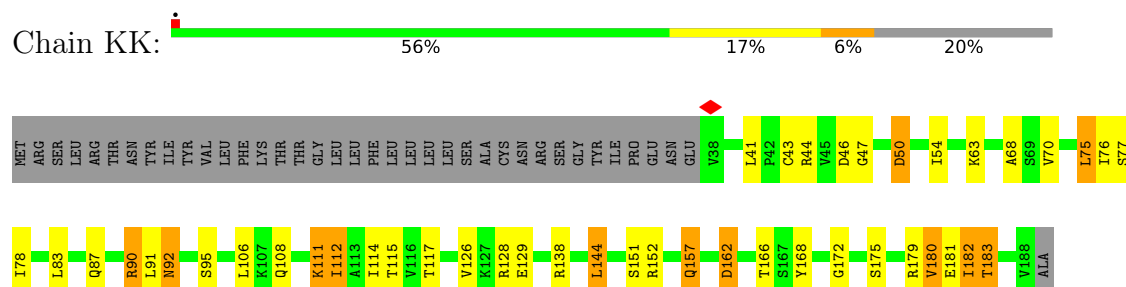


• Molecule 5: Inner membrane lipoprotein YiaD

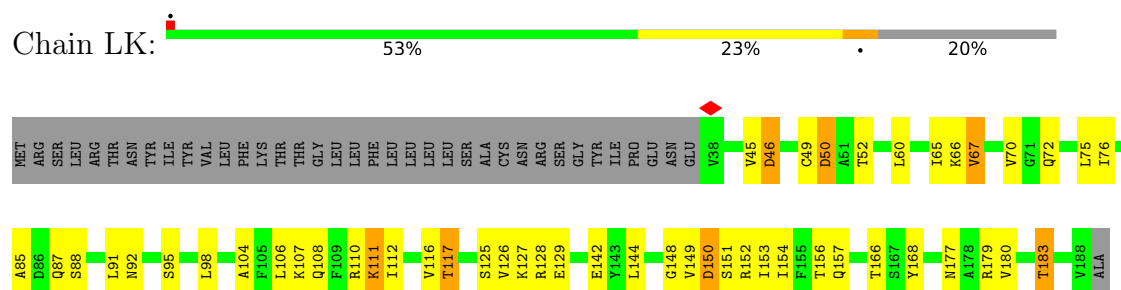
- Molecule 5: Inner membrane lipoprotein YiaD

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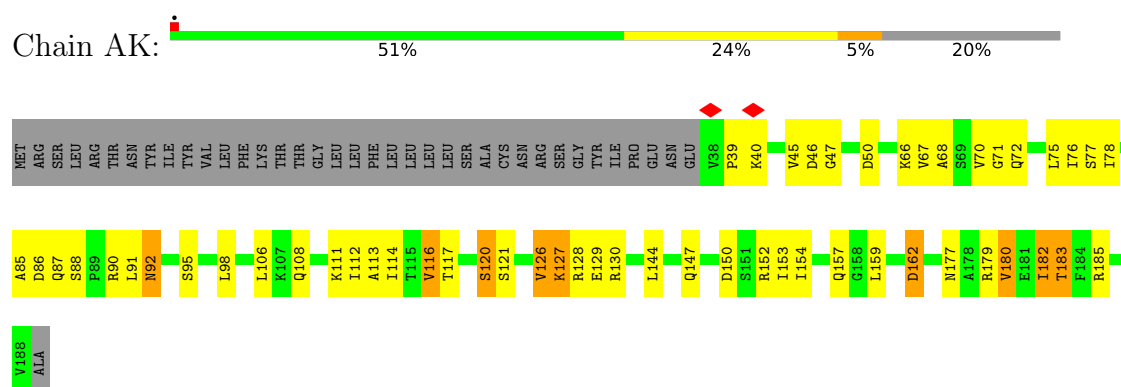
- Molecule 5: Inner membrane lipoprotein YiaD



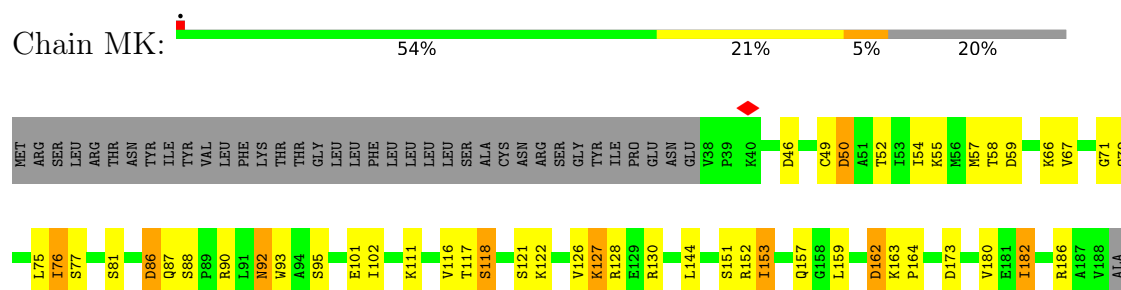
- Molecule 5: Inner membrane lipoprotein YiaD



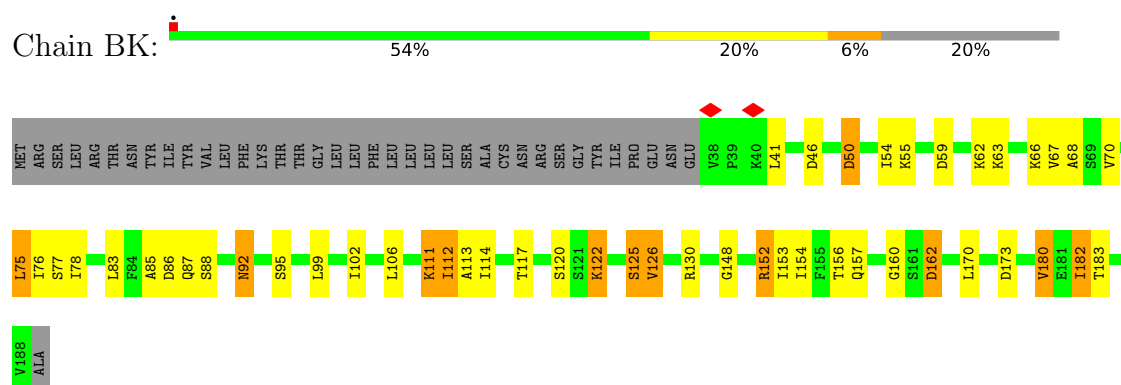
- Molecule 5: Inner membrane lipoprotein YiaD



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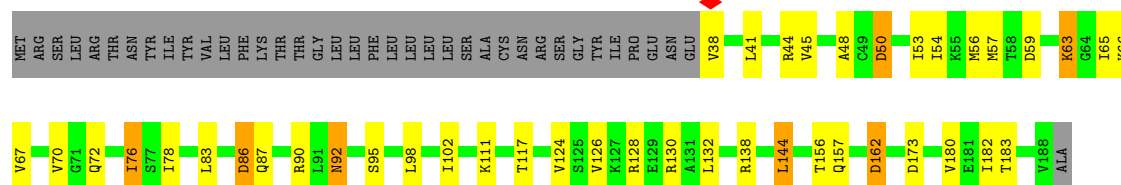


- Molecule 5: Inner membrane lipoprotein YiaD



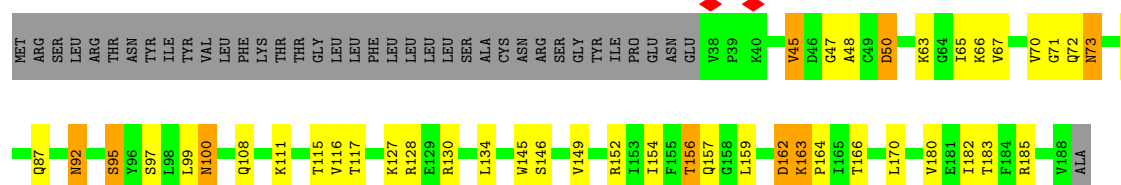
- Molecule 5: Inner membrane lipoprotein YiaD

Chain CK: 



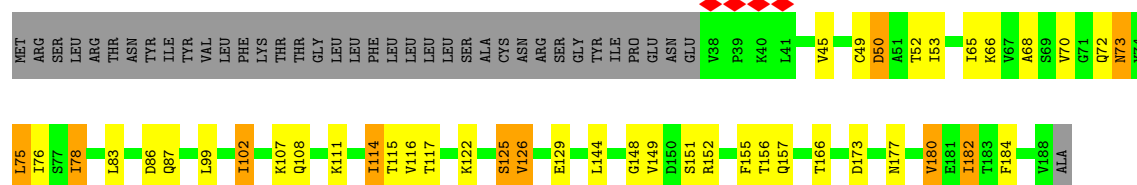
• Molecule 5: Inner membrane lipoprotein YiaD

Chain DK: 



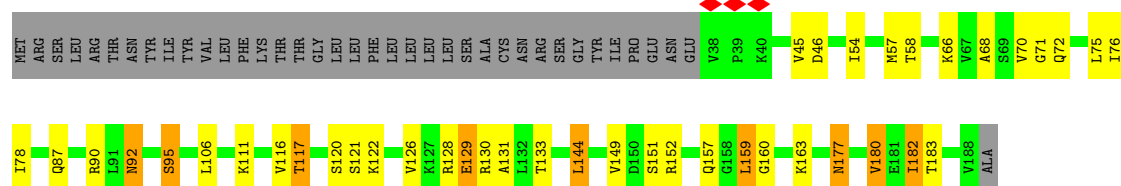
• Molecule 5: Inner membrane lipoprotein YiaD

Chain EK: 



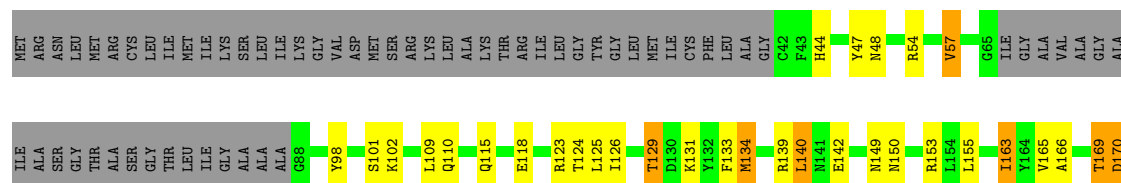
• Molecule 5: Inner membrane lipoprotein YiaD

Chain FK: 



• Molecule 6: Outer membrane protein, OmpA family protein

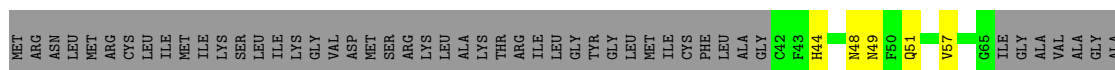
Chain GL: 





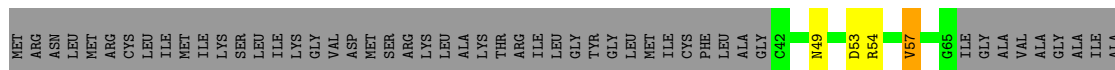
- Molecule 6: Outer membrane protein, OmpA family protein

Chain HL: 51% 16% 31%



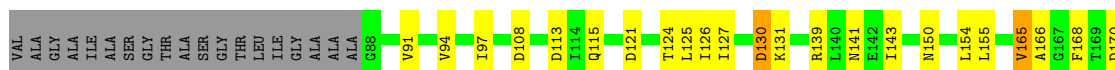
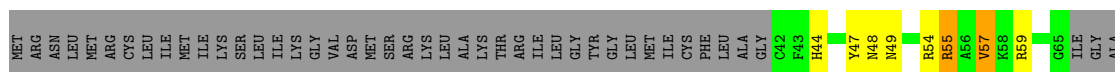
- Molecule 6: Outer membrane protein, OmpA family protein

Chain IL: 52% 15% 31%



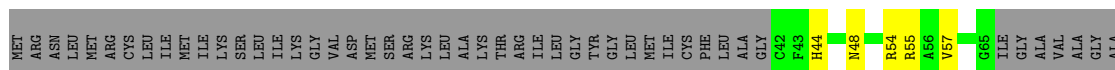
- Molecule 6: Outer membrane protein, OmpA family protein

Chain JL: 48% 19% 31%



- Molecule 6: Outer membrane protein, OmpA family protein

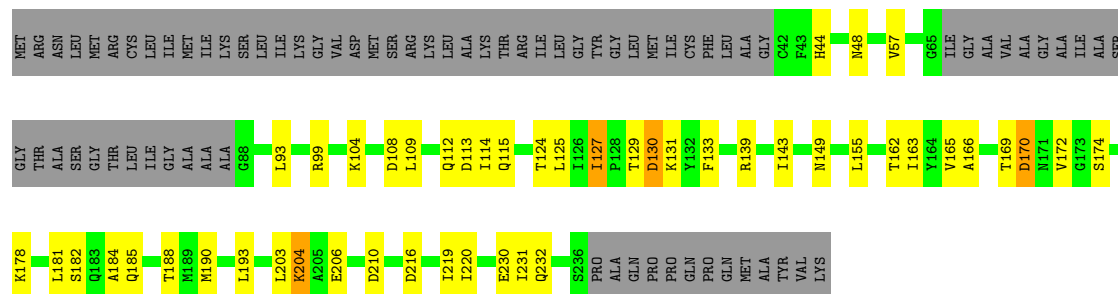
Chain KL: 50% 17% 31%





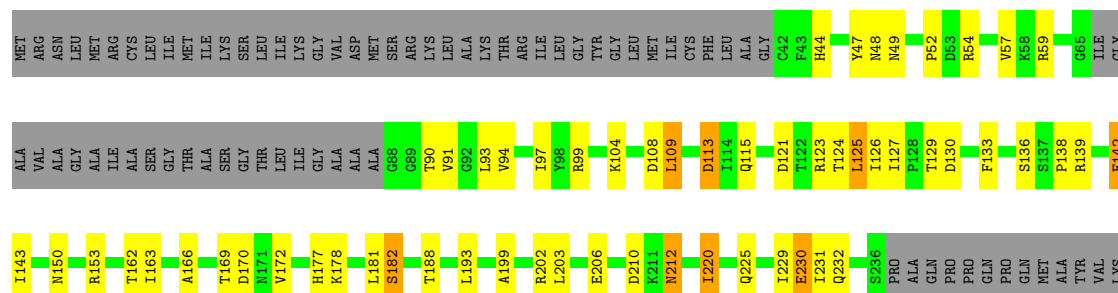
- Molecule 6: Outer membrane protein, OmpA family protein

Chain LL: 50% 18% 31%



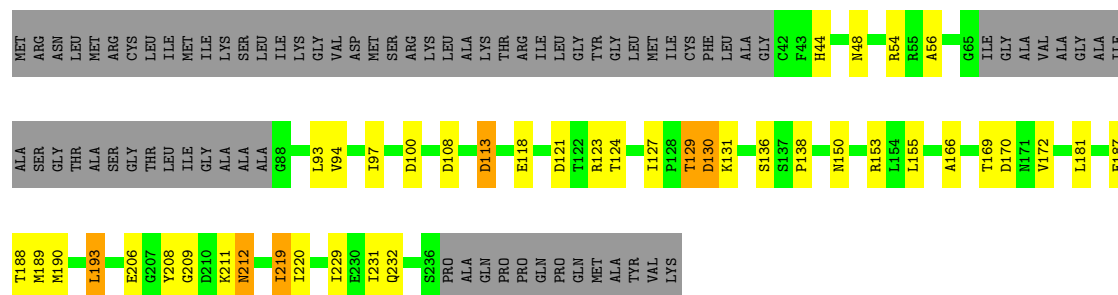
- Molecule 6: Outer membrane protein, OmpA family protein

Chain ML: 46% 20% 31%



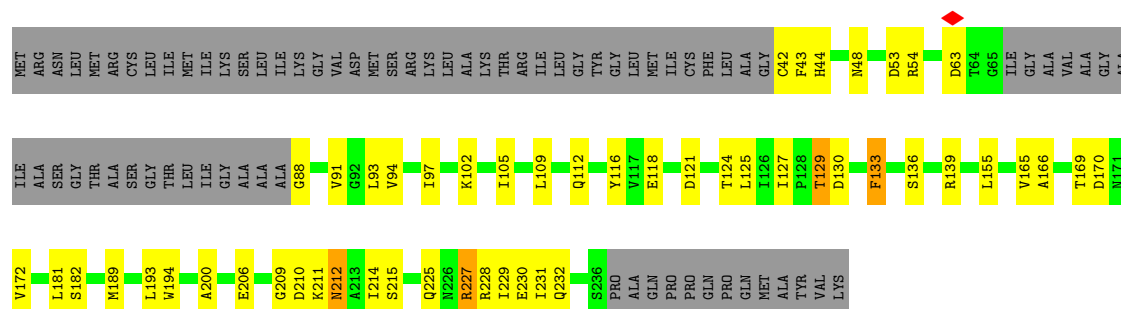
- Molecule 6: Outer membrane protein, OmpA family protein

Chain AL: 52% 15% 31%



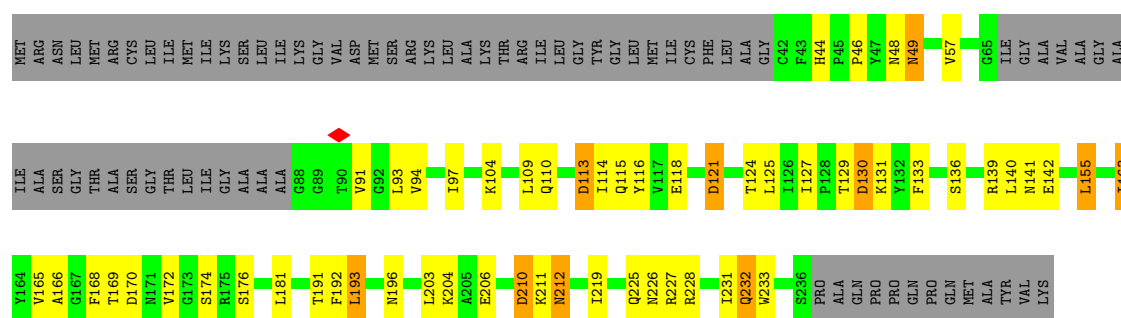
- Molecule 6: Outer membrane protein, OmpA family protein

Chain BL: 48% 20% 31%



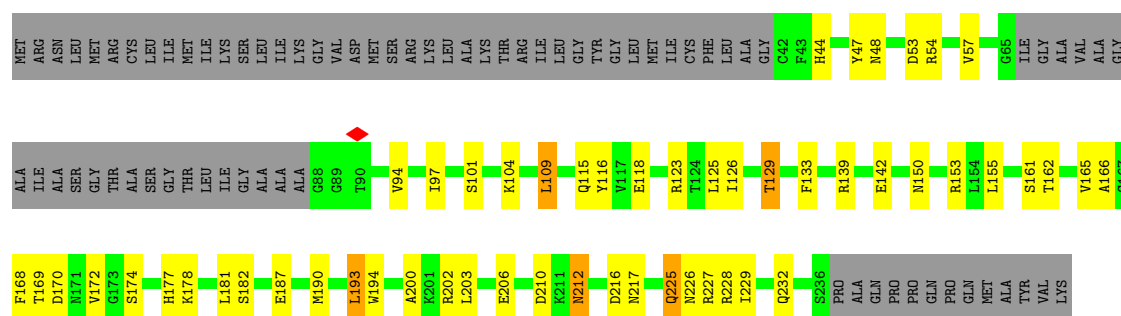
- Molecule 6: Outer membrane protein, OmpA family protein

Chain CL: 46% 20% . 31%



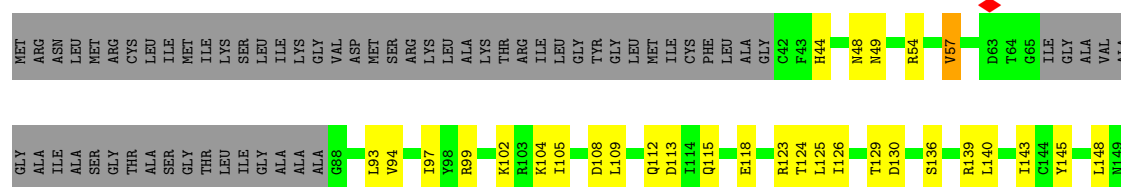
- Molecule 6: Outer membrane protein, OmpA family protein

Chain DL: 47% 20% . 31%



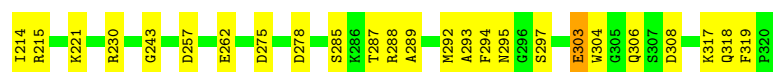
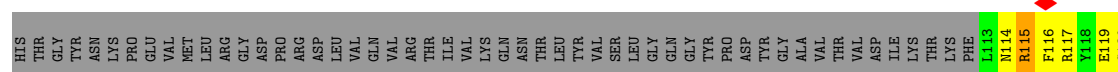
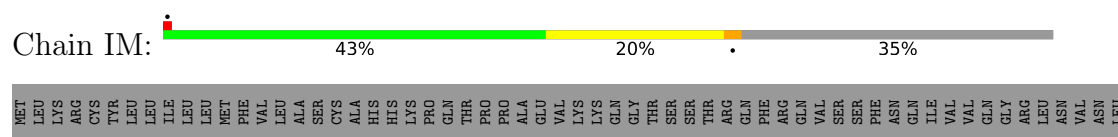
- Molecule 6: Outer membrane protein, OmpA family protein

Chain EL: 47% 20% . 31%

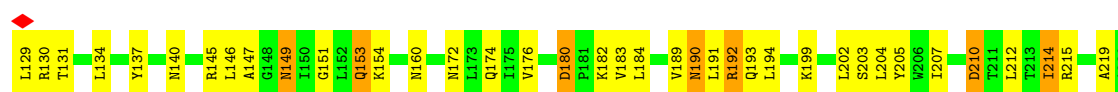
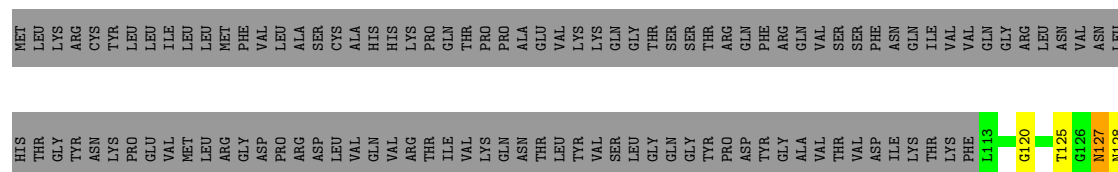




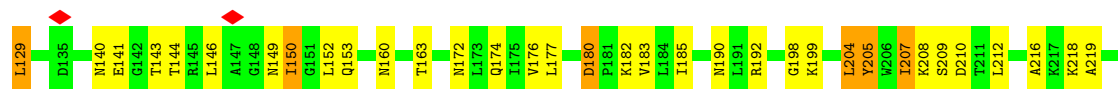
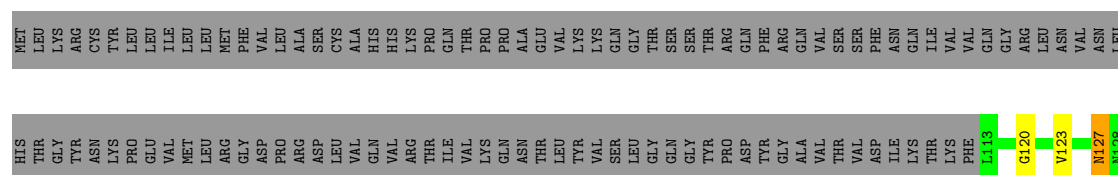
• Molecule 7: DUF2807 domain-containing protein



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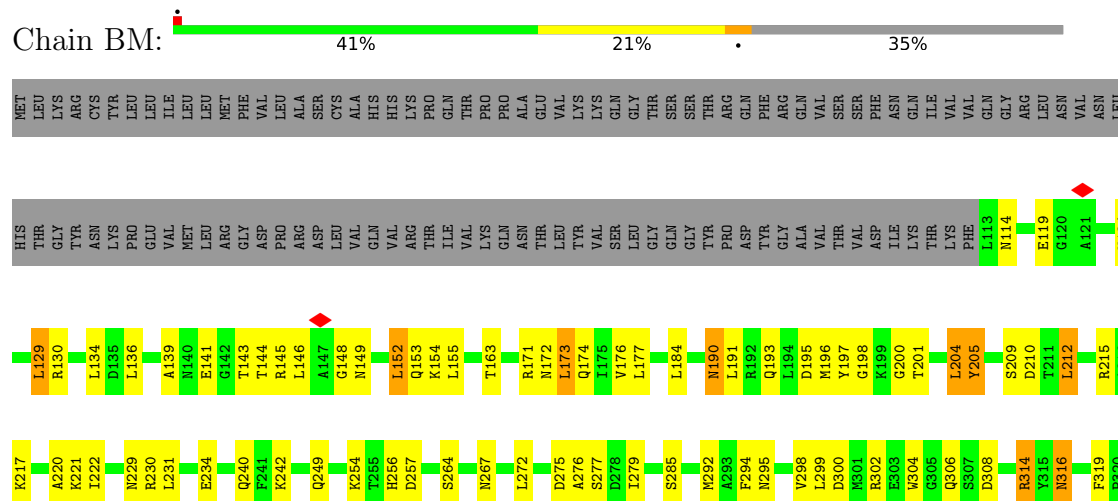


• Molecule 7: DUF2807 domain-containing protein

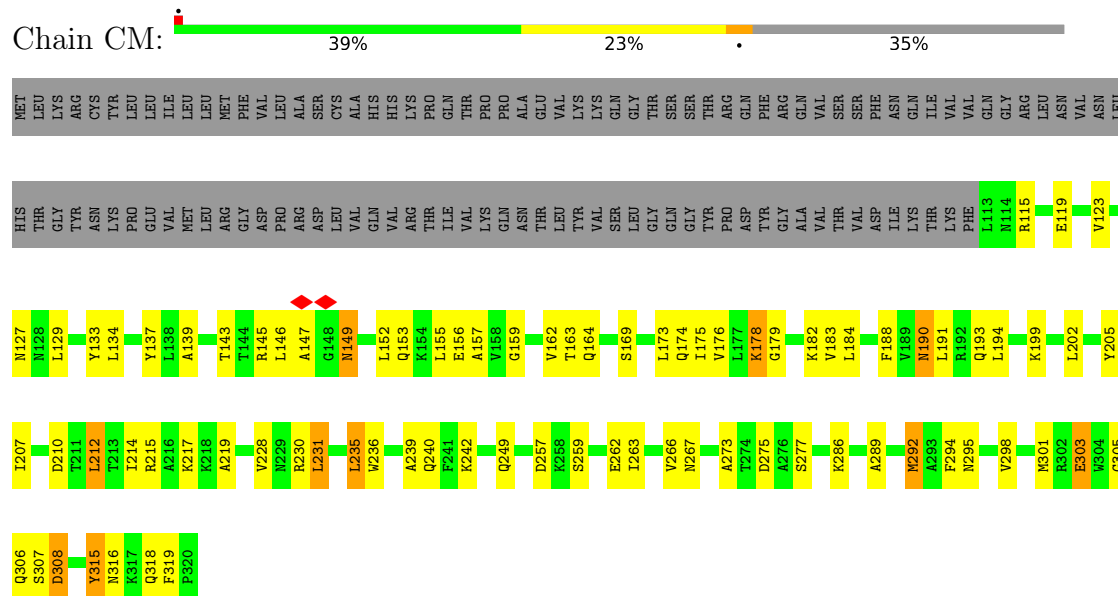




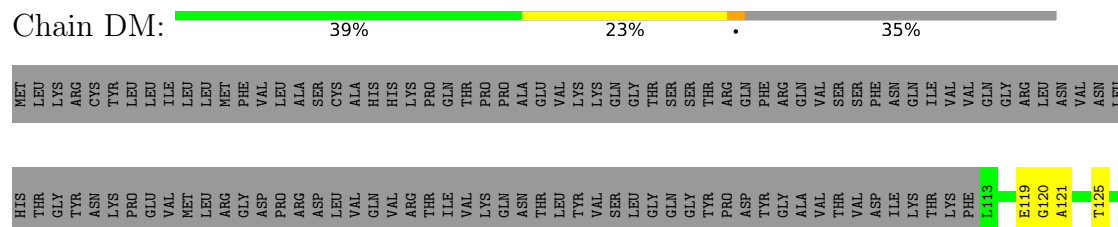
• Molecule 7: DUF2807 domain-containing protein

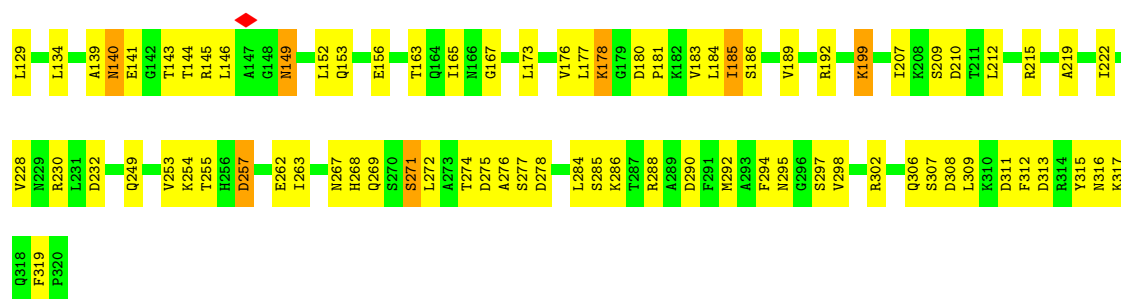


• Molecule 7: DUF2807 domain-containing protein

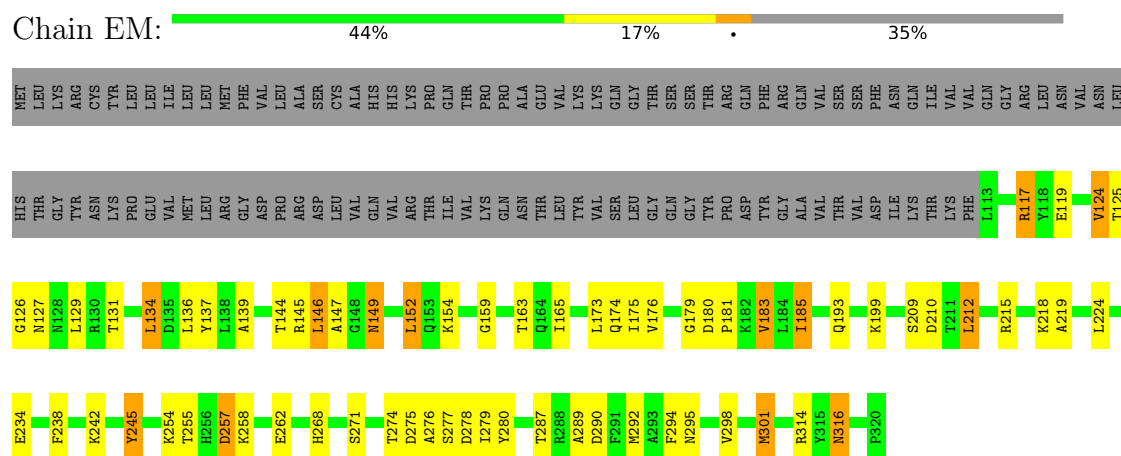


• Molecule 7: DUF2807 domain-containing protein

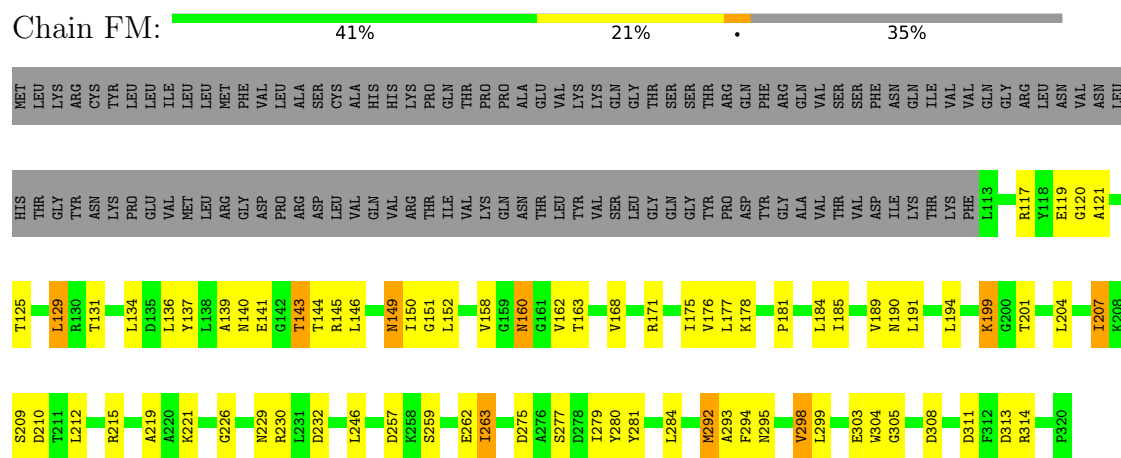




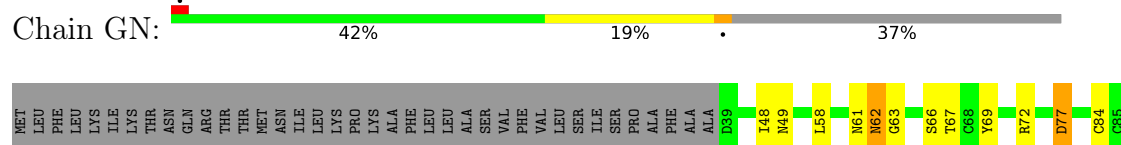
- Molecule 7: DUF2807 domain-containing protein



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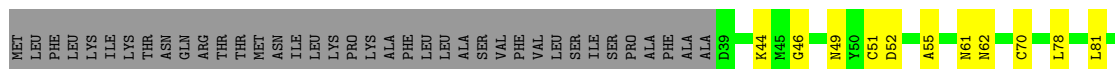


- Molecule 8: Neurogenic locus notch

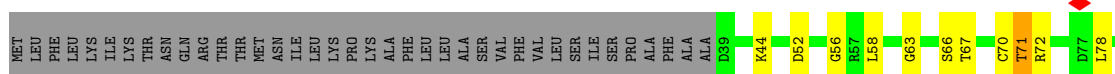




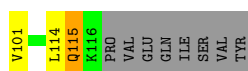
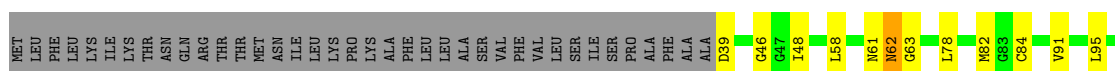
- Molecule 8: Neurogenic locus notch



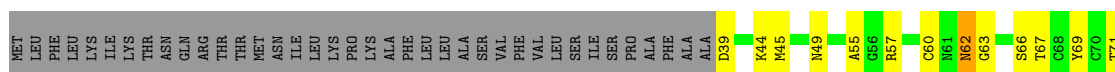
- Molecule 8: Neurogenic locus notch



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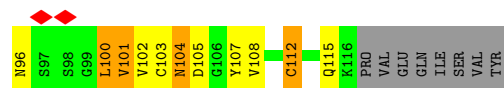
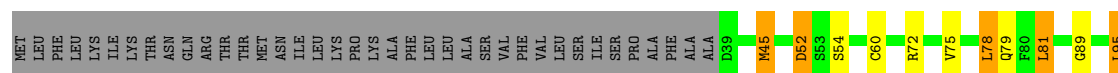


- Molecule 8: Neurogenic locus notch

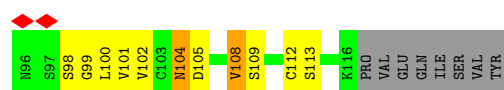
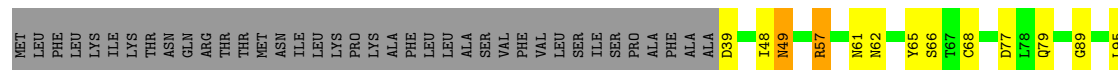


- Molecule 8: Neurogenic locus notch

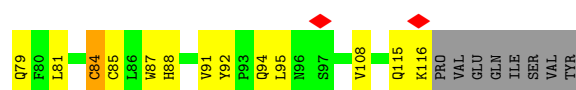
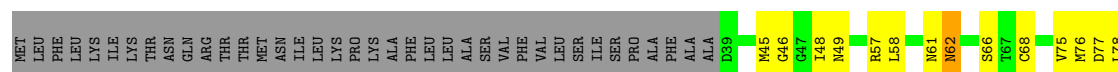




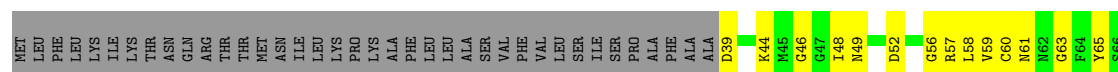
- Molecule 8: Neurogenic locus notch



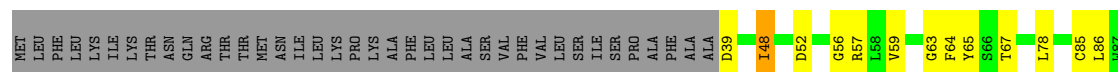
- Molecule 8: Neurogenic locus notch



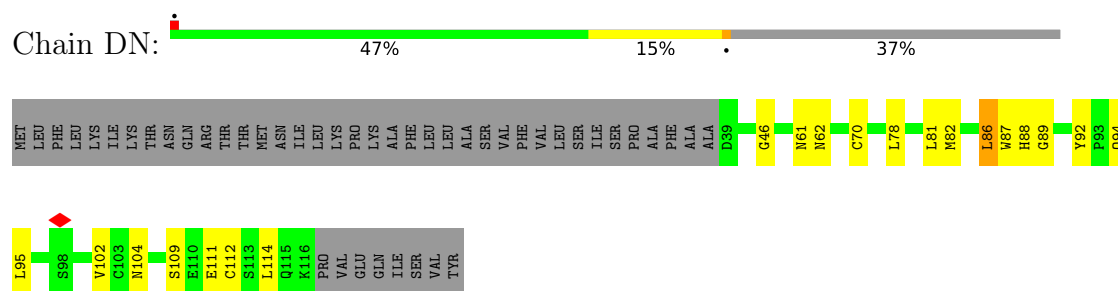
- Molecule 8: Neurogenic locus notch



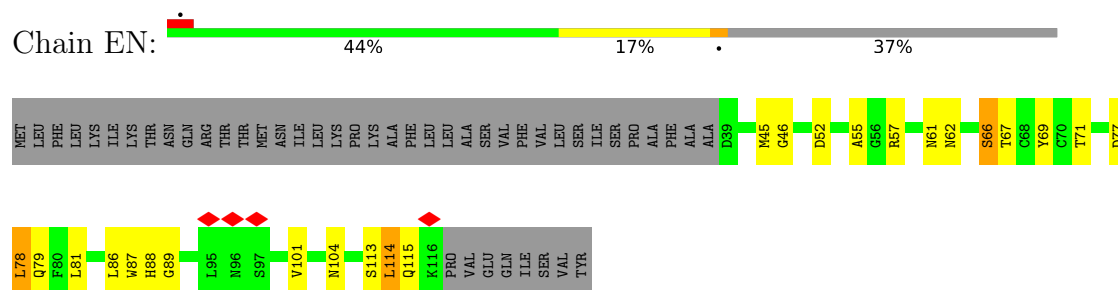
- Molecule 8: Neurogenic locus notch



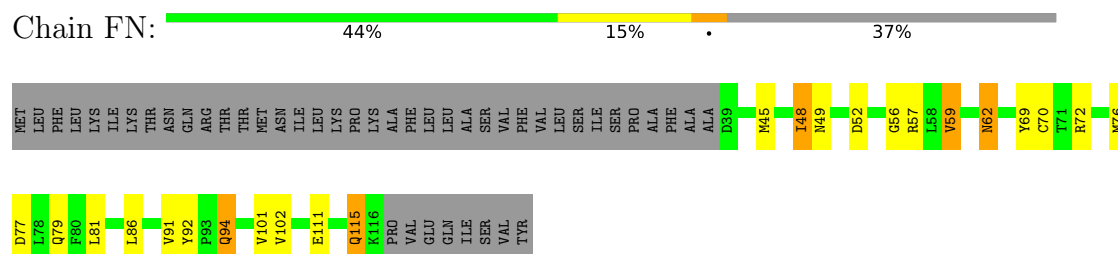
- Molecule 8: Neurogenic locus notch



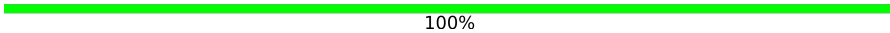
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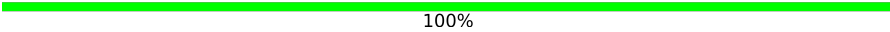


- Molecule 9: Unknown protein fragment

Chain GU:  100%

There are no outlier residues recorded for this chain.

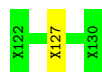
- Molecule 9: Unknown protein fragment

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:  100%

There are no outlier residues recorded for this chain.

- Molecule 9: Unknown protein fragment

Chain KU:  89% 11%



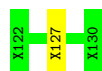
- Molecule 9: Unknown protein fragment

Chain LU:  78% 22%



- Molecule 9: Unknown protein fragment

Chain MU:  89% 11%



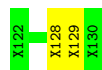
- Molecule 9: Unknown protein fragment

Chain AU:  78% 22%



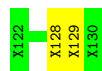
- Molecule 9: Unknown protein fragment

Chain BU:  78% 22%



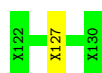
- Molecule 9: Unknown protein fragment

Chain CU:  78% 22%



- Molecule 9: Unknown protein fragment

Chain DU:  89% 11%



- Molecule 9: Unknown protein fragment

Chain EU: 100%

There are no outlier residues recorded for this chain.

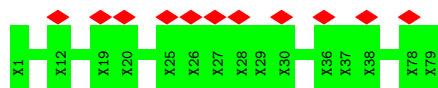
- Molecule 9: Unknown protein fragment

Chain FU: 100%

There are no outlier residues recorded for this chain.

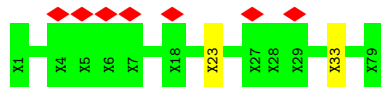
- Molecule 10: Unknown protein fragment

Chain GX: 23% 100%



- Molecule 10: Unknown protein fragment

Chain HX: 15% 96%



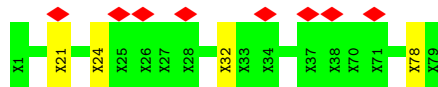
- Molecule 10: Unknown protein fragment

Chain IX: 10% 96%



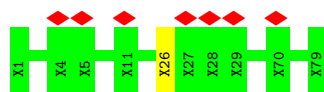
- Molecule 10: Unknown protein fragment

Chain JX: 17% 92% 8%

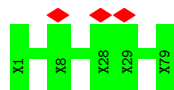


- Molecule 10: Unknown protein fragment

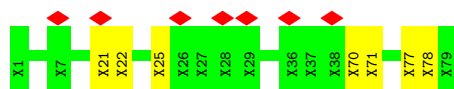
Chain KX: 15% 98%



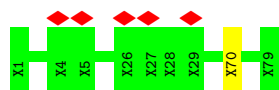
- Molecule 10: Unknown protein fragment



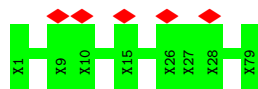
- Molecule 10: Unknown protein fragment



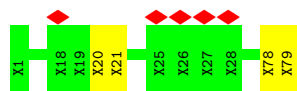
- Molecule 10: Unknown protein fragment



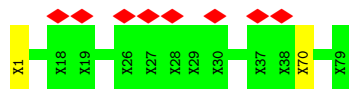
- Molecule 10: Unknown protein fragment



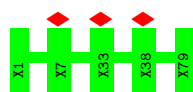
- Molecule 10: Unknown protein fragment



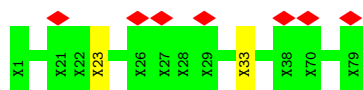
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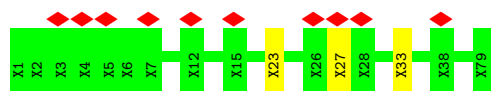
- Molecule 10: Unknown protein fragment



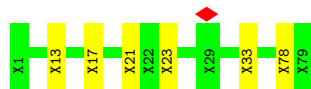
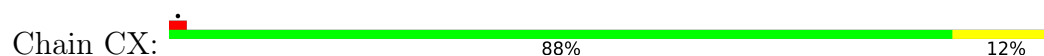
- Molecule 10: Unknown protein fragment



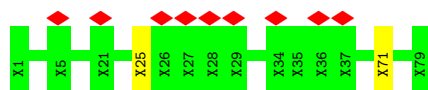
- Molecule 10: Unknown protein fragment



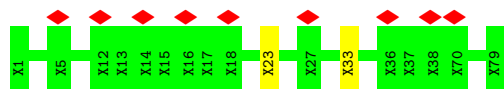
- Molecule 10: Unknown protein fragment



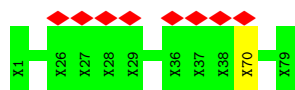
- Molecule 10: Unknown protein fragment



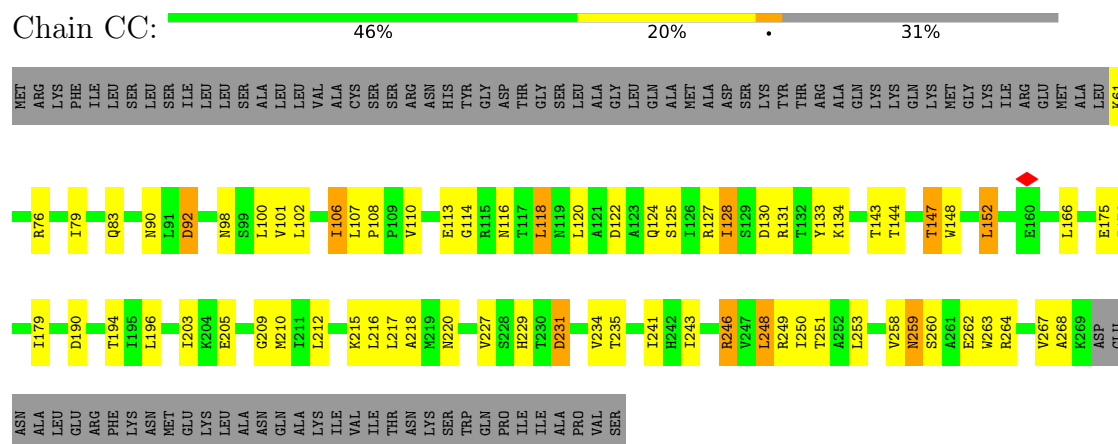
- Molecule 10: Unknown protein fragment



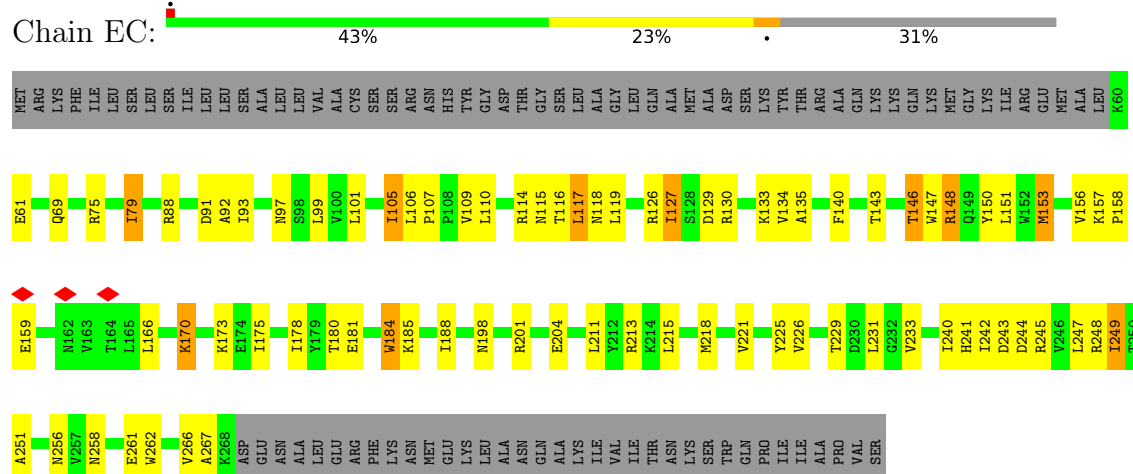
- Molecule 10: Unknown protein fragment



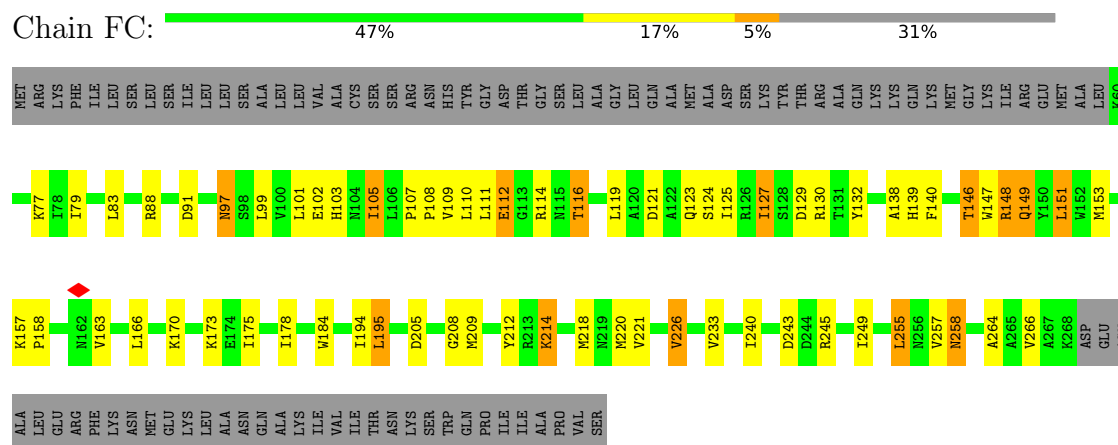
- Molecule 11: DotC



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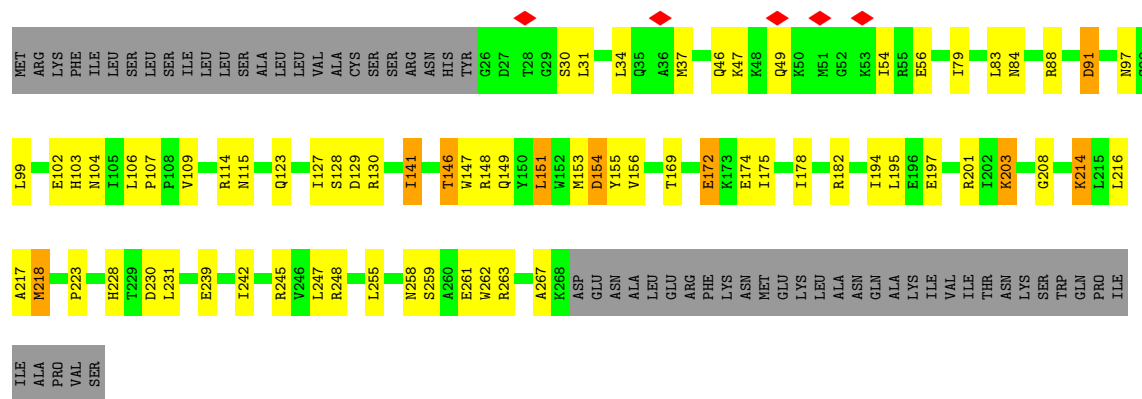


- Molecule 11: DotC



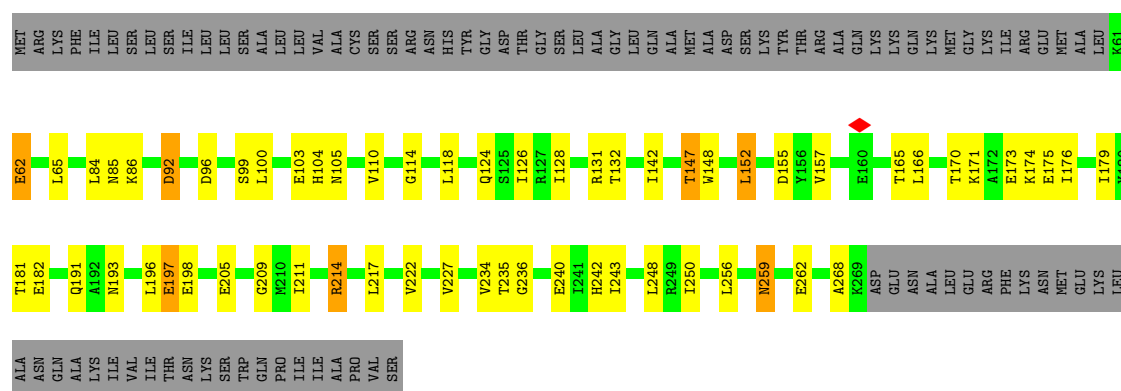
- Molecule 11: DotC





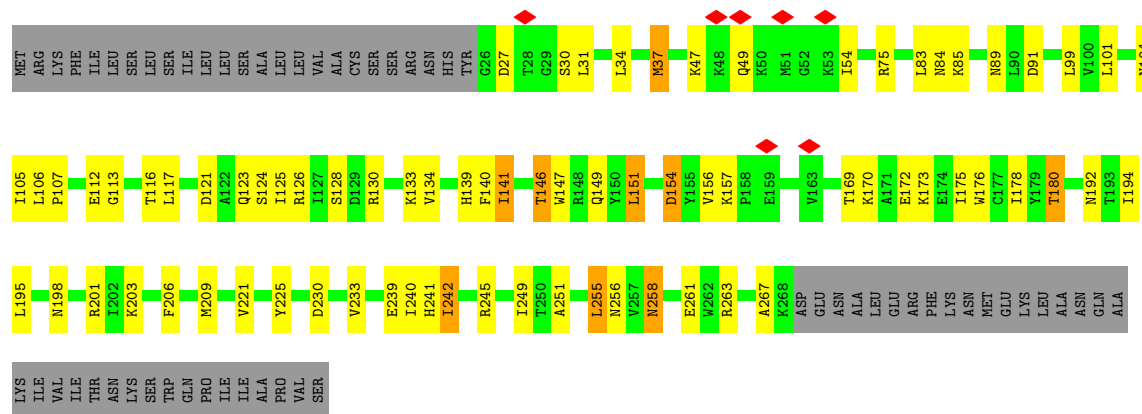
• Molecule 11: DotC

Chain GC: 49% 18% 31%



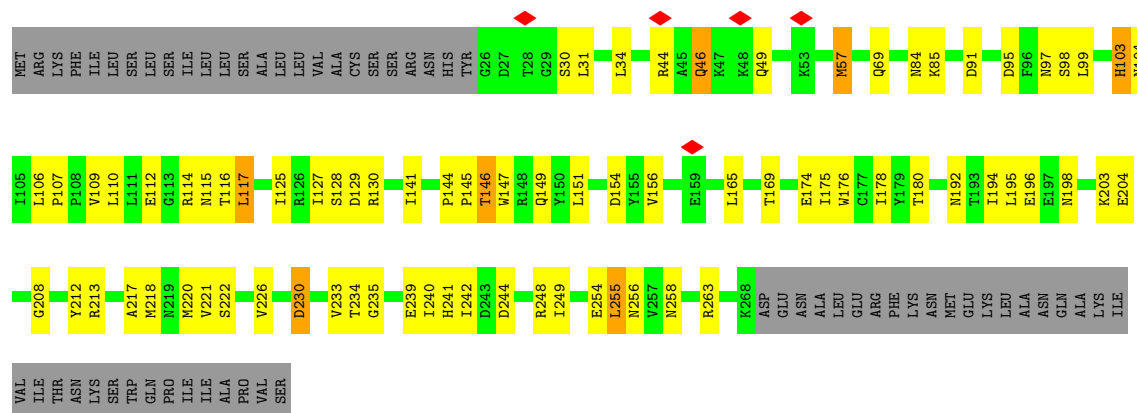
• Molecule 11: DotC

Chain HC: 55% 22% 20%



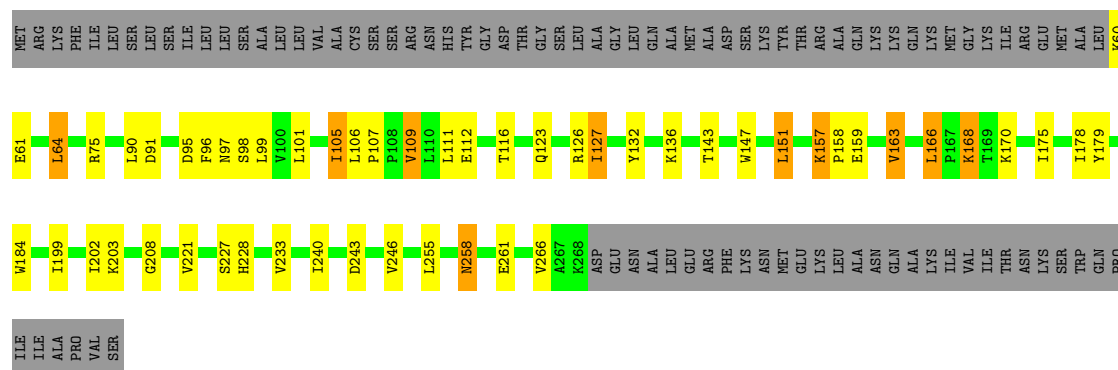
• Molecule 11: DotC

Chain MC: 54% 24% 20%



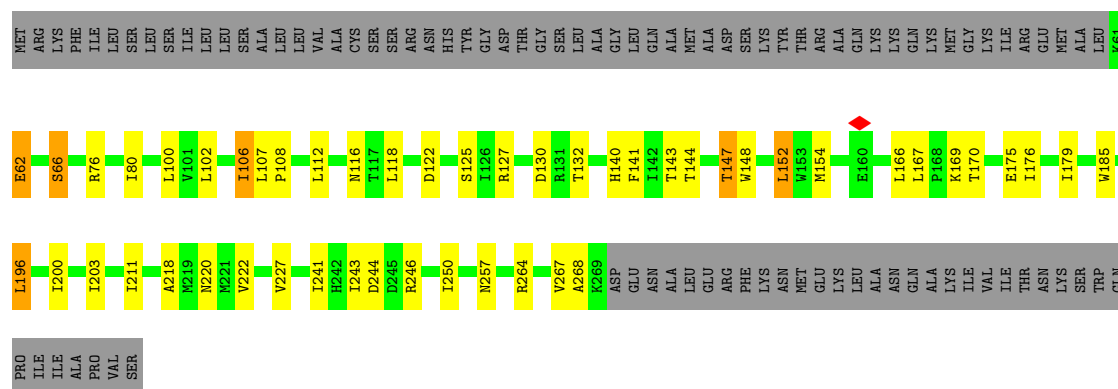
• Molecule 11: DotC

Chain JC: 51% 14% . 31%



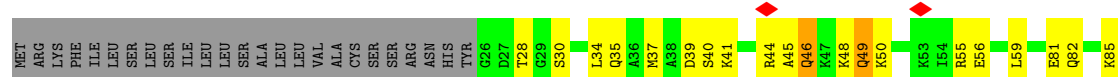
• Molecule 11: DotC

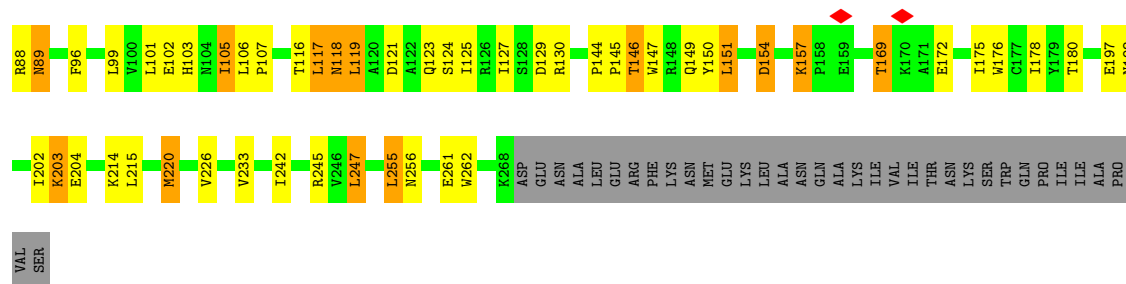
Chain KC: 52% 15% . 31%



• Molecule 11: DotC

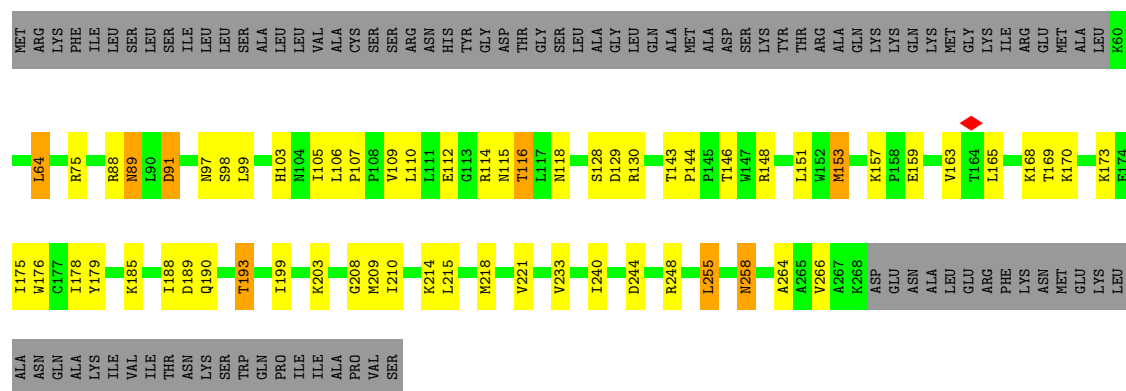
Chain LC: 56% 19% 5% 20%





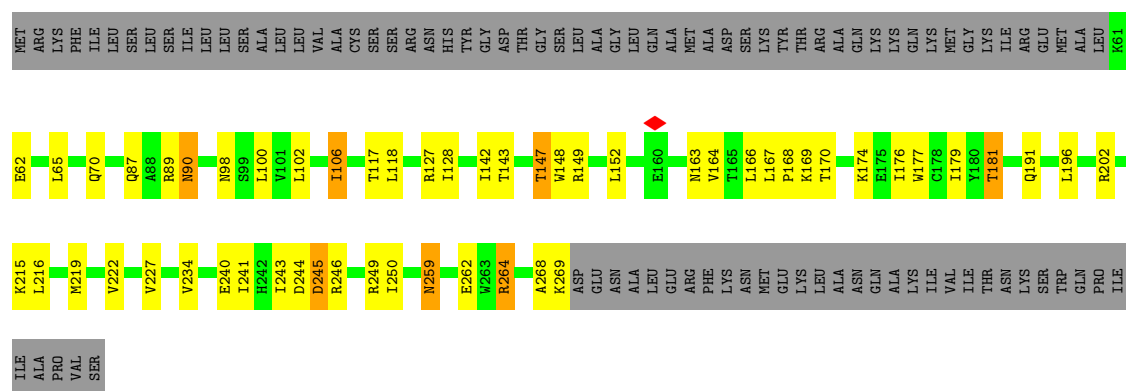
- Molecule 11: DotC

Chain AC: 49% 18% 31%



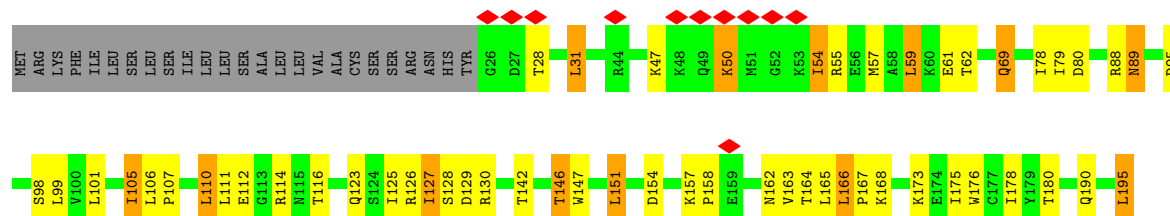
- Molecule 11: DotC

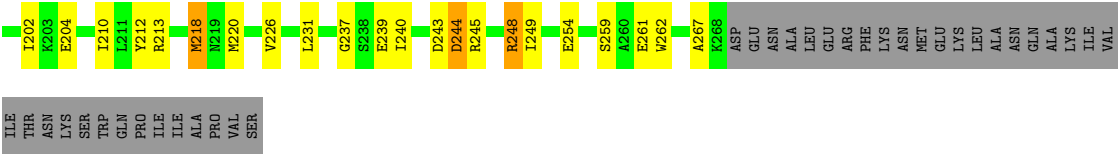
Chain BC: 51% 16% 31%



- Molecule 11: DotC

Chain IC: 54% 20% 5% 20%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	75959	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	9.010	Depositor
Minimum map value	-4.020	Depositor
Average map value	0.091	Depositor
Map value standard deviation	0.547	Depositor
Recommended contour level	2	Depositor
Map size (Å)	561.0, 561.0, 561.0	wwPDB
Map dimensions	250, 250, 250	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.244, 2.244, 2.244	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AG	0.23	0/1250	0.56	0/1699
1	Ag	0.18	0/278	0.37	0/377
1	BG	0.25	0/1250	0.59	0/1699
1	Bg	0.21	0/278	0.37	0/377
1	CG	0.24	0/1250	0.55	0/1699
1	Cg	0.20	0/278	0.35	0/377
1	DG	0.25	0/1250	0.59	0/1699
1	Dg	0.18	0/278	0.37	0/377
1	EG	0.24	0/1250	0.57	1/1699 (0.1%)
1	Eg	0.18	0/278	0.35	0/377
1	FG	0.25	0/1250	0.59	0/1699
1	Fg	0.18	0/278	0.39	0/377
1	GG	0.25	0/1250	0.58	0/1699
1	Gg	0.21	0/278	0.36	0/377
1	HG	0.24	0/1250	0.56	0/1699
1	Hg	0.20	0/278	0.42	0/377
1	IG	0.24	0/1250	0.58	0/1699
1	Ig	0.22	0/278	0.36	0/377
1	JG	0.25	0/1250	0.59	0/1699
1	Jg	0.19	0/278	0.40	0/377
1	KG	0.23	0/1250	0.58	1/1699 (0.1%)
1	Kg	0.20	0/278	0.37	0/377
1	LG	0.25	0/1250	0.58	0/1699
1	Lg	0.18	0/278	0.34	0/377
1	MG	0.22	0/1250	0.56	0/1699
1	Mg	0.20	0/278	0.37	0/377
1	NG	0.24	0/1250	0.58	0/1699
1	OG	0.23	0/1250	0.59	1/1699 (0.1%)
1	PG	0.24	0/1250	0.57	0/1699
1	VG	0.22	0/278	0.53	0/377
1	WG	0.21	0/278	0.48	0/377
1	XG	0.21	0/278	0.47	0/377
1	YG	0.21	0/278	0.46	0/377
1	ZG	0.20	0/278	0.49	0/377

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	AD	0.25	0/1107	0.51	0/1502
2	Ad	0.23	0/1078	0.43	0/1463
2	BD	0.26	0/1107	0.50	0/1502
2	Bd	0.25	0/1078	0.45	0/1463
2	CD	0.30	1/1107 (0.1%)	0.48	0/1502
2	Cd	0.22	0/1078	0.41	0/1463
2	DD	0.26	0/1107	0.50	0/1502
2	Dd	0.22	0/1078	0.41	0/1463
2	ED	0.26	0/1107	0.55	2/1502 (0.1%)
2	Ed	0.21	0/1078	0.42	0/1463
2	FD	0.26	0/1107	0.52	0/1502
2	Fd	0.22	0/1078	0.42	0/1463
2	GD	0.26	0/1107	0.54	0/1502
2	Gd	0.23	0/1078	0.46	0/1463
2	HD	0.25	0/1107	0.52	0/1502
2	Hd	0.23	0/1078	0.41	0/1463
2	ID	0.26	0/1107	0.54	0/1502
2	Id	0.23	0/1078	0.44	0/1463
2	JD	0.27	0/1107	0.54	0/1502
2	Jd	0.24	0/1078	0.42	0/1463
2	KD	0.26	0/1107	0.50	0/1502
2	Kd	0.22	0/1078	0.42	0/1463
2	LD	0.26	0/1107	0.52	0/1502
2	Ld	0.26	0/1078	0.45	0/1463
2	MD	0.26	0/1107	0.51	0/1502
2	Md	0.22	0/1078	0.43	0/1463
3	AF	0.15	0/490	0.36	0/660
3	Af	0.17	0/456	0.37	0/615
3	BF	0.16	0/490	0.36	0/660
3	Bf	0.18	0/456	0.37	0/615
3	CF	0.15	0/490	0.36	0/660
3	Cf	0.19	0/456	0.37	0/615
3	DF	0.16	0/490	0.40	0/660
3	Df	0.19	0/456	0.45	0/615
3	EF	0.18	0/490	0.37	0/660
3	Ef	0.17	0/456	0.34	0/615
3	FF	0.16	0/490	0.39	0/660
3	Ff	0.17	0/456	0.30	0/615
3	GF	0.17	0/490	0.39	0/660
3	Gf	0.19	0/456	0.34	0/615
3	HF	0.17	0/490	0.37	0/660
3	Hf	0.17	0/456	0.38	0/615
3	IF	0.17	0/490	0.33	0/660

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	If	0.17	0/456	0.35	0/615
3	JF	0.17	0/490	0.38	0/660
3	Jf	0.18	0/456	0.33	0/615
3	KF	0.16	0/490	0.36	0/660
3	Kf	0.17	0/456	0.37	0/615
3	LF	0.16	0/490	0.37	0/660
3	Lf	0.18	0/456	0.32	0/615
3	MF	0.16	0/490	0.35	0/660
3	Mf	0.18	0/456	0.33	0/615
3	VF	0.16	0/490	0.39	0/660
3	WF	0.17	0/490	0.34	0/660
3	XF	0.16	0/490	0.35	0/660
3	YF	0.16	0/490	0.35	0/660
3	ZF	0.16	0/490	0.34	0/660
4	AH	0.22	0/2033	0.45	0/2775
4	BH	0.23	0/2033	0.43	0/2775
4	CH	0.22	0/2033	0.43	0/2775
4	DH	0.22	0/2033	0.41	0/2775
4	EH	0.21	0/2033	0.45	0/2775
4	FH	0.21	0/2033	0.40	0/2775
4	GH	0.23	0/2033	0.45	0/2775
4	HH	0.22	0/2033	0.43	0/2775
4	IH	0.23	0/2033	0.41	0/2775
4	JH	0.23	0/2033	0.43	0/2775
4	KH	0.23	0/2033	0.44	0/2775
4	LH	0.23	0/2033	0.44	0/2775
4	MH	0.22	0/2033	0.44	0/2775
4	VH	0.17	0/1921	0.39	0/2620
4	WH	0.17	0/1921	0.38	0/2620
4	XH	0.20	0/1921	0.42	0/2620
4	YH	0.17	0/1921	0.39	0/2620
4	ZH	0.20	0/1921	0.43	0/2620
5	AK	0.25	0/1195	0.43	0/1616
5	BK	0.26	0/1195	0.45	0/1616
5	CK	0.25	0/1195	0.44	0/1616
5	DK	0.26	0/1195	0.43	0/1616
5	EK	0.26	0/1195	0.42	0/1616
5	FK	0.26	0/1195	0.44	0/1616
5	GK	0.26	0/1195	0.46	0/1616
5	HK	0.25	0/1195	0.43	0/1616
5	IK	0.25	0/1195	0.43	0/1616
5	JK	0.25	0/1195	0.44	0/1616
5	KK	0.26	0/1195	0.44	0/1616

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	LK	0.25	0/1195	0.48	0/1616
5	MK	0.25	0/1195	0.43	0/1616
6	AL	0.23	0/1417	0.49	0/1912
6	BL	0.25	0/1417	0.48	0/1912
6	CL	0.25	0/1417	0.49	0/1912
6	DL	0.25	0/1417	0.49	0/1912
6	EL	0.24	0/1417	0.48	0/1912
6	FL	0.24	0/1417	0.47	0/1912
6	GL	0.25	0/1417	0.47	0/1912
6	HL	0.24	0/1417	0.47	0/1912
6	IL	0.24	0/1417	0.50	0/1912
6	JL	0.24	0/1417	0.48	0/1912
6	KL	0.25	0/1417	0.47	0/1912
6	LL	0.24	0/1417	0.47	0/1912
6	ML	0.25	0/1417	0.47	0/1912
7	AM	0.21	0/1678	0.44	0/2262
7	BM	0.21	0/1678	0.46	0/2262
7	CM	0.22	0/1678	0.45	0/2262
7	DM	0.23	0/1678	0.45	0/2262
7	EM	0.22	0/1678	0.46	0/2262
7	FM	0.23	0/1678	0.45	0/2262
7	GM	0.23	0/1678	0.44	0/2262
7	HM	0.22	0/1678	0.42	0/2262
7	IM	0.21	0/1678	0.43	0/2262
7	JM	0.22	0/1678	0.46	0/2262
7	KM	0.23	0/1678	0.47	0/2262
7	LM	0.22	0/1678	0.43	0/2262
7	MM	0.22	0/1678	0.45	0/2262
8	AN	0.23	0/593	0.40	0/799
8	BN	0.25	0/593	0.41	0/799
8	CN	0.25	0/593	0.44	0/799
8	DN	0.25	0/593	0.43	0/799
8	EN	0.24	0/593	0.38	0/799
8	FN	0.23	0/593	0.42	0/799
8	GN	0.25	0/593	0.42	0/799
8	HN	0.25	0/593	0.39	0/799
8	IN	0.24	0/593	0.44	0/799
8	JN	0.25	0/593	0.40	0/799
8	KN	0.24	0/593	0.42	0/799
8	LN	0.24	0/593	0.42	0/799
8	MN	0.22	0/593	0.39	0/799
11	AC	0.27	0/1702	0.46	0/2315
11	BC	0.25	0/1702	0.46	0/2315

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
11	CC	0.26	0/1702	0.41	0/2315
11	DC	0.26	0/1957	0.44	0/2651
11	EC	0.26	0/1702	0.43	0/2315
11	FC	0.26	0/1702	0.44	0/2315
11	GC	0.26	0/1702	0.43	0/2315
11	HC	0.26	0/1957	0.42	0/2651
11	IC	0.23	0/1957	0.43	0/2651
11	JC	0.29	0/1702	0.45	0/2315
11	KC	0.28	0/1702	0.44	0/2315
11	LC	0.27	0/1957	0.45	0/2651
11	MC	0.25	0/1957	0.44	0/2651
All	All	0.23	1/191071 (0.0%)	0.46	5/258997 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	CD	28	PRO	C-N	5.61	1.38	1.33

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	KG	939	THR	N-CA-C	-5.87	106.76	114.04
1	OG	939	THR	N-CA-C	-5.58	107.47	114.56
2	ED	62	ILE	CA-C-N	-5.33	115.97	122.64
2	ED	62	ILE	C-N-CA	-5.33	115.97	122.64
1	EG	939	THR	N-CA-C	-5.22	107.57	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	31	0
1	Ag	276	0	263	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BG	1229	0	1231	33	0
1	Bg	276	0	263	11	0
1	CG	1229	0	1231	29	0
1	Cg	276	0	263	9	0
1	DG	1229	0	1231	34	0
1	Dg	276	0	263	6	0
1	EG	1229	0	1231	31	0
1	Eg	276	0	263	10	0
1	FG	1229	0	1231	36	0
1	Fg	276	0	263	7	0
1	GG	1229	0	1231	35	0
1	Gg	276	0	263	8	0
1	HG	1229	0	1231	37	0
1	Hg	276	0	263	7	0
1	IG	1229	0	1231	28	0
1	Ig	276	0	263	6	0
1	JG	1229	0	1231	32	0
1	Jg	276	0	263	6	0
1	KG	1229	0	1231	26	0
1	Kg	276	0	263	6	0
1	LG	1229	0	1231	24	0
1	Lg	276	0	263	10	0
1	MG	1229	0	1231	26	0
1	Mg	276	0	263	17	0
1	NG	1229	0	1231	28	0
1	OG	1229	0	1231	31	0
1	PG	1229	0	1231	25	0
1	VG	276	0	263	4	0
1	WG	276	0	263	5	0
1	XG	276	0	263	4	0
1	YG	276	0	263	5	0
1	ZG	276	0	263	9	0
2	AD	1086	0	1121	30	0
2	Ad	1058	0	1092	25	0
2	BD	1086	0	1121	24	0
2	Bd	1058	0	1092	19	0
2	CD	1086	0	1121	34	0
2	Cd	1058	0	1092	12	0
2	DD	1086	0	1121	33	0
2	Dd	1058	0	1092	26	0
2	ED	1086	0	1121	25	0
2	Ed	1058	0	1092	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	FD	1086	0	1121	24	0
2	Fd	1058	0	1092	23	0
2	GD	1086	0	1121	34	0
2	Gd	1058	0	1092	28	0
2	HD	1086	0	1121	21	0
2	Hd	1058	0	1092	15	0
2	ID	1086	0	1121	23	0
2	Id	1058	0	1092	24	0
2	JD	1086	0	1121	27	0
2	Jd	1058	0	1092	19	0
2	KD	1086	0	1121	27	0
2	Kd	1058	0	1092	19	0
2	LD	1086	0	1121	33	0
2	Ld	1058	0	1092	14	0
2	MD	1086	0	1121	25	0
2	Md	1058	0	1092	20	0
3	AF	483	0	502	12	0
3	Af	449	0	474	12	0
3	BF	483	0	502	14	0
3	Bf	449	0	474	7	0
3	CF	483	0	502	13	0
3	Cf	449	0	474	17	0
3	DF	483	0	502	12	0
3	Df	449	0	474	10	0
3	EF	483	0	502	10	0
3	Ef	449	0	474	8	0
3	FF	483	0	502	15	0
3	Ff	449	0	474	7	0
3	GF	483	0	502	11	0
3	Gf	449	0	474	11	0
3	HF	483	0	502	12	0
3	Hf	449	0	474	10	0
3	IF	483	0	502	9	0
3	If	449	0	474	10	0
3	JF	483	0	502	16	0
3	Jf	449	0	474	10	0
3	KF	483	0	502	19	0
3	Kf	449	0	474	9	0
3	LF	483	0	502	13	0
3	Lf	449	0	474	6	0
3	MF	483	0	502	9	0
3	Mf	449	0	474	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	VF	483	0	502	17	0
3	WF	483	0	502	14	0
3	XF	483	0	502	14	0
3	YF	483	0	502	11	0
3	ZF	483	0	502	15	0
4	AH	1983	0	2009	40	0
4	BH	1983	0	2009	50	0
4	CH	1983	0	2009	44	0
4	DH	1983	0	2009	44	0
4	EH	1983	0	2009	39	0
4	FH	1983	0	2009	45	0
4	GH	1983	0	2009	40	0
4	HH	1983	0	2009	43	0
4	IH	1983	0	2009	41	0
4	JH	1983	0	2009	45	0
4	KH	1983	0	2009	47	0
4	LH	1983	0	2009	55	0
4	MH	1983	0	2009	50	0
4	VH	1875	0	1900	42	0
4	WH	1875	0	1900	37	0
4	XH	1875	0	1900	41	0
4	YH	1875	0	1900	35	0
4	ZH	1875	0	1900	48	0
5	AK	1175	0	1221	32	0
5	BK	1175	0	1221	27	0
5	CK	1175	0	1221	18	0
5	DK	1175	0	1221	26	0
5	EK	1175	0	1221	25	0
5	FK	1175	0	1221	28	0
5	GK	1175	0	1221	27	0
5	HK	1175	0	1221	24	0
5	IK	1175	0	1221	29	0
5	JK	1175	0	1221	27	0
5	KK	1175	0	1221	28	0
5	LK	1175	0	1221	26	0
5	MK	1175	0	1221	31	0
6	AL	1388	0	1378	26	0
6	BL	1388	0	1378	29	0
6	CL	1388	0	1378	34	0
6	DL	1388	0	1378	31	0
6	EL	1388	0	1378	25	0
6	FL	1388	0	1378	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	GL	1388	0	1378	31	0
6	HL	1388	0	1378	28	0
6	IL	1388	0	1378	23	0
6	JL	1388	0	1378	37	0
6	KL	1388	0	1378	30	0
6	LL	1388	0	1378	25	0
6	ML	1388	0	1378	35	0
7	AM	1650	0	1658	45	0
7	BM	1650	0	1658	44	0
7	CM	1650	0	1658	42	0
7	DM	1650	0	1658	43	0
7	EM	1650	0	1658	37	0
7	FM	1650	0	1658	44	0
7	GM	1650	0	1658	38	0
7	HM	1650	0	1658	43	0
7	IM	1650	0	1658	36	0
7	JM	1650	0	1658	36	0
7	KM	1650	0	1658	41	0
7	LM	1650	0	1658	34	0
7	MM	1650	0	1658	42	0
8	AN	582	0	530	15	0
8	BN	582	0	530	14	0
8	CN	582	0	530	8	0
8	DN	582	0	530	12	0
8	EN	582	0	530	13	0
8	FN	582	0	530	11	0
8	GN	582	0	530	18	0
8	HN	582	0	530	10	0
8	IN	582	0	530	16	0
8	JN	582	0	530	6	0
8	KN	582	0	530	16	0
8	LN	582	0	530	11	0
8	MN	582	0	530	13	0
9	AU	45	0	12	2	0
9	BU	45	0	13	2	0
9	CU	45	0	12	2	0
9	DU	45	0	12	1	0
9	EU	45	0	12	0	0
9	FU	45	0	12	0	0
9	GU	45	0	12	0	0
9	HU	45	0	12	0	0
9	IU	45	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	JU	45	0	12	0	0
9	KU	45	0	14	1	0
9	LU	45	0	13	2	0
9	MU	45	0	13	1	0
10	AX	240	0	55	1	0
10	BX	240	0	56	2	0
10	CX	240	0	57	3	0
10	DX	240	0	56	1	0
10	EX	240	0	57	1	0
10	FX	240	0	55	1	0
10	GX	240	0	56	0	0
10	HX	240	0	56	1	0
10	IX	240	0	56	2	0
10	JX	240	0	54	3	0
10	KX	240	0	54	1	0
10	LX	240	0	53	0	0
10	MX	240	0	56	4	0
10	VX	240	0	56	1	0
10	WX	240	0	59	0	0
10	XX	240	0	54	3	0
10	YX	240	0	57	2	0
10	ZX	240	0	57	0	0
11	AC	1667	0	1682	27	0
11	BC	1667	0	1682	28	0
11	CC	1667	0	1682	43	0
11	DC	1921	0	1952	40	0
11	EC	1667	0	1682	54	0
11	FC	1667	0	1682	43	0
11	GC	1667	0	1682	34	0
11	HC	1921	0	1952	39	0
11	IC	1921	0	1952	43	0
11	JC	1667	0	1682	34	0
11	KC	1667	0	1682	26	0
11	LC	1921	0	1952	48	0
11	MC	1921	0	1952	41	0
All	All	192370	0	190626	3794	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 (3794) 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:BL:129:THR:O	6:BL:133:PHE:HB2	1.71	0.89
11:GC:148:TRP:O	11:GC:152:LEU:HB2	1.76	0.85
6:EL:166:ALA:HA	6:EL:206:GLU:O	1.77	0.84
1:EG:1019:ALA:O	1:EG:1023:PHE:HB2	1.78	0.84
1:DG:1019:ALA:O	1:DG:1023:PHE:HB2	1.78	0.82
6:KL:166:ALA:HA	6:KL:206:GLU:O	1.81	0.79
5:BK:117:THR:HA	5:BK:157:GLN:O	1.83	0.78
6:HL:166:ALA:HA	6:HL:206:GLU:O	1.82	0.78
6:LL:166:ALA:HA	6:LL:206:GLU:O	1.84	0.77
6:DL:166:ALA:HA	6:DL:206:GLU:O	1.84	0.77
5:AK:117:THR:HA	5:AK:157:GLN:O	1.84	0.77
6:AL:166:ALA:HA	6:AL:206:GLU:O	1.85	0.76
6:CL:166:ALA:HA	6:CL:206:GLU:O	1.86	0.75
6:ML:166:ALA:HA	6:ML:206:GLU:O	1.87	0.74
1:MG:886:LEU:HA	1:MG:899:LEU:O	1.87	0.74
6:BL:166:ALA:HA	6:BL:206:GLU:O	1.88	0.74
6:JL:166:ALA:HA	6:JL:206:GLU:O	1.88	0.74
1:HG:876:SER:H	1:IG:940:ALA:HB1	1.53	0.74
5:GK:117:THR:HA	5:GK:157:GLN:O	1.88	0.73
5:MK:117:THR:HA	5:MK:157:GLN:O	1.87	0.73
4:GH:189:TRP:HE1	4:GH:232:GLY:H	1.37	0.72
4:MH:345:LEU:HB2	4:MH:356:LEU:HB2	1.72	0.72
7:LM:306:GLN:HG2	7:LM:308:ASP:H	1.55	0.71
5:EK:117:THR:HA	5:EK:157:GLN:O	1.90	0.71
6:FL:166:ALA:HA	6:FL:206:GLU:O	1.90	0.71
2:ID:87:TRP:O	2:ID:120:SER:HA	1.91	0.71
1:OG:898:LYS:HE2	1:PG:864:LYS:HB3	1.72	0.71
6:GL:166:ALA:HA	6:GL:206:GLU:O	1.91	0.71
1:CG:1019:ALA:O	1:CG:1023:PHE:HB2	1.91	0.71
2:Gd:142:LYS:H	2:Gd:142:LYS:HZ3	1.38	0.70
11:EC:248:ARG:HH22	11:FC:125:ILE:HG12	1.57	0.70
4:CH:203:ASN:HB3	4:CH:216:GLN:HB3	1.73	0.70
5:FK:117:THR:HA	5:FK:157:GLN:O	1.92	0.69
2:AD:105:ARG:HB2	2:AD:153:VAL:HG12	1.75	0.69
3:Gf:219:ARG:HA	3:Gf:232:VAL:O	1.92	0.69
1:GG:886:LEU:HA	1:GG:899:LEU:O	1.93	0.68
4:EH:189:TRP:HE1	4:EH:232:GLY:H	1.40	0.68
5:CK:117:THR:HA	5:CK:157:GLN:O	1.94	0.68
5:CK:162:ASP:OD1	5:CK:162:ASP:N	2.26	0.68
7:LM:275:ASP:HB3	7:LM:294:PHE:HB2	1.75	0.68
1:CG:886:LEU:HA	1:CG:899:LEU:O	1.93	0.67
6:JL:115:GLN:HB3	6:JL:126:ILE:HB	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FG:951:HIS:H	1:FG:1027:THR:HG22	1.58	0.67
7:HM:120:GLY:H	7:HM:140:ASN:HB2	1.59	0.67
5:JK:117:THR:HA	5:JK:157:GLN:O	1.93	0.67
7:AM:306:GLN:HG2	7:AM:308:ASP:H	1.59	0.66
7:FM:120:GLY:H	7:FM:140:ASN:HB2	1.61	0.66
5:GK:148:GLY:H	2:Gd:30:ILE:HD13	1.58	0.66
2:Ad:97:ARG:HH12	11:JC:266:VAL:HG12	1.60	0.66
7:JM:275:ASP:HB3	7:JM:294:PHE:HB2	1.76	0.66
6:FL:54:ARG:HH21	6:FL:57:VAL:HG13	1.61	0.66
1:HG:1024:ASN:OD1	1:HG:1024:ASN:N	2.27	0.66
4:MH:203:ASN:HB3	4:MH:216:GLN:HB2	1.76	0.66
7:GM:302:ARG:HH11	7:GM:309:LEU:HD11	1.61	0.66
3:JF:222:LEU:O	3:JF:229:THR:HA	1.96	0.66
1:OG:951:HIS:H	1:OG:1027:THR:HG22	1.61	0.65
5:GK:70:VAL:HG22	6:HL:214:ILE:HG12	1.77	0.65
4:HH:183:ASP:HA	4:HH:256:VAL:HB	1.78	0.65
4:WH:189:TRP:HE1	4:WH:232:GLY:H	1.44	0.65
8:CN:57:ARG:HH21	8:CN:67:THR:HA	1.60	0.65
3:JF:246:LEU:HB3	3:JF:255:LEU:HD12	1.78	0.65
5:KK:117:THR:HA	5:KK:157:GLN:O	1.96	0.65
4:XH:183:ASP:HA	4:XH:256:VAL:HG12	1.77	0.65
7:CM:275:ASP:HB3	7:CM:294:PHE:HB2	1.79	0.65
7:DM:120:GLY:H	7:DM:140:ASN:HB2	1.62	0.65
2:Gd:84:SER:H	11:CC:268:ALA:HB3	1.62	0.65
1:BG:899:LEU:HD13	1:BG:919:MET:HG2	1.79	0.65
7:MM:306:GLN:HG3	7:MM:308:ASP:H	1.61	0.64
5:BK:54:ILE:HD11	8:BN:44:LYS:HB3	1.79	0.64
6:BL:127:ILE:HB	6:BL:229:ILE:HB	1.80	0.64
1:FG:899:LEU:HD13	1:FG:919:MET:HG2	1.77	0.64
11:CC:124:GLN:HE21	11:BC:250:ILE:HB	1.63	0.64
3:Cf:209:ILE:HG22	3:Cf:225:SER:HB3	1.80	0.64
4:JH:189:TRP:HE1	4:JH:232:GLY:H	1.44	0.64
6:LL:114:ILE:HD12	6:LL:127:ILE:HG13	1.80	0.64
5:MK:127:LYS:H	5:MK:127:LYS:HZ2	1.45	0.64
7:EM:316:ASN:OD1	7:EM:316:ASN:N	2.31	0.64
7:AM:120:GLY:H	7:AM:140:ASN:HB2	1.61	0.64
5:BK:113:ALA:HA	5:BK:153:ILE:O	1.97	0.64
7:BM:201:THR:HG22	7:BM:221:LYS:HB3	1.80	0.63
1:Dg:793:GLU:O	1:Dg:797:ARG:NH2	2.31	0.63
11:EC:231:LEU:HB2	11:EC:244:ASP:HB2	1.79	0.63
4:AH:179:LEU:HB2	4:AH:213:LEU:HB3	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:FH:219:LYS:HZ3	4:FH:220:LEU:H	1.47	0.63
6:GL:129:THR:O	6:GL:133:PHE:HB2	1.98	0.63
7:AM:276:ALA:H	7:AM:295:ASN:HB2	1.64	0.63
7:GM:308:ASP:OD1	7:GM:308:ASP:N	2.31	0.63
7:BM:240:GLN:HB3	7:BM:242:LYS:HE3	1.80	0.63
4:FH:354:MET:HE3	4:FH:355:GLN:H	1.63	0.63
11:DC:146:THR:OG1	11:DC:147:TRP:N	2.32	0.63
7:GM:306:GLN:HG3	7:GM:308:ASP:H	1.63	0.63
4:ZH:183:ASP:HA	4:ZH:256:VAL:HG22	1.79	0.63
2:Dd:142:LYS:HZ3	2:Dd:142:LYS:H	1.47	0.63
1:NG:947:ARG:NH2	1:NG:1030:GLU:OE1	2.31	0.63
4:GH:324:TRP:HA	4:GH:339:MET:HG3	1.81	0.62
7:HM:308:ASP:N	7:HM:308:ASP:OD1	2.32	0.62
3:IF:241:TYR:HB3	3:IF:256:THR:HG21	1.81	0.62
4:KH:189:TRP:HE1	4:KH:232:GLY:H	1.46	0.62
4:XH:114:ASP:HA	4:XH:117:ARG:HD3	1.81	0.62
11:MC:146:THR:OG1	11:MC:147:TRP:N	2.32	0.62
7:FM:275:ASP:HB3	7:FM:294:PHE:HB2	1.81	0.62
3:AF:265:SER:HB3	3:AF:268:ASP:HB2	1.81	0.62
7:JM:120:GLY:H	7:JM:140:ASN:HB2	1.62	0.62
3:VF:209:ILE:H	3:VF:225:SER:HB3	1.62	0.62
1:EG:921:ILE:HD12	1:EG:926:LYS:HD2	1.82	0.62
2:Md:29:PRO:HB2	2:Md:32:ASN:HB3	1.82	0.62
4:IH:205:GLN:HB2	4:IH:214:MET:HB2	1.80	0.62
7:MM:131:THR:HG23	7:MM:151:GLY:H	1.65	0.62
9:BU:128:UNK:HA	6:CL:232:GLN:HE22	1.64	0.62
6:GL:163:ILE:HG23	6:GL:233:TRP:HB3	1.81	0.62
4:DH:225:ASN:HD21	4:EH:176:VAL:H	1.45	0.62
1:KG:899:LEU:HG	1:KG:916:PHE:HB3	1.82	0.62
6:GL:169:THR:OG1	6:GL:170:ASP:N	2.33	0.62
3:Jf:222:LEU:HB2	3:Jf:230:LEU:HB2	1.81	0.62
7:FM:262:GLU:HA	7:FM:280:TYR:O	1.99	0.62
2:Hd:110:GLY:HA3	2:Hd:158:TYR:HB2	1.81	0.62
5:DK:73:ASN:HD21	5:DK:185:ARG:HH21	1.48	0.62
1:JG:969:GLY:HA3	1:JG:1009:ALA:HB2	1.82	0.62
2:JD:24:LYS:H	2:JD:24:LYS:HZ2	1.48	0.62
2:Jd:107:ARG:O	2:Jd:155:GLU:HA	1.99	0.62
2:Kd:73:ILE:HG12	2:Kd:133:ARG:HH21	1.64	0.62
11:HC:225:TYR:HB3	11:HC:251:ALA:HB3	1.81	0.62
1:Hg:794:ILE:HG23	4:IH:110:LYS:HE2	1.82	0.61
4:KH:326:ALA:HB3	4:KH:338:GLU:HB3	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:GC:214:ARG:HH22	11:GC:217:LEU:HD23	1.64	0.61
5:EK:50:ASP:OD1	5:EK:50:ASP:N	2.33	0.61
5:DK:87:GLN:HB3	5:DK:128:ARG:HH12	1.64	0.61
2:GD:81:ALA:HB3	2:GD:128:LEU:HD11	1.81	0.61
2:Id:107:ARG:O	2:Id:155:GLU:HA	2.00	0.61
1:Cg:797:ARG:HD3	4:VH:117:ARG:HH21	1.65	0.61
2:AD:70:THR:HA	2:AD:133:ARG:HH21	1.65	0.61
1:JG:921:ILE:HD12	1:JG:926:LYS:HD2	1.80	0.61
1:CG:881:GLU:OE1	1:DG:904:ASN:ND2	2.33	0.61
1:GG:898:LYS:HZ1	1:GG:920:SER:HB3	1.65	0.61
4:FH:149:PRO:HB2	4:FH:248:VAL:HG22	1.80	0.61
2:Fd:142:LYS:H	2:Fd:142:LYS:HZ2	1.46	0.61
4:GH:183:ASP:HA	4:GH:256:VAL:HG22	1.82	0.61
4:KH:108:ASP:N	4:KH:108:ASP:OD1	2.32	0.61
4:YH:294:ARG:HH22	4:YH:304:ALA:H	1.48	0.61
6:JL:44:HIS:HB2	6:JL:48:ASN:HA	1.81	0.61
11:CC:217:LEU:O	11:CC:264:ARG:NH2	2.34	0.61
2:CD:160:LYS:NZ	2:Cd:137:TYR:O	2.33	0.61
4:WH:183:ASP:HA	4:WH:256:VAL:HG12	1.82	0.61
7:BM:275:ASP:HB3	7:BM:294:PHE:HB2	1.83	0.61
3:GF:219:ARG:HH22	4:HH:150:LYS:HA	1.66	0.61
6:HL:190:MET:HE2	6:HL:203:LEU:HB3	1.82	0.61
4:CH:183:ASP:HA	4:CH:256:VAL:HG22	1.82	0.61
4:HH:162:PRO:HA	4:XH:251:ARG:HH22	1.65	0.61
4:VH:187:ALA:HB1	4:VH:262:ASN:HB2	1.83	0.61
1:FG:880:ASP:OD1	1:FG:880:ASP:N	2.34	0.61
11:HC:54:ILE:HG12	1:JG:872:VAL:HG22	1.83	0.61
7:CM:190:ASN:N	7:CM:190:ASN:OD1	2.34	0.61
5:HK:111:LYS:HD2	5:HK:114:ILE:HD11	1.81	0.60
8:JN:46:GLY:HA3	8:JN:61:ASN:HB2	1.81	0.60
4:KH:249:ASP:OD1	4:KH:249:ASP:N	2.34	0.60
6:LL:181:LEU:O	6:LL:185:GLN:NE2	2.33	0.60
1:GG:912:MET:HB3	1:GG:944:LEU:HB2	1.82	0.60
2:Gd:29:PRO:HB2	2:Gd:32:ASN:HB3	1.83	0.60
11:MC:146:THR:H	11:MC:149:GLN:HE22	1.47	0.60
5:AK:68:ALA:HB3	5:AK:75:LEU:HB3	1.83	0.60
3:Af:254:ILE:O	3:Af:261:VAL:HA	2.01	0.60
1:Dg:806:THR:O	1:Dg:810:GLN:NE2	2.34	0.60
6:DL:44:HIS:HB2	6:DL:48:ASN:HA	1.82	0.60
5:GK:114:ILE:HG23	5:GK:184:PHE:HB3	1.81	0.60
2:Dd:60:LYS:NZ	2:DD:136:ASP:O	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Df:254:ILE:HB	3:Df:262:ILE:HG23	1.83	0.60
11:JC:221:VAL:HG12	11:JC:255:LEU:HG	1.83	0.60
6:CL:210:ASP:OD1	6:CL:210:ASP:N	2.34	0.60
11:CC:102:LEU:HB2	11:CC:106:ILE:HG23	1.84	0.60
4:LH:321:SER:HB2	11:FC:148:ARG:HH11	1.66	0.60
5:BK:148:GLY:H	2:Bd:30:ILE:HD13	1.65	0.60
11:LC:48:LYS:HA	1:OG:938:ASN:HD21	1.66	0.60
4:DH:150:LYS:H	4:DH:247:ALA:HA	1.66	0.60
6:EL:54:ARG:HH21	6:EL:57:VAL:HG13	1.66	0.60
1:MG:900:ILE:HD11	1:NG:865:THR:HG22	1.83	0.60
11:AC:153:MET:N	11:AC:153:MET:SD	2.75	0.60
11:CC:147:THR:OG1	11:CC:148:TRP:N	2.31	0.60
1:EG:880:ASP:N	1:EG:880:ASP:OD1	2.34	0.60
8:AN:57:ARG:NH1	8:AN:66:SER:O	2.35	0.60
2:FD:29:PRO:HG2	6:FL:225:GLN:HA	1.84	0.60
2:Gd:105:ARG:HB2	2:Gd:153:VAL:HG23	1.84	0.60
5:JK:138:ARG:HH12	7:JM:320:PRO:HD2	1.67	0.60
4:AH:115:MET:HE3	1:Mg:801:MET:HG2	1.83	0.60
4:LH:182:LEU:HB2	4:LH:255:ARG:HG3	1.84	0.60
6:AL:127:ILE:HB	6:AL:229:ILE:HB	1.84	0.60
1:KG:899:LEU:HD13	1:KG:919:MET:HG2	1.84	0.60
1:KG:912:MET:HB3	1:KG:944:LEU:HB2	1.83	0.60
2:CD:77:TYR:O	2:CD:78:ASN:ND2	2.35	0.60
11:HC:146:THR:OG1	11:HC:147:TRP:N	2.33	0.60
1:MG:876:SER:HB3	1:NG:941:ARG:HG2	1.83	0.60
1:Ig:807:GLN:O	1:Ig:810:GLN:NE2	2.35	0.59
4:IH:183:ASP:HA	4:IH:256:VAL:HG12	1.83	0.59
8:KN:82:MET:N	8:KN:82:MET:SD	2.75	0.59
1:Bg:793:GLU:O	1:Bg:796:GLN:NE2	2.32	0.59
5:IK:46:ASP:OD1	5:IK:46:ASP:N	2.35	0.59
5:LK:150:ASP:OD1	5:LK:150:ASP:N	2.32	0.59
4:MH:316:ASN:OD1	4:MH:316:ASN:N	2.35	0.59
11:JC:127:ILE:HG23	11:IC:245:ARG:HB2	1.82	0.59
5:JK:47:GLY:O	5:JK:108:GLN:NE2	2.35	0.59
2:Bd:105:ARG:HB2	2:Bd:153:VAL:HG23	1.84	0.59
6:CL:192:PHE:O	6:CL:196:ASN:ND2	2.34	0.59
5:DK:50:ASP:N	5:DK:50:ASP:OD1	2.36	0.59
5:JK:50:ASP:OD1	5:JK:50:ASP:N	2.34	0.59
5:KK:90:ARG:NH2	7:KM:292:MET:O	2.36	0.59
4:MH:183:ASP:HA	4:MH:256:VAL:HG22	1.84	0.59
1:EG:899:LEU:HA	1:EG:918:THR:O	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Fd:105:ARG:HB3	2:Fd:153:VAL:HG23	1.84	0.59
5:GK:162:ASP:OD1	5:GK:162:ASP:N	2.31	0.59
2:Dd:71:LEU:O	2:Dd:133:ARG:NH1	2.36	0.59
3:KF:219:ARG:NH1	4:YH:149:PRO:O	2.36	0.59
2:Ld:108:VAL:HG12	2:Ld:156:LEU:HB3	1.84	0.59
5:MK:163:LYS:NZ	5:MK:164:PRO:O	2.35	0.59
3:Mf:221:TRP:HE1	3:Mf:229:THR:HB	1.67	0.59
4:XH:126:GLN:HA	4:XH:129:LYS:HG2	1.83	0.59
11:MC:114:ARG:HG2	11:MC:130:ARG:HG2	1.83	0.59
4:EH:284:LEU:O	4:EH:314:ARG:NH2	2.36	0.59
1:PG:972:PHE:HB3	1:PG:1005:VAL:HG22	1.84	0.59
2:Gd:108:VAL:HG12	2:Gd:156:LEU:HB3	1.85	0.59
3:KF:233:ARG:NH2	4:YH:148:PRO:O	2.35	0.59
6:FL:212:ASN:OD1	6:FL:212:ASN:N	2.36	0.59
6:IL:166:ALA:HA	6:IL:206:GLU:O	2.03	0.59
1:CG:951:HIS:H	1:CG:1027:THR:HG22	1.67	0.59
2:ED:23:MET:N	2:ED:23:MET:SD	2.75	0.59
1:OG:1017:GLN:NE2	1:OG:1018:GLN:OE1	2.35	0.59
2:Dd:110:GLY:HA3	2:Dd:158:TYR:HB2	1.83	0.59
3:If:210:TYR:HB3	3:If:222:LEU:HD12	1.85	0.59
1:Mg:797:ARG:NH1	1:Mg:797:ARG:O	2.36	0.59
2:ED:27:LYS:NZ	5:DK:71:GLY:O	2.36	0.59
11:HC:245:ARG:HB2	11:IC:127:ILE:HG12	1.84	0.59
8:EN:78:LEU:H	4:FH:354:MET:HE1	1.66	0.59
5:BK:112:ILE:HD12	5:BK:152:ARG:HG3	1.83	0.59
11:MC:57:MET:SD	11:MC:57:MET:N	2.74	0.59
11:MC:194:ILE:O	11:MC:198:ASN:ND2	2.36	0.59
6:DL:212:ASN:N	6:DL:212:ASN:OD1	2.35	0.59
6:HL:212:ASN:OD1	6:HL:212:ASN:N	2.35	0.59
4:JH:256:VAL:HG13	4:JH:258:GLY:H	1.67	0.59
2:Kd:110:GLY:HA3	2:Kd:158:TYR:HB2	1.85	0.59
2:Ld:68:ASP:OD1	2:Ld:68:ASP:N	2.36	0.59
5:AK:162:ASP:OD1	5:AK:162:ASP:N	2.35	0.59
2:BD:77:TYR:O	2:BD:78:ASN:ND2	2.35	0.59
6:FL:192:PHE:O	6:FL:196:ASN:ND2	2.35	0.59
1:HG:899:LEU:HD13	1:HG:919:MET:HG2	1.84	0.59
1:AG:871:ALA:HB2	1:AG:889:ILE:HD13	1.85	0.58
6:GL:115:GLN:HB3	6:GL:126:ILE:HB	1.85	0.58
4:HH:157:PHE:HA	4:HH:255:ARG:HB2	1.85	0.58
5:JK:166:THR:HG22	5:JK:168:TYR:H	1.68	0.58
2:MD:23:MET:N	2:MD:23:MET:SD	2.76	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:HC:221:VAL:HA	11:HC:255:LEU:HA	1.85	0.58
4:DH:326:ALA:HB3	4:DH:338:GLU:HB3	1.84	0.58
1:HG:900:ILE:HG13	1:HG:918:THR:HB	1.84	0.58
4:MH:184:SER:O	4:MH:255:ARG:NH1	2.36	0.58
7:AM:248:ALA:HB3	7:AM:265:ALA:HA	1.85	0.58
11:IC:243:ASP:OD1	11:IC:243:ASP:N	2.36	0.58
4:LH:138:GLU:HG3	4:LH:141:LYS:HZ3	1.68	0.58
7:AM:306:GLN:HB3	7:AM:309:LEU:HB2	1.86	0.58
3:Ef:210:TYR:HA	3:Ef:224:GLY:HA2	1.86	0.58
3:FF:245:LYS:HE3	3:FF:257:SER:HA	1.85	0.58
8:FN:115:GLN:HE21	8:FN:115:GLN:H	1.51	0.58
6:HL:129:THR:O	6:HL:133:PHE:HB2	2.04	0.58
7:IM:243:GLY:H	7:IM:262:GLU:HB2	1.68	0.58
3:If:247:ILE:HA	3:If:254:ILE:HG22	1.84	0.58
4:LH:293:ARG:NH1	4:LH:306:LEU:O	2.37	0.58
4:BH:209:THR:HA	4:BH:231:ARG:HH22	1.69	0.58
1:Eg:792:GLN:O	1:Eg:795:GLN:NE2	2.36	0.58
7:FM:177:LEU:HD22	7:FM:181:PRO:HG2	1.85	0.58
2:Hd:148:TYR:HB2	2:Hd:153:VAL:HG12	1.84	0.58
6:IL:169:THR:HG21	6:IL:178:LYS:HB2	1.85	0.58
6:ML:129:THR:O	6:ML:133:PHE:HB2	2.03	0.58
11:FC:157:LYS:NZ	11:FC:158:PRO:O	2.37	0.58
2:ED:150:ASN:N	2:ED:150:ASN:OD1	2.35	0.58
1:JG:919:MET:HE3	1:JG:928:ILE:HD11	1.86	0.58
7:HM:275:ASP:HB3	7:HM:294:PHE:HB2	1.86	0.58
1:BG:886:LEU:HA	1:BG:899:LEU:O	2.02	0.58
11:CC:124:GLN:NE2	11:BC:250:ILE:O	2.36	0.58
3:ZF:219:ARG:HH12	3:ZF:233:ARG:HE	1.51	0.58
11:GC:155:ASP:OD1	11:GC:155:ASP:N	2.34	0.58
7:FM:119:GLU:HG3	7:FM:139:ALA:HB3	1.86	0.58
7:GM:115:ARG:HG3	7:GM:135:ASP:HB3	1.86	0.58
1:ZG:811:ASP:O	1:ZG:814:GLN:NE2	2.36	0.58
2:Ad:68:ASP:OD1	2:Ad:68:ASP:N	2.37	0.58
2:BD:32:ASN:N	2:BD:32:ASN:OD1	2.37	0.58
11:JC:243:ASP:N	11:JC:243:ASP:OD1	2.36	0.58
5:FK:117:THR:HG23	5:FK:157:GLN:HB3	1.85	0.58
4:IH:325:LEU:N	4:IH:338:GLU:O	2.36	0.58
5:LK:50:ASP:N	5:LK:50:ASP:OD1	2.37	0.58
2:Md:60:LYS:NZ	2:Md:61:VAL:O	2.37	0.58
3:XF:207:ARG:HH21	3:XF:240:GLY:HA3	1.69	0.58
7:AM:145:ARG:HH22	7:AM:162:VAL:HG23	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GD:29:PRO:HG2	6:GL:225:GLN:HA	1.85	0.58
2:Gd:144:SER:HB2	2:Gd:157:ARG:HB3	1.85	0.58
10:VX:70:UNK:H2	4:DH:146:GLY:H	1.50	0.58
11:GC:147:THR:OG1	11:GC:148:TRP:N	2.33	0.58
7:CM:119:GLU:HG3	7:CM:139:ALA:HB3	1.86	0.58
5:DK:162:ASP:OD1	5:DK:162:ASP:N	2.37	0.58
2:HD:23:MET:N	2:HD:23:MET:SD	2.77	0.58
4:IH:319:ILE:HD11	4:IH:345:LEU:HD22	1.84	0.58
3:ZF:219:ARG:HH22	3:ZF:233:ARG:HH21	1.51	0.58
3:ZF:254:ILE:HB	3:ZF:262:ILE:HB	1.85	0.58
11:DC:154:ASP:OD1	11:DC:154:ASP:N	2.36	0.58
11:HC:101:LEU:HB2	11:HC:105:ILE:HB	1.85	0.58
6:EL:108:ASP:O	6:EL:112:GLN:NE2	2.37	0.58
4:FH:347:VAL:HG13	4:FH:354:MET:HB3	1.85	0.58
1:HG:898:LYS:NZ	1:IG:865:THR:O	2.37	0.58
1:HG:1017:GLN:NE2	1:IG:1020:GLN:OE1	2.37	0.58
7:LM:119:GLU:HG3	7:LM:139:ALA:HB3	1.85	0.57
5:BK:50:ASP:OD1	5:BK:50:ASP:N	2.36	0.57
5:MK:50:ASP:OD1	5:MK:50:ASP:N	2.37	0.57
11:JC:221:VAL:HA	11:JC:255:LEU:HA	1.86	0.57
4:FH:180:VAL:HA	4:FH:211:ASN:O	2.03	0.57
3:IF:231:THR:HG23	4:JH:150:LYS:HE3	1.85	0.57
5:AK:66:LYS:HB3	5:AK:77:SER:HB3	1.86	0.57
3:ZF:251:GLN:O	3:ZF:263:LYS:NZ	2.37	0.57
4:CH:159:ASN:OD1	4:CH:257:GLN:NE2	2.37	0.57
6:FL:109:LEU:HB2	6:FL:114:ILE:HG13	1.85	0.57
3:Gf:244:VAL:HA	3:Gf:256:THR:HA	1.86	0.57
6:ML:121:ASP:O	6:ML:123:ARG:NH1	2.38	0.57
11:EC:249:ILE:HB	11:FC:123:GLN:HE22	1.69	0.57
11:JC:109:VAL:HG23	11:JC:208:GLY:HA3	1.85	0.57
4:DH:159:ASN:HD22	4:DH:257:GLN:HG2	1.69	0.57
4:FH:230:LEU:HB2	4:FH:233:LEU:HB3	1.86	0.57
5:FK:68:ALA:HB3	5:FK:75:LEU:HB2	1.85	0.57
2:Hd:84:SER:H	11:DC:267:ALA:HB3	1.70	0.57
5:IK:152:ARG:HB2	5:IK:153:ILE:HD12	1.86	0.57
2:LD:132:LEU:HD12	2:LD:145:ILE:HG21	1.86	0.57
4:LH:155:SER:OG	4:LH:255:ARG:NH1	2.37	0.57
2:CD:24:LYS:HB2	6:CL:110:GLN:HE22	1.70	0.57
8:BN:49:ASN:OD1	8:BN:61:ASN:ND2	2.37	0.57
6:CL:124:THR:HA	6:CL:231:ILE:O	2.04	0.57
8:DN:92:TYR:HD1	8:DN:94:GLN:H	1.52	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:KM:288:ARG:NH2	7:KM:316:ASN:O	2.37	0.57
7:LM:174:GLN:NE2	7:LM:193:GLN:O	2.38	0.57
4:VH:203:ASN:N	4:VH:203:ASN:OD1	2.37	0.57
4:BH:273:PRO:O	11:JC:126:ARG:NH2	2.37	0.57
11:JC:163:VAL:HG12	11:JC:166:LEU:HD11	1.87	0.57
7:CM:210:ASP:OD1	7:CM:210:ASP:N	2.37	0.57
4:IH:204:ILE:HD11	4:IH:213:LEU:HD12	1.87	0.57
2:JD:148:TYR:O	2:JD:152:GLN:N	2.37	0.57
4:AH:108:ASP:OD1	4:AH:108:ASP:N	2.38	0.57
5:KK:166:THR:HG22	5:KK:168:TYR:H	1.70	0.57
6:KL:165:VAL:HG12	6:KL:231:ILE:HG12	1.85	0.57
7:LM:279:ILE:HB	7:LM:298:VAL:HG22	1.86	0.57
7:MM:215:ARG:NH2	7:MM:232:ASP:OD2	2.37	0.57
3:ZF:213:GLN:O	4:ZH:245:GLN:NE2	2.37	0.57
11:MC:217:ALA:O	11:MC:263:ARG:NH1	2.37	0.57
6:DL:169:THR:OG1	6:DL:170:ASP:N	2.37	0.57
4:FH:316:ASN:N	4:FH:316:ASN:OD1	2.37	0.57
8:FN:115:GLN:HE21	8:FN:115:GLN:N	2.03	0.57
2:GD:136:ASP:O	2:Gd:60:LYS:NZ	2.36	0.57
2:JD:30:ILE:O	6:JL:131:LYS:NZ	2.38	0.57
4:JH:284:LEU:O	4:JH:314:ARG:NH2	2.37	0.57
2:CD:26:LYS:O	6:CL:115:GLN:NE2	2.38	0.57
11:EC:133:LYS:NZ	11:EC:134:VAL:O	2.37	0.57
7:EM:276:ALA:H	7:EM:295:ASN:HB2	1.68	0.57
1:HG:874:ASP:N	1:HG:874:ASP:OD1	2.37	0.57
6:GL:170:ASP:N	6:GL:170:ASP:OD1	2.38	0.57
6:HL:115:GLN:HB3	6:HL:126:ILE:HB	1.85	0.57
8:IN:97:SER:O	1:FG:893:LYS:NZ	2.37	0.57
4:LH:159:ASN:OD1	4:LH:257:GLN:NE2	2.38	0.57
4:WH:250:TYR:HB3	4:FH:238:MET:HG3	1.86	0.57
3:BF:216:ILE:HG13	3:BF:219:ARG:HB2	1.87	0.57
7:EM:119:GLU:HG3	7:EM:139:ALA:HB3	1.87	0.57
7:GM:125:THR:HG23	7:GM:145:ARG:HB2	1.86	0.57
5:IK:66:LYS:HB3	5:IK:77:SER:HB3	1.87	0.57
5:KK:90:ARG:NH1	7:KM:293:ALA:O	2.38	0.57
1:Lg:807:GLN:O	1:Lg:810:GLN:NE2	2.38	0.57
2:AD:73:ILE:O	2:AD:133:ARG:NH2	2.38	0.57
4:DH:203:ASN:ND2	4:DH:216:GLN:OE1	2.38	0.57
5:EK:76:ILE:HB	5:EK:182:ILE:HG23	1.87	0.57
6:EL:192:PHE:O	6:EL:196:ASN:ND2	2.38	0.57
1:IG:1017:GLN:NE2	1:IG:1018:GLN:OE1	2.36	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Fd:150:ASN:OD1	2:Fd:150:ASN:N	2.38	0.57
2:Gd:148:TYR:HB2	2:Gd:153:VAL:HG12	1.87	0.56
2:JD:23:MET:N	2:JD:23:MET:SD	2.78	0.56
6:JL:54:ARG:HH21	6:JL:57:VAL:HG13	1.68	0.56
4:MH:324:TRP:HA	4:MH:339:MET:HG3	1.85	0.56
5:MK:162:ASP:N	5:MK:162:ASP:OD1	2.36	0.56
4:ZH:262:ASN:OD1	4:ZH:262:ASN:N	2.38	0.56
7:BM:200:GLY:O	7:BM:220:ALA:HA	2.04	0.56
3:EF:210:TYR:HA	3:EF:224:GLY:HA2	1.86	0.56
1:JG:898:LYS:NZ	1:KG:865:THR:O	2.38	0.56
3:AF:250:LEU:HG	3:AF:251:GLN:HG3	1.87	0.56
6:KL:134:MET:HB2	6:KL:139:ARG:HB2	1.86	0.56
8:KN:57:ARG:NH1	8:KN:66:SER:O	2.38	0.56
6:AL:169:THR:OG1	6:AL:170:ASP:N	2.38	0.56
7:AM:286:LYS:O	7:AM:316:ASN:ND2	2.38	0.56
6:BL:42:CYS:SG	6:BL:43:PHE:N	2.78	0.56
6:BL:124:THR:HA	6:BL:231:ILE:O	2.04	0.56
7:DM:163:THR:HB	7:DM:183:VAL:HG12	1.86	0.56
6:EL:136:SER:O	7:EM:314:ARG:NH1	2.36	0.56
8:EN:45:MET:SD	8:EN:62:ASN:ND2	2.74	0.56
5:FK:121:SER:OG	5:FK:122:LYS:N	2.38	0.56
8:FN:77:ASP:OD1	8:FN:79:GLN:NE2	2.39	0.56
2:GD:158:TYR:O	2:Gd:137:TYR:OH	2.23	0.56
4:HH:324:TRP:HA	4:HH:339:MET:HG3	1.87	0.56
5:JK:76:ILE:HG13	5:JK:182:ILE:HB	1.87	0.56
5:JK:177:ASN:O	5:JK:179:ARG:NH1	2.37	0.56
6:JL:168:PHE:HB2	6:JL:228:ARG:HG2	1.86	0.56
7:JM:210:ASP:N	7:JM:210:ASP:OD1	2.38	0.56
1:Kg:811:ASP:O	1:Kg:814:GLN:NE2	2.36	0.56
5:KK:50:ASP:OD1	5:KK:50:ASP:N	2.36	0.56
3:LF:245:LYS:NZ	3:LF:256:THR:O	2.37	0.56
1:Cg:807:GLN:O	1:Cg:810:GLN:NE2	2.39	0.56
9:MU:127:UNK:O	6:AL:232:GLN:NE2	2.38	0.56
1:EG:899:LEU:HD13	1:EG:919:MET:HG2	1.88	0.56
7:AM:288:ARG:NH2	7:AM:316:ASN:O	2.37	0.56
4:BH:181:PHE:O	4:BH:211:ASN:ND2	2.33	0.56
4:BH:315:THR:OG1	4:BH:316:ASN:N	2.37	0.56
1:FG:921:ILE:HD12	1:FG:926:LYS:HD2	1.86	0.56
6:CL:226:ASN:O	6:CL:228:ARG:NH1	2.38	0.56
2:DD:23:MET:SD	2:DD:23:MET:N	2.79	0.56
5:EK:86:ASP:OD1	5:EK:86:ASP:N	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:EK:148:GLY:H	2:Ed:30:ILE:HD13	1.70	0.56
4:FH:345:LEU:O	4:FH:355:GLN:HA	2.05	0.56
7:FM:143:THR:HG22	7:FM:145:ARG:HH12	1.70	0.56
7:FM:189:VAL:HB	7:FM:207:ILE:HG22	1.87	0.56
2:GD:142:LYS:O	2:GD:159:ALA:HB2	2.05	0.56
8:HN:84:CYS:SG	8:HN:85:CYS:N	2.79	0.56
4:VH:170:ARG:H	4:VH:170:ARG:HE	1.51	0.56
3:CF:245:LYS:HE3	3:CF:257:SER:HA	1.87	0.56
6:AL:118:GLU:HG2	6:AL:123:ARG:HG2	1.88	0.56
7:AM:119:GLU:HG3	7:AM:139:ALA:HB3	1.87	0.56
9:AU:127:UNK:O	6:BL:232:GLN:NE2	2.36	0.56
6:BL:200:ALA:O	7:BM:230:ARG:NH2	2.38	0.56
4:CH:345:LEU:HB2	4:CH:356:LEU:HB2	1.87	0.56
3:Cf:246:LEU:HB3	3:Cf:255:LEU:HB3	1.88	0.56
7:DM:285:SER:H	7:DM:288:ARG:HE	1.54	0.56
8:DN:89:GLY:O	8:DN:104:ASN:ND2	2.39	0.56
4:FH:238:MET:N	4:FH:238:MET:SD	2.78	0.56
1:IG:999:SER:HB2	1:JG:972:PHE:HZ	1.70	0.56
4:GH:108:ASP:OD1	4:GH:108:ASP:N	2.39	0.56
6:LL:108:ASP:O	6:LL:112:GLN:NE2	2.38	0.56
5:AK:92:ASN:OD1	5:AK:92:ASN:N	2.38	0.56
7:MM:282:TYR:HE1	7:MM:301:MET:HG3	1.69	0.56
10:MX:22:UNK:HA	10:MX:77:UNK:HA	1.87	0.56
7:BM:279:ILE:HB	7:BM:298:VAL:HG22	1.85	0.56
11:DC:147:TRP:O	11:DC:151:LEU:HB2	2.06	0.56
3:EF:267:GLU:O	4:EH:150:LYS:NZ	2.38	0.56
3:Ef:219:ARG:HD2	3:Ef:233:ARG:HH21	1.70	0.56
1:PG:921:ILE:HD12	1:PG:926:LYS:HD2	1.86	0.56
5:HK:46:ASP:OD1	5:HK:46:ASP:N	2.39	0.56
2:Id:110:GLY:HA3	2:Id:158:TYR:HB2	1.88	0.56
3:LF:213:GLN:HG3	4:LH:170:ARG:HH21	1.69	0.56
4:VH:148:PRO:O	3:CF:233:ARG:NH1	2.39	0.56
3:Af:246:LEU:HB3	3:Af:255:LEU:HB2	1.88	0.56
11:MC:104:ASN:ND2	11:MC:141:ILE:O	2.39	0.56
5:CK:50:ASP:N	5:CK:50:ASP:OD1	2.37	0.56
2:DD:83:ALA:HA	5:DK:154:ILE:O	2.06	0.56
4:DH:183:ASP:HA	4:DH:256:VAL:HG12	1.87	0.56
1:GG:899:LEU:HB2	1:GG:919:MET:HG2	1.87	0.56
1:BG:912:MET:HB3	1:BG:944:LEU:HB2	1.86	0.56
5:LK:72:GLN:OE1	6:ML:225:GLN:NE2	2.38	0.56
8:LN:101:VAL:HG11	8:LN:112:CYS:HB3	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Cg:793:GLU:O	1:Cg:796:GLN:NE2	2.38	0.56
11:EC:157:LYS:NZ	11:EC:158:PRO:O	2.38	0.56
11:DC:217:ALA:O	11:DC:263:ARG:NH1	2.38	0.56
11:MC:235:GLY:HA3	11:MC:240:ILE:HA	1.87	0.56
11:KC:243:ILE:HD11	11:LC:129:ASP:HB3	1.87	0.56
1:Eg:807:GLN:O	1:Eg:810:GLN:NE2	2.39	0.56
7:FM:226:GLY:H	7:FM:246:LEU:HA	1.71	0.56
6:GL:165:VAL:HG12	6:GL:231:ILE:HG12	1.88	0.56
2:LD:66:SER:OG	2:LD:67:LYS:NZ	2.39	0.56
3:LF:254:ILE:HB	3:LF:262:ILE:HB	1.88	0.56
2:Ld:84:SER:H	11:HC:267:ALA:HB3	1.71	0.56
1:DG:951:HIS:H	1:DG:1027:THR:HG22	1.71	0.56
4:XH:238:MET:SD	4:XH:238:MET:N	2.78	0.56
11:GC:259:ASN:OD1	11:GC:259:ASN:N	2.36	0.56
11:HC:242:ILE:HD11	11:IC:129:ASP:HB3	1.87	0.56
3:EF:254:ILE:O	3:EF:261:VAL:HA	2.05	0.56
6:EL:115:GLN:HB3	6:EL:126:ILE:HB	1.87	0.56
1:NG:898:LYS:NZ	1:OG:865:THR:O	2.39	0.56
4:GH:324:TRP:HB3	4:GH:339:MET:HE2	1.88	0.56
7:GM:214:ILE:O	7:GM:215:ARG:NH1	2.36	0.56
7:BM:306:GLN:NE2	7:BM:308:ASP:OD1	2.37	0.56
4:CH:315:THR:HG23	4:CH:317:LEU:H	1.69	0.56
1:HG:912:MET:HB3	1:HG:944:LEU:HB2	1.87	0.56
1:NG:1003:ASN:HA	1:NG:1006:ILE:HD12	1.88	0.56
4:GH:313:VAL:HG12	4:GH:337:TYR:HB2	1.88	0.56
1:BG:910:ASP:OD1	1:BG:910:ASP:N	2.37	0.56
3:KF:207:ARG:NH1	3:KF:240:GLY:O	2.39	0.56
1:Mg:792:GLN:O	1:Mg:795:GLN:NE2	2.39	0.56
4:MH:183:ASP:OD1	4:MH:187:ALA:N	2.37	0.56
3:YF:243:MET:N	3:YF:243:MET:SD	2.79	0.56
8:AN:62:ASN:OD1	8:AN:62:ASN:N	2.38	0.56
2:BD:47:SER:OG	11:JC:203:LYS:NZ	2.39	0.56
9:BU:129:UNK:O	6:CL:204:LYS:NZ	2.38	0.56
1:IG:901:GLY:HA3	1:IG:916:PHE:HA	1.87	0.56
5:GK:78:ILE:HB	5:GK:180:VAL:HG23	1.87	0.55
8:GN:49:ASN:HD21	8:GN:61:ASN:HA	1.70	0.55
7:HM:288:ARG:NH2	7:HM:316:ASN:O	2.39	0.55
2:Id:105:ARG:HB3	2:Id:153:VAL:HG23	1.87	0.55
2:Id:148:TYR:HB2	2:Id:153:VAL:HG12	1.88	0.55
8:KN:62:ASN:OD1	8:KN:62:ASN:N	2.39	0.55
1:Lg:791:GLN:N	1:Lg:793:GLU:OE2	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:MF:254:ILE:HB	3:MF:262:ILE:HB	1.88	0.55
1:Mg:807:GLN:O	1:Mg:810:GLN:NE2	2.39	0.55
6:ML:115:GLN:HB3	6:ML:126:ILE:HB	1.88	0.55
4:XH:125:GLU:OE2	4:XH:126:GLN:NE2	2.38	0.55
4:BH:301:ASP:OD1	4:BH:301:ASP:N	2.37	0.55
1:MG:912:MET:HB3	1:MG:944:LEU:HB2	1.88	0.55
2:GD:54:GLU:OE1	11:BC:215:LYS:NZ	2.39	0.55
8:GN:62:ASN:OD1	8:GN:62:ASN:N	2.40	0.55
2:JD:67:LYS:HZ1	2:Jd:62:ILE:H	1.52	0.55
4:KH:155:SER:OG	4:KH:255:ARG:NH1	2.39	0.55
4:KH:301:ASP:OD1	4:KH:301:ASP:N	2.37	0.55
6:KL:212:ASN:OD1	6:KL:212:ASN:N	2.37	0.55
7:KM:292:MET:N	7:KM:292:MET:SD	2.79	0.55
4:ZH:108:ASP:OD1	4:ZH:108:ASP:N	2.37	0.55
11:EC:198:ASN:OD1	11:EC:201:ARG:NH2	2.39	0.55
2:DD:29:PRO:HG2	6:DL:225:GLN:HA	1.87	0.55
3:FF:253:ARG:HE	3:FF:261:VAL:HG11	1.71	0.55
11:BC:102:LEU:HB2	11:BC:106:ILE:HG23	1.88	0.55
5:IK:146:SER:HB2	2:Id:29:PRO:HG3	1.87	0.55
8:IN:89:GLY:HA3	8:IN:104:ASN:HB2	1.86	0.55
2:JD:141:LYS:NZ	2:Jd:61:VAL:O	2.39	0.55
6:JL:130:ASP:N	6:JL:130:ASP:OD1	2.39	0.55
1:CG:898:LYS:HE2	1:DG:864:LYS:HE2	1.86	0.55
4:KH:315:THR:OG1	4:KH:316:ASN:N	2.38	0.55
6:KL:177:HIS:HD1	7:KM:315:TYR:HH	1.53	0.55
7:KM:209:SER:OG	7:KM:210:ASP:N	2.39	0.55
4:LH:203:ASN:HB2	4:LH:216:GLN:HE21	1.71	0.55
5:LK:60:LEU:HD22	5:LK:65:ILE:HD11	1.88	0.55
7:LM:249:GLN:OE1	7:LM:267:ASN:ND2	2.40	0.55
2:CD:29:PRO:HG2	6:CL:225:GLN:HA	1.87	0.55
4:DH:238:MET:SD	4:EH:178:SER:OG	2.64	0.55
1:JG:880:ASP:OD1	1:JG:880:ASP:N	2.37	0.55
11:BC:244:ASP:OD1	11:BC:244:ASP:N	2.37	0.55
6:GL:44:HIS:HB2	6:GL:48:ASN:HA	1.88	0.55
3:JF:210:TYR:HA	3:JF:224:GLY:HA2	1.88	0.55
5:KK:92:ASN:OD1	5:KK:92:ASN:N	2.39	0.55
4:LH:146:GLY:HA2	10:YX:70:UNK:H2	1.72	0.55
2:CD:130:GLU:OE2	2:CD:133:ARG:NH1	2.39	0.55
4:MH:255:ARG:NH1	4:ZH:285:GLU:OE2	2.39	0.55
4:WH:168:VAL:HG12	4:WH:240:THR:HB	1.89	0.55
4:WH:204:ILE:HD11	4:WH:213:LEU:HD22	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FG:898:LYS:HE2	1:GG:864:LYS:HE2	1.88	0.55
4:EH:278:ASP:OD1	4:EH:278:ASP:N	2.37	0.55
1:IG:880:ASP:OD1	1:IG:880:ASP:N	2.37	0.55
4:GH:332:ASP:OD1	4:GH:332:ASP:N	2.39	0.55
6:GL:216:ASP:H	5:FK:72:GLN:HE22	1.54	0.55
7:GM:249:GLN:OE1	7:GM:267:ASN:ND2	2.40	0.55
5:HK:150:ASP:OD1	5:HK:152:ARG:NH2	2.39	0.55
6:HL:170:ASP:N	6:HL:170:ASP:OD1	2.40	0.55
3:JF:254:ILE:HB	3:JF:262:ILE:HB	1.88	0.55
1:Ag:811:ASP:O	1:Ag:814:GLN:NE2	2.33	0.55
2:DD:93:GLU:OE1	2:DD:97:ARG:NH2	2.40	0.55
3:DF:209:ILE:H	3:DF:225:SER:HB3	1.70	0.55
2:Gd:110:GLY:HA3	2:Gd:158:TYR:HB2	1.87	0.55
1:BG:886:LEU:HB3	1:BG:900:ILE:HG23	1.87	0.55
2:ID:82:ARG:NH2	2:ID:125:ASP:O	2.40	0.55
6:JL:212:ASN:N	6:JL:212:ASN:OD1	2.37	0.55
7:JM:257:ASP:N	7:JM:257:ASP:OD1	2.38	0.55
4:LH:108:ASP:OD1	4:LH:108:ASP:N	2.36	0.55
8:MN:102:VAL:HA	8:MN:108:VAL:HA	1.89	0.55
3:Mf:243:MET:O	3:Mf:245:LYS:NZ	2.40	0.55
3:XF:214:ALA:HB3	3:XF:221:TRP:HB3	1.89	0.55
5:CK:87:GLN:HB3	5:CK:128:ARG:HH12	1.72	0.55
2:FD:130:GLU:OE2	2:FD:133:ARG:NH1	2.40	0.55
2:FD:150:ASN:OD1	2:FD:150:ASN:N	2.39	0.55
7:GM:257:ASP:N	7:GM:257:ASP:OD1	2.40	0.55
4:IH:192:ALA:HB2	4:IH:231:ARG:HD3	1.88	0.55
11:CC:231:ASP:N	11:CC:231:ASP:OD1	2.39	0.55
7:DM:308:ASP:OD1	7:DM:308:ASP:N	2.40	0.55
4:EH:183:ASP:HA	4:EH:256:VAL:HG12	1.87	0.55
4:FH:207:ASP:OD1	4:FH:207:ASP:N	2.38	0.55
4:FH:315:THR:OG1	4:FH:316:ASN:N	2.40	0.55
2:GD:74:PRO:HD2	2:GD:147:VAL:HG23	1.88	0.55
4:GH:170:ARG:NH1	4:GH:249:ASP:OD1	2.40	0.55
3:If:245:LYS:NZ	3:If:256:THR:O	2.40	0.55
4:LH:291:GLY:O	4:LH:293:ARG:NH2	2.36	0.55
2:MD:36:ASP:OD1	2:MD:36:ASP:N	2.38	0.55
1:Mg:797:ARG:NH2	1:Mg:801:MET:SD	2.80	0.55
3:CF:214:ALA:HB3	3:CF:221:TRP:HB2	1.88	0.55
11:EC:245:ARG:HB3	11:FC:127:ILE:HG23	1.88	0.55
7:EM:275:ASP:HB3	7:EM:294:PHE:HB2	1.89	0.55
1:AG:867:ASP:OD1	1:AG:867:ASP:N	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GD:23:MET:SD	2:GD:23:MET:N	2.80	0.55
2:Gd:111:LYS:NZ	2:Gd:112:SER:O	2.39	0.55
4:JH:190:PRO:HA	4:JH:211:ASN:HB3	1.89	0.55
6:JL:124:THR:HA	6:JL:231:ILE:O	2.06	0.55
6:JL:210:ASP:N	6:JL:210:ASP:OD1	2.39	0.55
1:CG:922:PRO:HB3	1:DG:864:LYS:HE3	1.89	0.55
7:KM:275:ASP:HB3	7:KM:294:PHE:HB2	1.88	0.55
4:BH:278:ASP:OD1	4:BH:278:ASP:N	2.40	0.55
1:FG:877:VAL:HG23	1:GG:942:THR:HG21	1.88	0.55
11:LC:151:LEU:HD21	11:LC:202:ILE:HG21	1.89	0.55
3:Cf:210:TYR:HB3	3:Cf:222:LEU:HD22	1.88	0.55
7:DM:209:SER:OG	7:DM:210:ASP:N	2.40	0.55
4:EH:266:MET:N	4:EH:266:MET:SD	2.80	0.55
3:Ef:245:LYS:NZ	3:Ef:256:THR:O	2.40	0.55
2:GD:130:GLU:OE2	2:GD:133:ARG:NH1	2.40	0.55
8:GN:77:ASP:N	8:GN:77:ASP:OD1	2.40	0.55
3:HF:245:LYS:HE3	3:HF:257:SER:HA	1.89	0.55
4:HH:185:THR:O	4:HH:264:LYS:NZ	2.38	0.55
2:ID:124:LYS:O	7:IM:317:LYS:NZ	2.40	0.55
4:JH:117:ARG:O	4:JH:117:ARG:NH1	2.38	0.55
4:AH:273:PRO:O	11:IC:126:ARG:NH1	2.40	0.55
2:CD:28:PRO:HG3	6:CL:115:GLN:HB2	1.89	0.55
2:Ld:29:PRO:HG2	2:Ld:32:ASN:HB3	1.89	0.55
5:AK:177:ASN:O	5:AK:179:ARG:NH1	2.40	0.55
4:MH:315:THR:OG1	4:MH:316:ASN:N	2.40	0.55
6:AL:150:ASN:OD1	6:AL:153:ARG:NH2	2.40	0.55
6:BL:194:TRP:O	7:BM:254:LYS:NZ	2.40	0.55
3:EF:246:LEU:HB3	3:EF:255:LEU:HD12	1.89	0.55
8:EN:46:GLY:HA3	8:EN:61:ASN:HB2	1.87	0.55
1:PG:951:HIS:H	1:PG:1027:THR:HG22	1.71	0.55
2:Fd:76:ALA:O	2:Fd:80:GLN:NE2	2.37	0.55
11:BC:259:ASN:ND2	11:BC:262:GLU:OE2	2.40	0.55
2:Jd:150:ASN:N	2:Jd:150:ASN:OD1	2.40	0.54
5:KK:46:ASP:N	5:KK:46:ASP:OD1	2.38	0.54
2:LD:23:MET:N	2:LD:23:MET:SD	2.79	0.54
5:AK:47:GLY:O	5:AK:108:GLN:NE2	2.40	0.54
7:MM:306:GLN:OE1	3:Mf:253:ARG:NH2	2.41	0.54
7:MM:308:ASP:OD1	7:MM:308:ASP:N	2.41	0.54
8:MN:49:ASN:HD21	8:MN:61:ASN:HA	1.72	0.54
7:AM:249:GLN:OE1	7:AM:267:ASN:ND2	2.40	0.54
7:BM:249:GLN:OE1	7:BM:267:ASN:ND2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:EC:170:LYS:HA	11:EC:173:LYS:HE2	1.89	0.54
11:EC:247:LEU:HB2	11:FC:125:ILE:HD11	1.88	0.54
11:DC:175:ILE:HA	11:DC:178:ILE:HG12	1.89	0.54
7:CM:163:THR:HB	7:CM:183:VAL:HG12	1.89	0.54
8:EN:66:SER:OG	8:EN:67:THR:N	2.40	0.54
1:IG:1003:ASN:HA	1:IG:1006:ILE:HD12	1.90	0.54
11:AC:258:ASN:OD1	11:AC:258:ASN:N	2.38	0.54
1:Gg:791:GLN:N	1:Gg:793:GLU:OE1	2.40	0.54
6:HL:169:THR:O	6:HL:226:ASN:ND2	2.41	0.54
1:Bg:808:LEU:HA	1:Bg:811:ASP:HB2	1.88	0.54
6:IL:108:ASP:OD2	6:IL:150:ASN:ND2	2.40	0.54
7:IM:163:THR:HB	7:IM:183:VAL:HG12	1.88	0.54
2:Jd:68:ASP:N	2:Jd:68:ASP:OD1	2.38	0.54
3:KF:213:GLN:O	4:KH:170:ARG:NH1	2.40	0.54
4:LH:315:THR:OG1	4:LH:316:ASN:N	2.40	0.54
7:LM:186:SER:HA	7:LM:205:TYR:HB2	1.88	0.54
11:JC:123:GLN:O	11:IC:248:ARG:NH2	2.40	0.54
1:GG:958:SER:O	1:GG:962:SER:OG	2.25	0.54
1:HG:958:SER:O	1:HG:962:SER:OG	2.26	0.54
7:FM:303:GLU:OE1	3:Ff:251:GLN:NE2	2.40	0.54
8:FN:52:ASP:O	8:FN:56:GLY:N	2.37	0.54
4:IH:155:SER:OG	4:IH:255:ARG:NH2	2.40	0.54
8:IN:63:GLY:HA3	2:JD:27:LYS:HB2	1.88	0.54
4:AH:284:LEU:O	4:AH:314:ARG:NH1	2.40	0.54
1:Kg:792:GLN:O	1:Kg:795:GLN:NE2	2.41	0.54
4:KH:341:LYS:HB2	4:KH:361:LEU:HD13	1.90	0.54
7:KM:268:HIS:ND1	7:KM:287:THR:OG1	2.39	0.54
1:DG:912:MET:HB3	1:DG:944:LEU:HB2	1.88	0.54
4:MH:319:ILE:HG12	4:MH:339:MET:HE1	1.90	0.54
7:MM:214:ILE:O	7:MM:215:ARG:NH1	2.38	0.54
2:Bd:36:ASP:OD1	2:Bd:36:ASP:N	2.40	0.54
11:MC:69:GLN:NE2	8:EN:115:GLN:OE1	2.40	0.54
5:DK:163:LYS:NZ	5:DK:164:PRO:O	2.41	0.54
7:DM:119:GLU:HG3	7:DM:139:ALA:HB3	1.90	0.54
4:EH:207:ASP:N	4:EH:207:ASP:OD1	2.39	0.54
2:Ed:66:SER:OG	2:Ed:67:LYS:NZ	2.41	0.54
2:FD:23:MET:N	2:FD:23:MET:SD	2.81	0.54
4:FH:158:VAL:HB	4:FH:256:VAL:HA	1.88	0.54
1:LG:972:PHE:HB3	1:LG:1005:VAL:HG22	1.88	0.54
1:MG:873:LEU:HD23	1:MG:1037:LEU:HD22	1.88	0.54
2:Gd:36:ASP:OD1	2:Gd:36:ASP:N	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:ID:23:MET:N	2:ID:23:MET:SD	2.81	0.54
1:Ig:792:GLN:O	1:Ig:795:GLN:NE2	2.37	0.54
4:KH:191:ILE:HG22	4:KH:211:ASN:HA	1.89	0.54
3:LF:233:ARG:NH1	3:MF:269:SER:OG	2.41	0.54
5:MK:66:LYS:HB3	5:MK:77:SER:HB3	1.89	0.54
6:ML:124:THR:HA	6:ML:231:ILE:O	2.06	0.54
10:MX:25:UNK:N	10:MX:71:UNK:O	2.41	0.54
2:Md:84:SER:H	11:IC:267:ALA:HB3	1.72	0.54
4:VH:117:ARG:NH1	4:VH:118:ASN:OD1	2.41	0.54
4:XH:159:ASN:OD1	4:XH:257:GLN:NE2	2.40	0.54
3:ZF:214:ALA:HB3	3:ZF:221:TRP:HB2	1.90	0.54
7:AM:257:ASP:N	7:AM:257:ASP:OD1	2.38	0.54
6:CL:113:ASP:N	6:CL:113:ASP:OD1	2.41	0.54
5:EK:68:ALA:HB3	5:EK:75:LEU:HB3	1.89	0.54
7:FM:215:ARG:NH1	7:FM:232:ASP:OD1	2.37	0.54
6:GL:174:SER:HG	6:GL:176:SER:HG	1.54	0.54
2:Dd:148:TYR:HB2	2:Dd:153:VAL:HG12	1.90	0.54
7:HM:146:LEU:HB2	7:HM:165:ILE:HG12	1.89	0.54
1:BG:1019:ALA:O	1:BG:1023:PHE:HB2	2.07	0.54
3:IF:233:ARG:NH2	4:JH:148:PRO:O	2.40	0.54
4:IH:148:PRO:O	3:XF:233:ARG:NH1	2.41	0.54
8:IN:72:ARG:NH1	4:JH:298:SER:OG	2.38	0.54
2:Id:68:ASP:OD1	2:Id:68:ASP:N	2.36	0.54
2:Jd:81:ALA:HB3	2:Jd:128:LEU:HD11	1.89	0.54
5:BK:114:ILE:HB	5:BK:154:ILE:HG22	1.90	0.54
11:EC:146:THR:OG1	11:EC:147:TRP:N	2.35	0.54
11:MC:109:VAL:HG13	11:MC:208:GLY:HA3	1.89	0.54
11:MC:230:ASP:OD1	11:MC:230:ASP:N	2.40	0.54
7:DM:210:ASP:N	7:DM:210:ASP:OD1	2.39	0.54
6:FL:115:GLN:HB3	6:FL:126:ILE:HB	1.88	0.54
2:ID:77:TYR:OH	5:IK:130:ARG:NH1	2.40	0.54
4:IH:210:SER:OG	4:IH:211:ASN:N	2.40	0.54
1:Mg:797:ARG:HH12	1:Mg:801:MET:HB2	1.72	0.54
4:WH:159:ASN:OD1	4:WH:257:GLN:NE2	2.40	0.54
4:XH:125:GLU:OE1	4:XH:129:LYS:NZ	2.41	0.54
3:BF:213:GLN:HB2	3:BF:221:TRP:HB3	1.89	0.54
11:HC:113:GLY:O	11:HC:130:ARG:HA	2.08	0.54
7:CM:257:ASP:OD1	7:CM:257:ASP:N	2.40	0.54
2:DD:130:GLU:OE2	2:DD:133:ARG:NH1	2.39	0.54
1:GG:972:PHE:HB3	1:GG:1005:VAL:HG22	1.90	0.54
6:EL:169:THR:OG1	6:EL:170:ASP:N	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:GH:249:ASP:OD1	4:GH:249:ASP:N	2.40	0.54
7:GM:163:THR:HB	7:GM:183:VAL:HG12	1.90	0.54
2:HD:125:ASP:O	7:HM:317:LYS:NZ	2.40	0.54
1:Bg:824:THR:H	4:AH:208:LYS:HD2	1.71	0.54
5:IK:125:SER:HG	5:IK:128:ARG:H	1.55	0.54
6:IL:169:THR:OG1	6:IL:170:ASP:N	2.40	0.54
3:Jf:245:LYS:NZ	3:Jf:256:THR:O	2.39	0.54
7:KM:307:SER:OG	3:Kf:253:ARG:NH2	2.39	0.54
6:LL:124:THR:HA	6:LL:231:ILE:O	2.06	0.54
2:MD:77:TYR:OH	5:MK:130:ARG:NH1	2.40	0.54
3:VF:207:ARG:NH1	3:VF:241:TYR:OH	2.41	0.54
3:WF:263:LYS:HD3	3:WF:264:PHE:H	1.71	0.54
3:ZF:247:ILE:HG12	3:ZF:254:ILE:HG23	1.89	0.54
2:Ad:150:ASN:N	2:Ad:150:ASN:OD1	2.40	0.54
3:Af:211:TYR:O	3:Af:213:GLN:NE2	2.41	0.54
5:BK:85:ALA:HB3	5:BK:88:SER:HB2	1.90	0.54
11:DC:228:HIS:HB3	11:DC:247:LEU:HG	1.89	0.54
11:GC:92:ASP:OD1	11:GC:148:TRP:NE1	2.39	0.54
4:CH:249:ASP:OD1	4:CH:249:ASP:N	2.39	0.54
3:DF:265:SER:HB3	3:DF:268:ASP:HB3	1.88	0.54
1:GG:931:SER:O	1:GG:1042:THR:OG1	2.26	0.54
1:GG:1017:GLN:NE2	1:GG:1018:GLN:OE1	2.39	0.54
1:HG:880:ASP:OD1	1:HG:880:ASP:N	2.39	0.54
1:IG:958:SER:O	1:IG:962:SER:OG	2.26	0.54
3:AF:254:ILE:O	3:AF:261:VAL:HA	2.08	0.54
2:Gd:76:ALA:O	2:Gd:80:GLN:NE2	2.39	0.54
4:IH:173:GLN:NE2	4:IH:218:THR:O	2.41	0.54
7:IM:117:ARG:NH2	7:IM:119:GLU:OE2	2.40	0.54
2:JD:136:ASP:HB3	2:Jd:60:LYS:HE2	1.90	0.54
4:JH:251:ARG:NH1	4:JH:253:ASP:OD2	2.41	0.54
4:XH:315:THR:OG1	4:XH:316:ASN:N	2.41	0.54
6:AL:187:GLU:OE2	7:AM:268:HIS:ND1	2.41	0.54
9:CU:128:UNK:HA	6:DL:232:GLN:HE22	1.72	0.54
4:DH:204:ILE:HG12	4:DH:215:ILE:HG23	1.89	0.54
6:DL:226:ASN:O	6:DL:228:ARG:NH1	2.39	0.54
4:EH:249:ASP:N	4:EH:249:ASP:OD1	2.41	0.54
4:EH:315:THR:OG1	4:EH:316:ASN:N	2.40	0.54
6:EL:124:THR:HA	6:EL:231:ILE:O	2.08	0.54
2:ID:118:LEU:O	11:DC:97:ASN:ND2	2.40	0.54
5:JK:92:ASN:N	5:JK:92:ASN:OD1	2.40	0.54
4:AH:203:ASN:OD1	4:AH:216:GLN:NE2	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:KD:36:ASP:OD1	2:KD:36:ASP:N	2.41	0.54
2:Kd:29:PRO:O	2:Kd:32:ASN:ND2	2.41	0.54
5:LK:151:SER:OG	5:LK:152:ARG:N	2.41	0.54
2:MD:124:LYS:O	7:MM:317:LYS:NZ	2.40	0.54
6:ML:178:LYS:O	6:ML:182:SER:OG	2.24	0.54
2:Md:150:ASN:OD1	2:Md:150:ASN:N	2.41	0.54
4:VH:149:PRO:HB2	4:VH:248:VAL:HG12	1.90	0.54
4:CH:114:ASP:O	4:CH:118:ASN:ND2	2.41	0.54
2:DD:77:TYR:OH	5:DK:130:ARG:NH1	2.41	0.54
1:HG:881:GLU:HB2	1:IG:911:LYS:HZ3	1.73	0.54
11:BC:62:GLU:HA	11:BC:65:LEU:HD12	1.89	0.54
8:GN:48:ILE:HD12	8:GN:58:LEU:HD13	1.89	0.54
2:ID:47:SER:OG	11:DC:203:LYS:NZ	2.41	0.54
2:JD:140:GLY:O	2:Jd:60:LYS:NZ	2.40	0.54
5:JK:138:ARG:NH2	7:JM:320:PRO:O	2.41	0.54
1:CG:972:PHE:HB3	1:CG:1005:VAL:HG22	1.90	0.54
3:XF:254:ILE:HB	3:XF:262:ILE:HB	1.89	0.54
4:ZH:207:ASP:OD1	4:ZH:207:ASP:N	2.39	0.54
4:BH:190:PRO:HB2	4:BH:231:ARG:HD3	1.90	0.54
1:FG:958:SER:O	1:FG:962:SER:OG	2.26	0.54
11:FC:243:ASP:OD1	11:FC:243:ASP:N	2.40	0.54
11:GC:103:GLU:OE2	11:GC:104:HIS:ND1	2.41	0.54
5:DK:66:LYS:NZ	5:DK:67:VAL:O	2.41	0.54
1:JG:901:GLY:HA3	1:JG:916:PHE:HA	1.89	0.54
7:FM:279:ILE:O	7:FM:298:VAL:HA	2.08	0.54
1:AG:941:ARG:HG2	1:PG:876:SER:HB3	1.89	0.53
4:IH:108:ASP:OD1	4:IH:108:ASP:N	2.40	0.53
7:IM:308:ASP:N	7:IM:308:ASP:OD1	2.41	0.53
2:MD:85:VAL:HG12	5:MK:153:ILE:HG13	1.90	0.53
5:MK:87:GLN:HB3	5:MK:128:ARG:HH12	1.71	0.53
2:AD:69:ASN:OD1	2:AD:69:ASN:N	2.41	0.53
2:Bd:76:ALA:O	2:Bd:80:GLN:NE2	2.37	0.53
7:DM:165:ILE:HB	7:DM:185:ILE:HG23	1.89	0.53
4:FH:292:SER:HB3	4:FH:307:SER:HB3	1.89	0.53
1:JG:1019:ALA:O	1:JG:1023:PHE:HB2	2.07	0.53
4:GH:170:ARG:HD3	4:GH:245:GLN:HG2	1.89	0.53
7:HM:127:ASN:OD1	7:HM:127:ASN:N	2.41	0.53
2:Hd:78:ASN:OD1	2:Hd:78:ASN:N	2.41	0.53
2:LD:40:LYS:HZ2	11:GC:197:GLU:HB3	1.73	0.53
5:AK:78:ILE:HB	5:AK:180:VAL:HG23	1.90	0.53
5:MK:46:ASP:N	5:MK:46:ASP:OD1	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:ML:212:ASN:OD1	6:ML:212:ASN:N	2.42	0.53
7:MM:275:ASP:HB3	7:MM:294:PHE:HB2	1.89	0.53
1:ZG:818:GLN:OE1	4:ZH:205:GLN:NE2	2.40	0.53
1:FG:884:PRO:HA	1:FG:901:GLY:O	2.08	0.53
3:Bf:246:LEU:HB3	3:Bf:255:LEU:HD21	1.90	0.53
11:KC:102:LEU:HB2	11:KC:106:ILE:HG13	1.89	0.53
3:Cf:245:LYS:NZ	3:Cf:256:THR:O	2.41	0.53
2:Ed:36:ASP:N	2:Ed:36:ASP:OD1	2.39	0.53
1:AG:958:SER:O	1:AG:962:SER:OG	2.27	0.53
2:HD:52:MET:HE1	2:Hd:48:VAL:HA	1.89	0.53
3:HF:213:GLN:HB3	3:HF:221:TRP:HD1	1.73	0.53
1:BG:900:ILE:HD11	1:CG:865:THR:HG22	1.90	0.53
7:IM:114:ASN:HB3	7:IM:115:ARG:HH21	1.74	0.53
6:JL:230:GLU:OE2	6:JL:232:GLN:NE2	2.41	0.53
2:Jd:36:ASP:OD1	2:Jd:36:ASP:N	2.40	0.53
5:KK:76:ILE:HB	5:KK:182:ILE:HG23	1.90	0.53
2:Kd:36:ASP:N	2:Kd:36:ASP:OD1	2.41	0.53
2:MD:111:LYS:HZ2	2:Md:120:SER:H	1.56	0.53
5:MK:116:VAL:HG22	5:MK:182:ILE:HG23	1.90	0.53
7:BM:124:VAL:HB	7:BM:144:THR:HG23	1.91	0.53
1:FG:912:MET:HB3	1:FG:944:LEU:HB2	1.90	0.53
5:DK:152:ARG:NH2	4:EH:351:GLY:O	2.41	0.53
1:Fg:818:GLN:NE2	4:FH:205:GLN:OE1	2.41	0.53
1:AG:886:LEU:HA	1:AG:899:LEU:O	2.08	0.53
4:HH:108:ASP:N	4:HH:108:ASP:OD1	2.41	0.53
2:KD:31:ASN:OD1	6:KL:131:LYS:NZ	2.40	0.53
1:CG:917:ASN:OD1	1:CG:917:ASN:N	2.42	0.53
5:LK:66:LYS:NZ	5:LK:67:VAL:O	2.41	0.53
4:YH:278:ASP:N	4:YH:278:ASP:OD1	2.42	0.53
2:AD:160:LYS:NZ	2:AD:162:TYR:O	2.41	0.53
11:LC:101:LEU:HB2	11:LC:105:ILE:HG23	1.90	0.53
1:IG:904:ASN:N	1:IG:904:ASN:OD1	2.41	0.53
3:Ff:244:VAL:HA	3:Ff:256:THR:HA	1.89	0.53
2:GD:24:LYS:O	6:GL:110:GLN:NE2	2.42	0.53
2:ID:86:ASP:OD1	2:ID:86:ASP:N	2.40	0.53
8:IN:107:TYR:OH	11:DC:201:ARG:NH1	2.42	0.53
5:JK:115:THR:HB	5:JK:183:THR:HG23	1.91	0.53
2:Jd:48:VAL:HG11	11:EC:93:ILE:HG13	1.91	0.53
4:KH:278:ASP:N	4:KH:278:ASP:OD1	2.41	0.53
4:KH:321:SER:OG	11:EC:148:ARG:NH1	2.42	0.53
5:LK:85:ALA:HB3	5:LK:88:SER:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AK:150:ASP:OD1	5:AK:152:ARG:NH2	2.41	0.53
1:Cg:792:GLN:HG2	1:Cg:793:GLU:HG3	1.91	0.53
7:MM:245:TYR:HH	3:Mf:249:SER:HG	1.56	0.53
4:WH:148:PRO:O	3:FF:233:ARG:NH2	2.41	0.53
4:ZH:191:ILE:HA	4:ZH:230:LEU:HA	1.90	0.53
11:MC:221:VAL:HG12	11:MC:255:LEU:HD23	1.91	0.53
6:CL:212:ASN:OD1	6:CL:212:ASN:N	2.40	0.53
3:FF:254:ILE:HB	3:FF:262:ILE:HB	1.90	0.53
7:FM:171:ARG:O	7:FM:190:ASN:ND2	2.40	0.53
2:GD:77:TYR:OH	5:GK:130:ARG:NH1	2.42	0.53
4:IH:160:LEU:O	4:JH:251:ARG:NH2	2.41	0.53
5:IK:177:ASN:O	5:IK:179:ARG:NH1	2.41	0.53
2:Id:134:ASP:O	2:Id:138:GLN:NE2	2.41	0.53
6:KL:130:ASP:OD1	6:KL:130:ASP:N	2.39	0.53
6:KL:184:ALA:O	6:KL:188:THR:OG1	2.26	0.53
3:Kf:212:ILE:HD11	3:Kf:262:ILE:HG13	1.91	0.53
5:LK:107:LYS:NZ	5:LK:148:GLY:O	2.38	0.53
2:CD:23:MET:N	2:CD:23:MET:SD	2.82	0.53
2:MD:76:ALA:O	2:MD:80:GLN:NE2	2.41	0.53
7:BM:285:SER:O	7:BM:316:ASN:ND2	2.42	0.53
7:CM:199:LYS:HA	7:CM:219:ALA:HB3	1.90	0.53
10:CX:21:UNK:O	10:CX:78:UNK:N	2.42	0.53
1:GG:1017:GLN:OE1	1:HG:1020:GLN:NE2	2.42	0.53
2:FD:27:LYS:HD3	2:FD:28:PRO:HD2	1.89	0.53
4:FH:284:LEU:HD11	4:FH:330:SER:HB3	1.91	0.53
5:FK:66:LYS:HB3	5:FK:77:SER:HB3	1.89	0.53
5:FK:151:SER:OG	5:FK:152:ARG:N	2.42	0.53
11:IC:151:LEU:HD21	11:IC:202:ILE:HG21	1.90	0.53
8:GN:62:ASN:ND2	2:HD:25:PHE:O	2.42	0.53
2:Gd:150:ASN:N	2:Gd:150:ASN:OD1	2.40	0.53
4:HH:315:THR:OG1	4:HH:316:ASN:N	2.42	0.53
2:ID:122:SER:HG	11:DC:88:ARG:HH21	1.53	0.53
4:IH:266:MET:SD	4:IH:266:MET:N	2.80	0.53
8:LN:96:ASN:ND2	8:LN:100:LEU:O	2.42	0.53
2:Ld:70:THR:OG1	2:Ld:71:LEU:N	2.41	0.53
3:VF:219:ARG:HB3	3:VF:233:ARG:HD3	1.91	0.53
1:EG:898:LYS:HE2	1:FG:864:LYS:HB3	1.89	0.53
4:YH:315:THR:OG1	4:YH:316:ASN:N	2.41	0.53
2:AD:149:PRO:O	2:AD:152:GLN:NE2	2.41	0.53
5:BK:130:ARG:NH2	5:BK:162:ASP:OD2	2.42	0.53
11:FC:110:LEU:HD23	11:FC:212:TYR:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LC:89:ASN:OD1	11:LC:89:ASN:N	2.37	0.53
7:CM:308:ASP:N	7:CM:308:ASP:OD1	2.41	0.53
1:LG:885:ILE:O	1:LG:900:ILE:HA	2.08	0.53
6:HL:124:THR:HG22	6:HL:232:GLN:HG2	1.89	0.53
2:ID:36:ASP:N	2:ID:36:ASP:OD1	2.40	0.53
7:JM:128:ASN:O	7:JM:130:ARG:NH1	2.42	0.53
4:KH:316:ASN:N	4:KH:316:ASN:OD1	2.42	0.53
4:KH:343:PRO:HG2	4:KH:344:VAL:HG12	1.89	0.53
4:LH:117:ARG:NH1	4:LH:117:ARG:O	2.42	0.53
2:CD:150:ASN:N	2:CD:150:ASN:OD1	2.40	0.53
6:ML:130:ASP:N	6:ML:130:ASP:OD1	2.41	0.53
8:MN:57:ARG:NH1	8:MN:68:CYS:O	2.42	0.53
7:DM:275:ASP:HB3	7:DM:294:PHE:HB2	1.90	0.53
4:FH:182:LEU:HB2	4:FH:255:ARG:HH21	1.73	0.53
1:NG:900:ILE:HD11	1:OG:865:THR:HG22	1.91	0.53
7:FM:144:THR:HB	7:FM:163:THR:HG23	1.89	0.53
6:GL:124:THR:HA	6:GL:231:ILE:O	2.09	0.53
6:GL:212:ASN:N	6:GL:212:ASN:OD1	2.41	0.53
7:HM:177:LEU:HD13	7:HM:181:PRO:HG2	1.90	0.53
7:HM:249:GLN:OE1	7:HM:267:ASN:ND2	2.42	0.53
4:IH:311:MET:HG3	4:IH:341:LYS:HA	1.90	0.53
4:IH:315:THR:OG1	4:IH:316:ASN:N	2.42	0.53
4:AH:315:THR:OG1	4:AH:316:ASN:N	2.42	0.53
1:Kg:817:THR:OG1	1:Kg:818:GLN:N	2.39	0.53
2:LD:76:ALA:H	2:LD:79:LEU:HD12	1.73	0.53
2:LD:105:ARG:HB2	2:LD:153:VAL:HG12	1.91	0.53
5:AK:86:ASP:N	5:AK:86:ASP:OD1	2.40	0.53
4:MH:195:ASP:OD1	1:ZG:818:GLN:NE2	2.41	0.53
4:ZH:200:SER:OG	4:ZH:219:LYS:NZ	2.40	0.53
1:FG:922:PRO:HB3	1:GG:864:LYS:HE3	1.91	0.53
11:FC:88:ARG:NH1	11:FC:91:ASP:OD2	2.42	0.53
11:DC:114:ARG:HG2	11:DC:130:ARG:HG2	1.91	0.53
11:JC:175:ILE:HA	11:JC:178:ILE:HG12	1.90	0.53
5:CK:54:ILE:HA	5:CK:57:MET:HG2	1.89	0.53
6:CL:174:SER:HG	6:CL:176:SER:HG	1.54	0.53
2:Cd:71:LEU:O	2:Cd:133:ARG:NH1	2.42	0.53
9:DU:127:UNK:O	6:EL:232:GLN:NE2	2.41	0.53
6:EL:130:ASP:N	6:EL:130:ASP:OD1	2.42	0.53
11:AC:244:ASP:OD2	11:BC:127:ARG:NH2	2.41	0.53
11:IC:50:LYS:O	11:IC:54:ILE:HB	2.08	0.53
3:Hf:208:ILE:HG13	3:Hf:225:SER:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Id:150:ASN:OD1	2:Id:150:ASN:N	2.42	0.53
4:LH:294:ARG:HH21	11:GC:198:GLU:HG3	1.74	0.53
1:DG:874:ASP:OD1	1:DG:874:ASP:N	2.42	0.53
3:ZF:213:GLN:O	4:ZH:170:ARG:NH1	2.42	0.53
7:AM:307:SER:OG	3:Af:253:ARG:NH2	2.41	0.53
11:EC:226:VAL:HB	11:EC:249:ILE:HG23	1.90	0.53
11:KC:241:ILE:HG12	11:LC:255:LEU:HD13	1.90	0.53
4:EH:114:ASP:O	4:EH:118:ASN:ND2	2.42	0.53
4:EH:264:LYS:NZ	4:EH:266:MET:O	2.42	0.53
5:FK:92:ASN:OD1	5:FK:92:ASN:N	2.41	0.53
7:HM:155:LEU:HB3	7:HM:175:ILE:HD13	1.92	0.52
2:Id:70:THR:OG1	2:Id:133:ARG:NH1	2.42	0.52
4:JH:207:ASP:N	4:JH:207:ASP:OD1	2.41	0.52
4:JH:292:SER:OG	4:JH:293:ARG:N	2.43	0.52
6:JL:49:ASN:ND2	7:JM:293:ALA:O	2.34	0.52
3:KF:208:ILE:HG13	3:KF:225:SER:H	1.73	0.52
1:Lg:811:ASP:O	1:Lg:814:GLN:NE2	2.39	0.52
7:LM:308:ASP:OD1	7:LM:308:ASP:N	2.42	0.52
3:WF:243:MET:N	3:WF:243:MET:SD	2.82	0.52
8:AN:46:GLY:HA3	8:AN:61:ASN:HB2	1.90	0.52
11:FC:97:ASN:OD1	11:FC:97:ASN:N	2.33	0.52
11:LC:203:LYS:NZ	2:DD:47:SER:OG	2.42	0.52
1:Kg:807:GLN:O	1:Kg:810:GLN:NE2	2.41	0.52
6:KL:230:GLU:OE2	6:KL:232:GLN:NE2	2.42	0.52
7:KM:257:ASP:OD1	7:KM:257:ASP:N	2.42	0.52
4:LH:148:PRO:HD2	3:YF:219:ARG:HG2	1.90	0.52
1:DG:880:ASP:OD1	1:DG:880:ASP:N	2.42	0.52
5:AK:90:ARG:HD3	7:AM:292:MET:HB2	1.91	0.52
6:ML:47:TYR:OH	6:ML:142:GLU:OE1	2.27	0.52
7:MM:256:HIS:O	7:MM:259:SER:OG	2.28	0.52
3:VF:219:ARG:NH1	4:DH:149:PRO:O	2.37	0.52
2:BD:140:GLY:O	2:Bd:60:LYS:NZ	2.40	0.52
11:GC:250:ILE:O	11:HC:123:GLN:NE2	2.43	0.52
6:CL:133:PHE:HA	6:CL:141:ASN:H	1.74	0.52
7:DM:285:SER:O	7:DM:288:ARG:NH2	2.42	0.52
7:DM:313:ASP:H	7:DM:316:ASN:HB2	1.74	0.52
1:Eg:799:SER:HA	1:Eg:802:LEU:HD12	1.90	0.52
2:FD:86:ASP:OD1	11:AC:88:ARG:NH1	2.42	0.52
2:Dd:36:ASP:OD1	2:Dd:36:ASP:N	2.37	0.52
7:IM:214:ILE:O	7:IM:215:ARG:NH1	2.41	0.52
4:AH:159:ASN:ND2	4:AH:257:GLN:OE1	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:AH:203:ASN:HB3	4:AH:216:GLN:HG2	1.92	0.52
2:MD:73:ILE:O	2:MD:133:ARG:NH2	2.39	0.52
8:MN:77:ASP:OD1	8:MN:79:GLN:NE2	2.42	0.52
4:VH:182:LEU:O	4:VH:255:ARG:HA	2.09	0.52
3:YF:237:LYS:NZ	3:YF:238:ILE:O	2.43	0.52
6:AL:54:ARG:HH12	6:AL:56:ALA:H	1.57	0.52
2:BD:36:ASP:OD1	11:JC:75:ARG:NH2	2.42	0.52
4:BH:226:LEU:O	4:BH:238:MET:HA	2.09	0.52
5:BK:78:ILE:HB	5:BK:180:VAL:HG23	1.92	0.52
6:BL:121:ASP:OD1	6:BL:121:ASP:N	2.42	0.52
11:EC:258:ASN:O	11:EC:262:TRP:NE1	2.38	0.52
11:HC:230:ASP:N	11:HC:230:ASP:OD1	2.41	0.52
11:MC:213:ARG:NH1	2:Ed:59:GLU:OE2	2.43	0.52
4:CH:266:MET:SD	4:CH:266:MET:N	2.82	0.52
5:EK:151:SER:OG	5:EK:152:ARG:N	2.40	0.52
3:FF:220:ALA:O	3:FF:231:THR:HA	2.09	0.52
1:OG:931:SER:O	1:OG:1042:THR:OG1	2.28	0.52
1:OG:1030:GLU:HG2	1:PG:941:ARG:HH21	1.74	0.52
7:FM:158:VAL:HG22	7:FM:178:LYS:HE2	1.90	0.52
6:HL:121:ASP:O	6:HL:123:ARG:NH1	2.42	0.52
7:HM:127:ASN:HB3	7:HM:147:ALA:HB3	1.90	0.52
2:JD:36:ASP:N	2:JD:36:ASP:OD1	2.36	0.52
8:KN:63:GLY:HA3	2:LD:27:LYS:HB2	1.91	0.52
1:DG:958:SER:O	1:DG:962:SER:OG	2.28	0.52
4:ZH:203:ASN:OD1	4:ZH:216:GLN:NE2	2.41	0.52
8:BN:49:ASN:HB2	8:BN:59:VAL:HG23	1.91	0.52
7:CM:273:ALA:HB1	7:CM:277:SER:HB2	1.91	0.52
1:IG:899:LEU:HD13	1:IG:919:MET:HG2	1.91	0.52
7:FM:121:ALA:HA	7:FM:141:GLU:HB3	1.90	0.52
2:GD:36:ASP:N	2:GD:36:ASP:OD1	2.42	0.52
5:IK:87:GLN:NE2	5:IK:173:ASP:OD1	2.38	0.52
6:JL:192:PHE:O	6:JL:196:ASN:ND2	2.41	0.52
7:JM:125:THR:HG23	7:JM:145:ARG:HB2	1.91	0.52
6:ML:136:SER:O	7:MM:314:ARG:NH1	2.42	0.52
2:AD:158:TYR:O	2:Ad:137:TYR:OH	2.25	0.52
3:Af:219:ARG:HA	3:Af:232:VAL:O	2.10	0.52
4:EH:313:VAL:HG13	4:EH:337:TYR:HB2	1.92	0.52
1:LG:910:ASP:OD1	1:LG:910:ASP:N	2.38	0.52
1:LG:1003:ASN:HA	1:LG:1006:ILE:HD12	1.90	0.52
3:GF:219:ARG:NH1	4:HH:148:PRO:O	2.42	0.52
2:Hd:125:ASP:OD1	2:Hd:125:ASP:N	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BG:911:LYS:HA	1:BG:943:ALA:HA	1.92	0.52
6:IL:54:ARG:HH21	6:IL:57:VAL:HG13	1.74	0.52
4:AH:176:VAL:HG22	4:AH:216:GLN:HB3	1.92	0.52
11:CC:220:ASN:ND2	11:CC:262:GLU:O	2.42	0.52
3:KF:210:TYR:HA	3:KF:224:GLY:HA2	1.92	0.52
8:MN:57:ARG:NH1	8:MN:66:SER:O	2.42	0.52
1:WG:791:GLN:O	1:WG:795:GLN:NE2	2.43	0.52
11:DC:146:THR:O	11:DC:149:GLN:NE2	2.41	0.52
8:EN:57:ARG:NH1	8:EN:66:SER:O	2.43	0.52
11:AC:157:LYS:HD2	11:AC:159:GLU:HG2	1.92	0.52
7:HM:201:THR:HG22	7:HM:221:LYS:HB2	1.91	0.52
5:IK:76:ILE:HG21	5:IK:102:ILE:HD11	1.92	0.52
7:IM:257:ASP:N	7:IM:257:ASP:OD1	2.43	0.52
11:CC:124:GLN:O	11:BC:249:ARG:NH1	2.43	0.52
5:LK:177:ASN:O	5:LK:179:ARG:NH1	2.39	0.52
3:Lf:245:LYS:HG3	3:Lf:255:LEU:HB3	1.92	0.52
3:YF:254:ILE:HB	3:YF:262:ILE:HB	1.91	0.52
4:YH:183:ASP:OD1	4:YH:187:ALA:N	2.42	0.52
8:BN:77:ASP:OD2	4:CH:352:LYS:NZ	2.42	0.52
11:KC:147:THR:OG1	11:KC:148:TRP:N	2.41	0.52
6:CL:44:HIS:HB2	6:CL:48:ASN:HA	1.92	0.52
6:CL:139:ARG:NH2	7:CM:319:PHE:O	2.42	0.52
5:DK:73:ASN:OD1	5:DK:73:ASN:N	2.43	0.52
1:IG:912:MET:HB3	1:IG:944:LEU:HB2	1.92	0.52
1:Gg:797:ARG:HD3	4:HH:117:ARG:HH21	1.75	0.52
6:HL:130:ASP:OD1	6:HL:130:ASP:N	2.41	0.52
3:If:217:PRO:O	3:If:219:ARG:NH2	2.43	0.52
4:KH:205:GLN:HB2	4:KH:214:MET:HB3	1.92	0.52
7:KM:275:ASP:HA	7:KM:295:ASN:H	1.75	0.52
6:LL:230:GLU:OE2	6:LL:232:GLN:NE2	2.43	0.52
5:AK:72:GLN:NE2	6:BL:214:ILE:O	2.42	0.52
4:VH:296:VAL:HG13	4:VH:359:GLU:HB2	1.91	0.52
3:CF:212:ILE:O	4:CH:170:ARG:NH2	2.43	0.52
4:DH:278:ASP:OD1	4:DH:278:ASP:N	2.41	0.52
5:DK:97:SER:O	5:DK:100:ASN:ND2	2.43	0.52
10:EX:23:UNK:HA	10:EX:33:UNK:HA	1.92	0.52
3:FF:267:GLU:O	4:FH:150:LYS:NZ	2.37	0.52
1:NG:958:SER:O	1:NG:962:SER:OG	2.27	0.52
11:AC:168:LYS:O	11:AC:173:LYS:NZ	2.43	0.52
1:BG:884:PRO:HA	1:BG:901:GLY:O	2.10	0.52
6:IL:212:ASN:OD1	6:IL:212:ASN:N	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:LH:189:TRP:HE1	4:LH:230:LEU:HG	1.74	0.52
1:DG:899:LEU:HD13	1:DG:919:MET:HG2	1.92	0.52
1:DG:910:ASP:OD1	1:DG:910:ASP:N	2.41	0.52
6:BL:210:ASP:N	6:BL:210:ASP:OD1	2.43	0.52
11:JC:157:LYS:NZ	11:JC:158:PRO:O	2.38	0.52
11:LC:197:GLU:OE2	4:DH:294:ARG:NH1	2.43	0.52
1:BG:955:ARG:NH1	1:BG:1023:PHE:O	2.39	0.52
2:Id:84:SER:H	11:EC:267:ALA:HB3	1.73	0.52
1:Jg:791:GLN:N	1:Jg:793:GLU:OE1	2.43	0.52
4:AH:229:ARG:HG2	4:AH:236:PRO:HB3	1.92	0.52
4:KH:226:LEU:HB2	4:KH:241:LEU:HD11	1.91	0.52
7:KM:129:LEU:HB2	7:KM:150:ILE:HD11	1.92	0.52
2:Ld:148:TYR:HB2	2:Ld:153:VAL:HG12	1.92	0.52
11:EC:225:TYR:H	11:EC:251:ALA:HB3	1.72	0.52
11:DC:104:ASN:ND2	11:DC:141:ILE:O	2.42	0.52
11:GC:259:ASN:ND2	11:GC:262:GLU:OE2	2.43	0.52
7:EM:268:HIS:ND1	7:EM:287:THR:OG1	2.37	0.52
1:OG:875:THR:HA	1:PG:940:ALA:HB1	1.91	0.52
1:OG:958:SER:O	1:OG:962:SER:OG	2.27	0.52
11:AC:75:ARG:HG3	11:AC:188:ILE:HA	1.92	0.52
7:FM:257:ASP:OD1	7:FM:257:ASP:N	2.41	0.52
8:FN:115:GLN:N	8:FN:115:GLN:NE2	2.57	0.52
7:JM:308:ASP:O	7:JM:310:LYS:NZ	2.38	0.51
8:MN:104:ASN:OD1	8:MN:104:ASN:N	2.43	0.51
4:VH:189:TRP:HE1	4:VH:231:ARG:HB2	1.75	0.51
7:BM:149:ASN:OD1	7:BM:149:ASN:N	2.42	0.51
8:BN:46:GLY:HA3	8:BN:61:ASN:HB2	1.92	0.51
11:DC:178:ILE:HG13	11:DC:182:ARG:HH12	1.74	0.51
5:CK:87:GLN:NE2	5:CK:173:ASP:OD1	2.43	0.51
5:DK:116:VAL:HG12	5:DK:182:ILE:HG22	1.92	0.51
6:DL:177:HIS:HD1	7:DM:315:TYR:HH	1.56	0.51
6:EL:212:ASN:N	6:EL:212:ASN:OD1	2.41	0.51
3:GF:220:ALA:HB3	3:GF:232:VAL:HG12	1.92	0.51
4:GH:315:THR:OG1	4:GH:316:ASN:N	2.43	0.51
2:HD:79:LEU:HG	2:HD:128:LEU:HB2	1.91	0.51
4:HH:126:GLN:HA	4:HH:129:LYS:HB2	1.93	0.51
5:HK:151:SER:OG	5:HK:152:ARG:N	2.43	0.51
6:HL:230:GLU:OE2	6:HL:232:GLN:NE2	2.44	0.51
5:JK:71:GLY:O	2:KD:27:LYS:NZ	2.43	0.51
7:JM:205:TYR:OH	3:Jf:219:ARG:NH2	2.42	0.51
2:KD:81:ALA:HB3	2:KD:128:LEU:HD11	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:KK:68:ALA:HB3	5:KK:75:LEU:HB3	1.92	0.51
7:LM:286:LYS:O	7:LM:316:ASN:ND2	2.44	0.51
3:MF:219:ARG:NH1	3:ZF:269:SER:O	2.43	0.51
5:MK:86:ASP:OD1	5:MK:86:ASP:N	2.37	0.51
3:Df:222:LEU:HD23	3:Df:232:VAL:HG11	1.92	0.51
2:Md:36:ASP:N	2:Md:36:ASP:OD1	2.43	0.51
2:Md:71:LEU:O	2:Md:133:ARG:NH1	2.38	0.51
4:WH:187:ALA:HB1	4:WH:262:ASN:HB2	1.92	0.51
4:ZH:114:ASP:O	4:ZH:118:ASN:ND2	2.43	0.51
11:DC:109:VAL:HG13	11:DC:208:GLY:HA3	1.92	0.51
4:FH:155:SER:OG	4:FH:255:ARG:NH1	2.43	0.51
1:PG:891:THR:OG1	1:PG:892:GLY:N	2.43	0.51
5:GK:90:ARG:NH1	5:GK:91:LEU:O	2.43	0.51
6:HL:199:ALA:HB3	6:HL:202:ARG:HG3	1.93	0.51
5:IK:60:LEU:HD22	5:IK:65:ILE:HD13	1.92	0.51
6:IL:124:THR:HA	6:IL:231:ILE:O	2.08	0.51
2:Id:150:ASN:O	2:Id:152:GLN:NE2	2.43	0.51
2:Jd:82:ARG:NH1	2:Jd:125:ASP:OD1	2.41	0.51
4:LH:236:PRO:HG2	4:MH:251:ARG:HH12	1.75	0.51
6:AL:54:ARG:HH22	6:AL:56:ALA:HB3	1.75	0.51
6:BL:63:ASP:OD1	6:BL:88:GLY:N	2.43	0.51
11:EC:256:ASN:N	11:EC:256:ASN:OD1	2.42	0.51
11:LC:146:THR:OG1	11:LC:147:TRP:N	2.43	0.51
6:CL:44:HIS:HB3	6:CL:46:PRO:HD2	1.93	0.51
4:DH:262:ASN:OD1	4:DH:262:ASN:N	2.43	0.51
7:EM:257:ASP:OD1	7:EM:257:ASP:N	2.41	0.51
2:FD:130:GLU:HA	2:FD:133:ARG:HD2	1.93	0.51
1:JG:958:SER:O	1:JG:962:SER:OG	2.27	0.51
1:NG:891:THR:OG1	1:NG:892:GLY:N	2.44	0.51
1:OG:891:THR:OG1	1:OG:892:GLY:N	2.44	0.51
4:HH:106:VAL:HA	4:HH:109:LYS:HE2	1.91	0.51
2:JD:123:THR:OG1	2:JD:124:LYS:N	2.43	0.51
4:AH:230:LEU:HD12	4:AH:233:LEU:HD12	1.91	0.51
4:KH:238:MET:HG3	4:YH:250:TYR:HB3	1.92	0.51
7:KM:313:ASP:HB2	7:KM:316:ASN:HD21	1.75	0.51
4:LH:322:PRO:HG2	4:LH:339:MET:HE1	1.93	0.51
6:BL:212:ASN:N	6:BL:212:ASN:OD1	2.41	0.51
8:BN:49:ASN:ND2	8:BN:60:CYS:O	2.43	0.51
2:Bd:130:GLU:HA	2:Bd:133:ARG:HB2	1.91	0.51
11:EC:175:ILE:HA	11:EC:178:ILE:HG12	1.92	0.51
11:HC:176:TRP:O	11:HC:180:THR:OG1	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:GG:1031:VAL:O	1:HG:941:ARG:NH2	2.44	0.51
1:Fg:807:GLN:O	1:Fg:810:GLN:NE2	2.43	0.51
2:Fd:139:ALA:O	2:Fd:142:LYS:NZ	2.43	0.51
11:IC:175:ILE:HA	11:IC:178:ILE:HG12	1.92	0.51
5:KK:162:ASP:N	5:KK:162:ASP:OD1	2.43	0.51
1:Ag:807:GLN:O	1:Ag:810:GLN:NE2	2.43	0.51
2:LD:36:ASP:N	2:LD:36:ASP:OD1	2.42	0.51
4:MH:275:SER:HA	11:HC:126:ARG:HD3	1.92	0.51
6:BL:44:HIS:HB2	6:BL:48:ASN:HA	1.91	0.51
2:ED:91:ILE:O	2:ED:95:THR:OG1	2.28	0.51
5:CK:87:GLN:OE1	5:CK:128:ARG:NH1	2.44	0.51
3:DF:246:LEU:HB3	3:DF:255:LEU:HB2	1.93	0.51
2:Ed:73:ILE:HG22	2:Ed:75:ASN:H	1.76	0.51
1:LG:951:HIS:O	1:LG:955:ARG:NE	2.42	0.51
11:BC:259:ASN:OD1	11:BC:259:ASN:N	2.35	0.51
8:GN:89:GLY:O	8:GN:104:ASN:ND2	2.38	0.51
5:HK:50:ASP:OD1	5:HK:50:ASP:N	2.44	0.51
1:Ig:810:GLN:HA	1:Ig:813:LYS:HB2	1.92	0.51
6:IL:49:ASN:ND2	7:IM:293:ALA:O	2.40	0.51
8:JN:63:GLY:HA3	2:KD:27:LYS:HB2	1.92	0.51
2:KD:123:THR:OG1	2:KD:126:GLU:OE1	2.28	0.51
11:CC:133:TYR:HB2	11:BC:241:ILE:HG22	1.93	0.51
4:LH:210:SER:HB2	4:YH:229:ARG:HH22	1.76	0.51
4:LH:225:ASN:HD21	4:MH:176:VAL:HB	1.76	0.51
2:CD:77:TYR:OH	5:CK:130:ARG:NH1	2.44	0.51
4:MH:273:PRO:O	11:HC:126:ARG:NH1	2.43	0.51
7:MM:242:LYS:HA	7:MM:262:GLU:HB2	1.93	0.51
2:Md:79:LEU:HA	2:Md:128:LEU:HD12	1.91	0.51
6:AL:212:ASN:N	6:AL:212:ASN:OD1	2.41	0.51
7:AM:163:THR:HB	7:AM:183:VAL:HG12	1.91	0.51
6:BL:169:THR:OG1	6:BL:170:ASP:N	2.41	0.51
7:EM:159:GLY:HA3	7:EM:179:GLY:HA3	1.93	0.51
1:KG:874:ASP:N	1:KG:874:ASP:OD1	2.44	0.51
4:IH:145:PRO:HB3	4:JH:132:GLN:HG2	1.91	0.51
4:IH:302:ALA:O	4:IH:303:ARG:NH1	2.39	0.51
6:IL:175:ARG:HA	6:IL:178:LYS:HE2	1.92	0.51
2:KD:125:ASP:OD1	5:KK:138:ARG:NH2	2.44	0.51
4:KH:159:ASN:OD1	4:KH:257:GLN:NE2	2.44	0.51
6:KL:44:HIS:HB3	6:KL:48:ASN:HA	1.91	0.51
1:DG:1030:GLU:OE2	1:EG:941:ARG:NE	2.40	0.51
6:AL:130:ASP:OD1	6:AL:130:ASP:N	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:BH:230:LEU:HD12	4:BH:233:LEU:HD12	1.92	0.51
7:BM:210:ASP:HA	7:BM:229:ASN:H	1.76	0.51
7:BM:306:GLN:HG3	7:BM:308:ASP:H	1.76	0.51
10:BX:23:UNK:HA	10:BX:33:UNK:HA	1.93	0.51
11:LC:56:GLU:HA	11:LC:59:LEU:HD12	1.91	0.51
6:CL:121:ASP:OD1	6:CL:121:ASP:N	2.43	0.51
4:DH:225:ASN:OD1	4:DH:225:ASN:N	2.44	0.51
4:GH:253:ASP:OD1	4:GH:253:ASP:N	2.43	0.51
4:IH:294:ARG:HH21	11:DC:197:GLU:HG3	1.75	0.51
6:KL:170:ASP:OD1	6:KL:170:ASP:N	2.37	0.51
5:LK:46:ASP:OD1	5:LK:46:ASP:N	2.43	0.51
1:DG:969:GLY:HA3	1:DG:1009:ALA:HB2	1.93	0.51
2:MD:150:ASN:N	2:MD:150:ASN:OD1	2.42	0.51
1:Mg:791:GLN:N	1:Mg:793:GLU:OE2	2.43	0.51
3:CF:210:TYR:HB2	3:CF:262:ILE:HD13	1.91	0.51
1:EG:958:SER:O	1:EG:962:SER:OG	2.27	0.51
4:XH:320:LEU:HD11	4:XH:348:SER:HB2	1.93	0.51
7:AM:127:ASN:HB3	7:AM:147:ALA:HB3	1.93	0.51
7:AM:133:TYR:HE1	7:AM:154:LYS:H	1.58	0.51
2:Ad:109:LEU:HD13	2:Ad:155:GLU:HG3	1.93	0.51
11:MC:234:THR:OG1	11:MC:235:GLY:N	2.44	0.51
1:Eg:793:GLU:O	1:Eg:796:GLN:NE2	2.44	0.51
11:BC:90:ASN:OD1	11:BC:90:ASN:N	2.43	0.51
7:GM:119:GLU:HG3	7:GM:139:ALA:HB3	1.93	0.51
2:Hd:68:ASP:OD1	2:Hd:68:ASP:N	2.40	0.51
3:LF:231:THR:HG23	4:MH:150:LYS:HE3	1.93	0.51
5:AK:126:VAL:HG23	5:AK:127:LYS:HD3	1.92	0.51
2:Md:105:ARG:HB3	2:Md:153:VAL:HG23	1.93	0.51
4:XH:278:ASP:O	4:XH:282:HIS:ND1	2.44	0.51
6:AL:136:SER:OG	7:AM:314:ARG:NH2	2.44	0.51
2:AD:52:MET:HE1	2:Ad:52:MET:HG2	1.91	0.51
2:Ad:86:ASP:HA	2:Ad:121:ILE:O	2.10	0.51
3:BF:254:ILE:HB	3:BF:262:ILE:HB	1.93	0.51
11:HC:104:ASN:ND2	11:HC:141:ILE:O	2.44	0.51
1:GG:910:ASP:OD1	1:GG:910:ASP:N	2.36	0.51
4:EH:289:PRO:O	4:EH:292:SER:OG	2.28	0.51
1:NG:966:GLN:O	1:NG:970:ASN:ND2	2.44	0.51
1:AG:1003:ASN:HA	1:AG:1006:ILE:HD12	1.93	0.51
7:GM:288:ARG:NH2	7:GM:318:GLN:OE1	2.44	0.51
4:HH:204:ILE:HG23	4:HH:213:LEU:HD11	1.93	0.51
3:Hf:251:GLN:OE1	3:Hf:253:ARG:NH1	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:IN:71:THR:OG1	8:IN:72:ARG:N	2.40	0.51
1:Jg:813:LYS:NZ	4:KH:138:GLU:OE1	2.42	0.51
5:JK:121:SER:OG	5:JK:122:LYS:N	2.43	0.51
2:MD:35:ASP:O	2:MD:38:THR:OG1	2.29	0.51
6:ML:44:HIS:HB2	6:ML:48:ASN:HA	1.93	0.51
3:YF:212:ILE:HG12	3:YF:264:PHE:HB3	1.93	0.51
4:YH:179:LEU:O	4:YH:212:THR:HA	2.12	0.51
3:Af:245:LYS:NZ	3:Af:256:THR:O	2.44	0.51
2:BD:130:GLU:HA	2:BD:133:ARG:HD2	1.93	0.51
5:BK:86:ASP:OD1	5:BK:86:ASP:N	2.38	0.51
11:KC:127:ARG:NH1	4:CH:273:PRO:O	2.36	0.51
7:CM:157:ALA:O	7:CM:178:LYS:NZ	2.43	0.51
1:GG:1005:VAL:O	1:GG:1009:ALA:HB2	2.10	0.51
2:FD:107:ARG:NH1	2:Fd:130:GLU:OE1	2.39	0.51
1:MG:891:THR:OG1	1:MG:892:GLY:N	2.44	0.51
11:AC:189:ASP:O	11:AC:193:THR:OG1	2.29	0.51
1:AG:865:THR:OG1	1:AG:1044:ASP:OD2	2.27	0.50
6:IL:226:ASN:O	6:IL:228:ARG:NH1	2.43	0.50
3:JF:207:ARG:HH12	3:JF:260:GLN:HE22	1.58	0.50
3:KF:251:GLN:OE1	10:YX:1:UNK:N	2.42	0.50
6:ML:230:GLU:OE2	6:ML:232:GLN:NE2	2.40	0.50
7:MM:127:ASN:HB3	7:MM:147:ALA:HB3	1.93	0.50
7:AM:308:ASP:N	7:AM:308:ASP:OD1	2.43	0.50
2:Ad:72:THR:OG1	2:Ad:73:ILE:N	2.43	0.50
11:HC:133:LYS:NZ	11:HC:134:VAL:O	2.44	0.50
11:BC:177:TRP:O	11:BC:181:THR:OG1	2.26	0.50
4:GH:219:LYS:HD3	4:GH:221:TYR:H	1.77	0.50
2:HD:139:ALA:O	2:HD:142:LYS:NZ	2.39	0.50
7:IM:190:ASN:N	7:IM:190:ASN:OD1	2.42	0.50
3:JF:219:ARG:HG2	4:KH:148:PRO:HD2	1.94	0.50
3:Kf:217:PRO:O	3:Kf:219:ARG:NH2	2.43	0.50
2:Md:76:ALA:O	2:Md:80:GLN:NE2	2.36	0.50
4:WH:301:ASP:OD1	4:WH:301:ASP:N	2.43	0.50
1:EG:919:MET:HB3	1:EG:928:ILE:HG13	1.93	0.50
5:BK:46:ASP:N	5:BK:46:ASP:OD1	2.43	0.50
11:EC:157:LYS:HZ1	11:EC:159:GLU:HG3	1.77	0.50
2:ED:79:LEU:HA	2:ED:128:LEU:HD12	1.94	0.50
11:HC:154:ASP:N	11:HC:154:ASP:OD1	2.43	0.50
4:CH:311:MET:HG3	4:CH:341:LYS:HA	1.92	0.50
7:DM:156:GLU:HB3	7:DM:178:LYS:HZ1	1.75	0.50
6:FL:210:ASP:OD1	6:FL:210:ASP:N	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:PG:916:PHE:HE2	1:PG:1037:LEU:HD11	1.76	0.50
4:JH:278:ASP:OD1	4:JH:278:ASP:N	2.42	0.50
1:CG:958:SER:O	1:CG:962:SER:OG	2.28	0.50
4:MH:319:ILE:HA	4:MH:347:VAL:HG12	1.94	0.50
7:MM:119:GLU:HG3	7:MM:139:ALA:HB3	1.92	0.50
7:CM:205:TYR:OH	3:Cf:219:ARG:NE	2.44	0.50
1:KG:898:LYS:NZ	1:LG:865:THR:O	2.44	0.50
1:LG:958:SER:O	1:LG:962:SER:OG	2.29	0.50
1:AG:1032:TYR:HD1	1:BG:941:ARG:HH22	1.58	0.50
7:GM:263:ILE:HD11	7:GM:279:ILE:HG22	1.93	0.50
8:HN:49:ASN:HD21	8:HN:61:ASN:HA	1.77	0.50
6:JL:174:SER:HG	6:JL:176:SER:HG	1.58	0.50
4:AH:155:SER:OG	4:AH:255:ARG:NH2	2.44	0.50
11:CC:143:THR:HG22	11:CC:144:THR:HG23	1.92	0.50
4:KH:259:TYR:HB3	4:KH:263:ALA:HB2	1.94	0.50
1:Lg:801:MET:HB3	4:MH:121:PRO:HB2	1.94	0.50
4:MH:228:VAL:HB	4:MH:237:VAL:HB	1.93	0.50
2:Md:70:THR:OG1	2:Md:71:LEU:N	2.45	0.50
3:WF:207:ARG:NH2	3:WF:239:PRO:O	2.44	0.50
7:AM:171:ARG:O	7:AM:192:ARG:NH2	2.44	0.50
4:BH:168:VAL:HA	4:BH:240:THR:O	2.12	0.50
5:BK:92:ASN:O	5:BK:95:SER:OG	2.29	0.50
7:BM:257:ASP:N	7:BM:257:ASP:OD1	2.43	0.50
11:EC:245:ARG:HG2	11:EC:247:LEU:HD21	1.93	0.50
2:ED:148:TYR:O	2:ED:152:GLN:N	2.45	0.50
4:CH:277:ASN:HD21	4:CH:279:LEU:HB2	1.76	0.50
5:DK:92:ASN:O	5:DK:95:SER:OG	2.29	0.50
5:DK:117:THR:HA	5:DK:157:GLN:O	2.10	0.50
2:FD:82:ARG:NH2	7:FM:311:ASP:OD2	2.45	0.50
3:FF:215:VAL:H	4:FH:245:GLN:HE22	1.58	0.50
11:IC:218:MET:HG2	11:IC:220:MET:HE2	1.94	0.50
3:AF:246:LEU:HB3	3:AF:255:LEU:HD12	1.92	0.50
2:Hd:79:LEU:HA	2:Hd:128:LEU:HD12	1.94	0.50
4:IH:280:LEU:HD21	4:IH:338:GLU:HG2	1.93	0.50
3:JF:251:GLN:O	3:JF:263:LYS:NZ	2.43	0.50
11:CC:259:ASN:N	11:CC:259:ASN:OD1	2.43	0.50
5:MK:152:ARG:HB2	5:MK:153:ILE:HD12	1.94	0.50
4:VH:292:SER:HB3	4:VH:307:SER:HB2	1.94	0.50
2:BD:47:SER:O	2:BD:51:SER:OG	2.28	0.50
7:BM:197:TYR:HA	7:BM:217:LYS:HB3	1.92	0.50
2:Bd:148:TYR:HB2	2:Bd:153:VAL:HG12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:EC:127:ILE:HG12	11:DC:245:ARG:HB2	1.94	0.50
11:LC:41:LYS:HD2	11:LC:44:ARG:HD2	1.92	0.50
7:CM:303:GLU:OE1	7:CM:306:GLN:N	2.42	0.50
3:DF:233:ARG:NH2	3:EF:266:GLN:O	2.45	0.50
1:MG:1003:ASN:HA	1:MG:1006:ILE:HD12	1.93	0.50
6:GL:118:GLU:OE2	6:GL:123:ARG:NH2	2.44	0.50
4:HH:219:LYS:HD2	4:HH:222:ASN:HB2	1.93	0.50
7:HM:290:ASP:HB3	7:HM:298:VAL:HG21	1.94	0.50
7:JM:214:ILE:HB	7:JM:233:VAL:HG22	1.94	0.50
7:JM:312:PHE:HB2	7:JM:317:LYS:HD3	1.94	0.50
11:CC:108:PRO:HG2	11:CC:210:MET:HG2	1.94	0.50
4:KH:280:LEU:HD23	4:KH:328:MET:HB2	1.93	0.50
5:LK:142:GLU:OE2	6:LL:139:ARG:NH1	2.44	0.50
5:AK:185:ARG:NH2	6:BL:214:ILE:O	2.45	0.50
4:MH:169:ILE:HD12	4:MH:252:VAL:HG21	1.94	0.50
4:ZH:183:ASP:OD1	4:ZH:187:ALA:N	2.45	0.50
6:BL:209:GLY:H	6:BL:211:LYS:HZ3	1.59	0.50
11:FC:170:LYS:HA	11:FC:173:LYS:HE2	1.94	0.50
11:MC:95:ASP:O	11:MC:98:SER:OG	2.29	0.50
7:DM:149:ASN:N	7:DM:149:ASN:OD1	2.45	0.50
1:NG:1006:ILE:O	1:NG:1010:THR:OG1	2.29	0.50
1:AG:941:ARG:HH21	1:PG:1030:GLU:HG2	1.76	0.50
5:JK:87:GLN:NE2	5:JK:173:ASP:OD1	2.44	0.50
4:AH:154:THR:HB	4:AH:156:GLN:HE22	1.77	0.50
3:LF:269:SER:OG	3:YF:233:ARG:NH1	2.45	0.50
6:LL:190:MET:HE1	6:LL:203:LEU:HB3	1.94	0.50
5:AK:88:SER:OG	7:AM:296:GLY:O	2.30	0.50
5:AK:130:ARG:NH1	2:AD:77:TYR:OH	2.43	0.50
4:MH:269:GLU:HB2	4:ZH:328:MET:HG2	1.93	0.50
5:MK:92:ASN:N	5:MK:92:ASN:OD1	2.43	0.50
6:ML:169:THR:OG1	6:ML:170:ASP:N	2.45	0.50
4:VH:315:THR:OG1	4:VH:316:ASN:N	2.43	0.50
3:WF:207:ARG:NH1	3:WF:208:ILE:O	2.44	0.50
4:WH:196:LEU:HD21	4:WH:202:PHE:HB2	1.94	0.50
7:BM:205:TYR:OH	3:Bf:219:ARG:NH1	2.45	0.50
1:FG:886:LEU:HD11	1:GG:1040:LEU:HB2	1.93	0.50
11:DC:46:GLN:OE1	11:DC:49:GLN:NE2	2.45	0.50
11:LC:55:ARG:NH1	1:OG:1034:GLY:O	2.45	0.50
4:CH:105:GLU:O	4:CH:109:LYS:NZ	2.35	0.50
7:CM:235:LEU:HD23	7:CM:259:SER:HB2	1.94	0.50
3:DF:213:GLN:OE1	4:DH:170:ARG:NH2	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:DH:315:THR:OG1	4:DH:316:ASN:N	2.45	0.50
5:EK:73:ASN:N	5:EK:73:ASN:OD1	2.44	0.50
5:EK:87:GLN:NE2	5:EK:173:ASP:OD1	2.45	0.50
1:OG:1003:ASN:HA	1:OG:1006:ILE:HD12	1.92	0.50
2:GD:114:SER:HB2	11:CC:118:LEU:HD22	1.94	0.50
4:GH:316:ASN:N	4:GH:316:ASN:OD1	2.45	0.50
2:Dd:68:ASP:OD1	2:Dd:68:ASP:N	2.44	0.50
5:HK:90:ARG:NH2	7:HM:293:ALA:O	2.44	0.50
7:IM:211:THR:HA	7:IM:230:ARG:O	2.12	0.50
2:JD:158:TYR:O	2:Jd:137:TYR:OH	2.29	0.50
3:JF:207:ARG:NH1	3:JF:240:GLY:O	2.41	0.50
4:JH:114:ASP:O	4:JH:118:ASN:ND2	2.39	0.50
8:JN:115:GLN:NE2	11:EC:69:GLN:OE1	2.45	0.50
5:KK:179:ARG:NE	5:KK:181:GLU:OE2	2.44	0.50
7:LM:288:ARG:O	7:LM:318:GLN:NE2	2.45	0.50
2:CD:149:PRO:O	2:CD:152:GLN:NE2	2.45	0.50
4:MH:182:LEU:HA	4:MH:188:PRO:HA	1.93	0.50
1:WG:791:GLN:N	1:WG:793:GLU:OE1	2.45	0.50
1:EG:871:ALA:HB1	1:EG:887:ALA:HB1	1.94	0.50
4:XH:308:ASN:OD1	4:XH:308:ASN:N	2.45	0.50
4:XH:322:PRO:HG2	4:XH:339:MET:HE3	1.93	0.50
8:AN:76:MET:N	8:AN:76:MET:SD	2.85	0.50
7:FM:149:ASN:OD1	7:FM:149:ASN:N	2.44	0.50
2:ID:77:TYR:O	2:ID:78:ASN:ND2	2.34	0.50
7:JM:153:GLN:OE1	7:JM:172:ASN:ND2	2.37	0.50
3:KF:254:ILE:HB	3:KF:262:ILE:HB	1.93	0.50
4:MH:225:ASN:HD21	4:ZH:176:VAL:HB	1.76	0.50
8:MN:98:SER:OG	8:MN:99:GLY:N	2.43	0.50
4:VH:132:GLN:NE2	10:BX:27:UNK:O	2.44	0.50
2:Ad:86:ASP:N	2:Ad:86:ASP:OD1	2.44	0.50
1:FG:867:ASP:OD1	1:FG:867:ASP:N	2.44	0.50
1:FG:1024:ASN:OD1	1:FG:1024:ASN:N	2.38	0.50
11:FC:112:GLU:OE1	11:FC:130:ARG:NH1	2.44	0.50
11:MC:175:ILE:HA	11:MC:178:ILE:HG12	1.94	0.50
11:KC:176:ILE:HA	11:KC:179:ILE:HG12	1.94	0.50
8:CN:63:GLY:HA3	2:DD:27:LYS:HB2	1.94	0.50
7:DM:285:SER:OG	7:DM:286:LYS:N	2.44	0.50
1:LG:920:SER:HA	1:LG:927:THR:HA	1.93	0.50
1:MG:999:SER:HB2	1:NG:972:PHE:HZ	1.76	0.50
11:IC:101:LEU:HB2	11:IC:105:ILE:HG23	1.93	0.50
5:GK:110:ARG:NH2	8:GN:69:TYR:OH	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:HH:143:ALA:O	4:XH:131:LYS:NZ	2.45	0.49
7:HM:278:ASP:OD1	7:HM:297:SER:OG	2.29	0.49
4:LH:148:PRO:HG2	3:YF:216:ILE:HD12	1.94	0.49
2:CD:114:SER:HB2	11:LC:117:LEU:HD22	1.94	0.49
2:Md:148:TYR:HB2	2:Md:153:VAL:HG12	1.94	0.49
4:VH:316:ASN:N	4:VH:316:ASN:OD1	2.44	0.49
1:EG:946:SER:OG	1:EG:1030:GLU:O	2.26	0.49
10:XX:21:UNK:O	10:XX:78:UNK:N	2.45	0.49
4:YH:183:ASP:HA	4:YH:256:VAL:HG12	1.94	0.49
1:Dg:820:TYR:HB2	4:DH:205:GLN:HG2	1.93	0.49
11:HC:258:ASN:OD1	11:HC:258:ASN:N	2.38	0.49
6:CL:165:VAL:HG12	6:CL:231:ILE:HG12	1.94	0.49
2:DD:82:ARG:NH1	7:DM:311:ASP:OD2	2.42	0.49
1:GG:880:ASP:OD1	1:GG:880:ASP:N	2.41	0.49
1:Eg:800:ASP:N	1:Eg:800:ASP:OD1	2.44	0.49
5:EK:177:ASN:N	5:EK:177:ASN:OD1	2.45	0.49
7:EM:125:THR:HG23	7:EM:145:ARG:HB2	1.94	0.49
5:FK:177:ASN:OD1	5:FK:177:ASN:N	2.45	0.49
1:MG:958:SER:O	1:MG:962:SER:OG	2.29	0.49
7:FM:125:THR:HG23	7:FM:145:ARG:HB2	1.93	0.49
4:HH:278:ASP:N	4:HH:278:ASP:OD1	2.45	0.49
2:Id:35:ASP:O	2:Id:38:THR:OG1	2.29	0.49
2:Id:71:LEU:O	2:Id:133:ARG:NH1	2.40	0.49
4:JH:108:ASP:OD1	4:JH:108:ASP:N	2.42	0.49
4:JH:222:ASN:OD1	4:JH:222:ASN:N	2.44	0.49
7:JM:215:ARG:NH1	7:JM:232:ASP:OD2	2.39	0.49
2:KD:87:TRP:CD1	2:KD:89:GLY:H	2.30	0.49
2:Kd:68:ASP:N	2:Kd:68:ASP:OD1	2.44	0.49
1:Lg:800:ASP:OD1	1:Lg:800:ASP:N	2.44	0.49
7:LM:141:GLU:OE2	7:LM:143:THR:OG1	2.30	0.49
6:BL:170:ASP:OD2	6:BL:227:ARG:NE	2.39	0.49
11:MC:176:TRP:O	11:MC:180:THR:OG1	2.28	0.49
11:LC:175:ILE:HA	11:LC:178:ILE:HG12	1.94	0.49
5:DK:47:GLY:O	5:DK:108:GLN:NE2	2.45	0.49
1:MG:966:GLN:O	1:MG:970:ASN:ND2	2.45	0.49
7:FM:129:LEU:HB3	7:FM:150:ILE:HD11	1.92	0.49
2:Fd:73:ILE:HG22	2:Fd:75:ASN:H	1.77	0.49
1:AG:931:SER:O	1:AG:1042:THR:OG1	2.29	0.49
2:GD:27:LYS:NZ	5:FK:71:GLY:O	2.40	0.49
5:IK:121:SER:OG	5:IK:122:LYS:N	2.43	0.49
5:LK:183:THR:HG21	9:LU:123:UNK:HA	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:LM:270:SER:HA	7:LM:289:ALA:HB3	1.95	0.49
2:MD:84:SER:OG	2:MD:124:LYS:NZ	2.40	0.49
6:ML:59:ARG:HH12	6:ML:99:ARG:HD2	1.77	0.49
4:WH:249:ASP:N	4:WH:249:ASP:OD1	2.45	0.49
1:ZG:817:THR:OG1	1:ZG:818:GLN:N	2.44	0.49
2:Ad:149:PRO:O	2:Ad:152:GLN:NE2	2.40	0.49
4:BH:229:ARG:NH1	4:CH:207:ASP:OD2	2.45	0.49
2:ED:119:ILE:HD12	2:ED:138:GLN:HG2	1.94	0.49
4:EH:185:THR:HB	4:EH:265:SER:HB3	1.93	0.49
2:FD:31:ASN:ND2	2:Fd:34:SER:O	2.44	0.49
1:JG:876:SER:OG	1:JG:1031:VAL:O	2.30	0.49
1:KG:882:PRO:HB3	1:KG:902:SER:HB2	1.93	0.49
2:Fd:82:ARG:HH12	2:Fd:127:SER:HA	1.77	0.49
11:IC:89:ASN:N	11:IC:89:ASN:OD1	2.44	0.49
7:IM:288:ARG:O	7:IM:318:GLN:NE2	2.45	0.49
1:CG:935:ILE:N	1:CG:1038:GLY:O	2.44	0.49
7:KM:120:GLY:H	7:KM:140:ASN:HB2	1.78	0.49
1:DG:900:ILE:HG13	1:DG:918:THR:HB	1.94	0.49
1:DG:1006:ILE:O	1:DG:1010:THR:OG1	2.30	0.49
4:YH:326:ALA:HB3	4:YH:338:GLU:HB3	1.93	0.49
4:DH:174:GLY:N	4:DH:217:ALA:O	2.42	0.49
5:EK:114:ILE:HG23	5:EK:184:PHE:HB3	1.93	0.49
6:FL:200:ALA:O	7:FM:230:ARG:NH2	2.45	0.49
1:KG:966:GLN:O	1:KG:970:ASN:ND2	2.45	0.49
2:GD:75:ASN:ND2	7:GM:306:GLN:O	2.45	0.49
1:BG:931:SER:O	1:BG:1042:THR:OG1	2.30	0.49
1:BG:999:SER:OG	1:BG:1000:THR:N	2.46	0.49
1:CG:899:LEU:HD13	1:CG:919:MET:HG2	1.94	0.49
5:KK:183:THR:HG21	9:KU:123:UNK:HA	1.93	0.49
2:CD:136:ASP:O	2:Cd:60:LYS:NZ	2.38	0.49
5:AK:106:LEU:O	5:AK:111:LYS:NZ	2.38	0.49
5:MK:93:TRP:NE1	2:Md:24:LYS:O	2.45	0.49
2:Ad:59:GLU:OE2	11:IC:213:ARG:NH1	2.45	0.49
4:CH:190:PRO:HB2	4:CH:231:ARG:HH11	1.77	0.49
5:EK:125:SER:OG	5:EK:126:VAL:N	2.43	0.49
6:EL:193:LEU:HA	6:EL:196:ASN:HD22	1.78	0.49
1:LG:889:ILE:HG21	1:LG:894:LEU:HB2	1.94	0.49
1:NG:876:SER:OG	1:NG:1031:VAL:O	2.28	0.49
7:FM:175:ILE:HB	7:FM:194:LEU:HD13	1.95	0.49
1:AG:880:ASP:OD1	1:AG:880:ASP:N	2.45	0.49
4:GH:273:PRO:O	11:BC:127:ARG:NH1	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Gd:97:ARG:HH22	11:CC:267:VAL:HB	1.76	0.49
5:HK:177:ASN:O	5:HK:179:ARG:NH1	2.43	0.49
2:Hd:150:ASN:OD1	2:Hd:150:ASN:N	2.44	0.49
5:JK:162:ASP:N	5:JK:162:ASP:OD1	2.45	0.49
4:AH:292:SER:OG	4:AH:293:ARG:N	2.46	0.49
2:LD:31:ASN:OD1	2:LD:31:ASN:N	2.46	0.49
2:CD:132:LEU:HD12	2:CD:145:ILE:HG21	1.94	0.49
5:AK:46:ASP:OD1	5:AK:46:ASP:N	2.45	0.49
8:MN:49:ASN:N	8:MN:49:ASN:OD1	2.45	0.49
3:CF:246:LEU:HB3	3:CF:255:LEU:HD12	1.94	0.49
4:YH:332:ASP:OD1	4:YH:332:ASP:N	2.41	0.49
1:ZG:794:ILE:HD12	4:BH:110:LYS:HD2	1.95	0.49
4:ZH:178:SER:HA	4:ZH:213:LEU:O	2.13	0.49
5:BK:162:ASP:N	5:BK:162:ASP:OD1	2.45	0.49
11:EC:150:TYR:O	11:EC:198:ASN:ND2	2.46	0.49
11:FC:175:ILE:HA	11:FC:178:ILE:HG12	1.94	0.49
8:CN:89:GLY:HA3	8:CN:104:ASN:HB2	1.93	0.49
3:Cf:254:ILE:H	3:Cf:261:VAL:HG23	1.76	0.49
6:DL:168:PHE:HB2	6:DL:228:ARG:HG2	1.95	0.49
1:PG:958:SER:O	1:PG:962:SER:OG	2.31	0.49
2:GD:72:THR:OG1	2:GD:146:HIS:ND1	2.38	0.49
5:IK:81:SER:OG	5:IK:173:ASP:O	2.30	0.49
3:KF:268:ASP:OD1	4:KH:150:LYS:NZ	2.45	0.49
6:KL:169:THR:OG1	6:KL:170:ASP:N	2.45	0.49
6:LL:99:ARG:HA	6:LL:104:LYS:HG2	1.95	0.49
6:LL:169:THR:OG1	6:LL:170:ASP:N	2.46	0.49
4:ZH:278:ASP:OD1	4:ZH:278:ASP:N	2.45	0.49
2:Ad:71:LEU:O	2:Ad:133:ARG:NH1	2.38	0.49
8:BN:48:ILE:HD12	8:BN:58:LEU:HD13	1.95	0.49
2:ED:87:TRP:HD1	2:ED:89:GLY:H	1.61	0.49
4:CH:330:SER:OG	4:CH:332:ASP:OD1	2.30	0.49
4:FH:319:ILE:HG12	4:FH:339:MET:HE1	1.94	0.49
11:AC:109:VAL:HG13	11:AC:208:GLY:HA3	1.95	0.49
7:GM:275:ASP:HA	7:GM:295:ASN:H	1.77	0.49
3:Gf:218:GLY:H	3:Gf:247:ILE:HD11	1.78	0.49
10:HX:23:UNK:HA	10:HX:33:UNK:HA	1.94	0.49
4:LH:182:LEU:HD12	4:LH:255:ARG:HE	1.77	0.49
8:LN:103:CYS:N	8:LN:107:TYR:O	2.44	0.49
3:MF:216:ILE:HD11	3:MF:219:ARG:HB2	1.95	0.49
4:WH:207:ASP:OD1	4:WH:207:ASP:N	2.46	0.49
10:XX:21:UNK:N	10:XX:78:UNK:O	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:BH:167:PRO:HB2	4:BH:239:LEU:HD23	1.93	0.49
11:GC:92:ASP:OD1	11:GC:92:ASP:N	2.44	0.49
4:DH:183:ASP:OD1	4:DH:187:ALA:N	2.45	0.49
7:EM:242:LYS:HA	7:EM:262:GLU:HG2	1.95	0.49
3:FF:233:ARG:HD3	3:FF:234:GLU:H	1.78	0.49
1:LG:946:SER:OG	1:LG:1030:GLU:O	2.28	0.49
2:HD:87:TRP:CD1	2:HD:89:GLY:H	2.31	0.49
2:HD:130:GLU:OE2	2:HD:133:ARG:NH1	2.38	0.49
5:IK:50:ASP:N	5:IK:50:ASP:OD1	2.43	0.49
8:IN:52:ASP:O	8:IN:56:GLY:N	2.45	0.49
4:AH:328:MET:HE1	11:IC:116:THR:HG23	1.94	0.49
5:KK:47:GLY:O	5:KK:108:GLN:NE2	2.41	0.49
5:LK:110:ARG:NH1	8:LN:75:VAL:O	2.40	0.49
7:LM:131:THR:HG23	7:LM:151:GLY:H	1.77	0.49
1:DG:1030:GLU:HG2	1:EG:941:ARG:HH21	1.78	0.49
3:VF:265:SER:HB3	3:VF:268:ASP:HB3	1.94	0.49
4:VH:153:ALA:HA	4:VH:251:ARG:O	2.12	0.49
4:WH:183:ASP:OD1	4:WH:187:ALA:N	2.46	0.49
4:XH:207:ASP:O	4:XH:210:SER:OG	2.30	0.49
2:AD:36:ASP:OD1	2:AD:36:ASP:N	2.42	0.49
7:AM:165:ILE:HB	7:AM:185:ILE:HG23	1.95	0.49
7:AM:262:GLU:HG3	7:AM:280:TYR:HB2	1.95	0.49
6:BL:116:TYR:OH	6:BL:118:GLU:OE1	2.31	0.49
11:GC:118:LEU:HA	11:GC:128:ILE:HG22	1.95	0.49
11:LC:124:SER:O	11:LC:124:SER:OG	2.30	0.49
6:CL:130:ASP:OD1	6:CL:130:ASP:N	2.39	0.49
2:Cd:76:ALA:O	2:Cd:80:GLN:NE2	2.43	0.49
7:DM:141:GLU:OE2	7:DM:143:THR:OG1	2.30	0.49
8:EN:77:ASP:OD1	8:EN:79:GLN:NE2	2.46	0.49
1:HG:869:MET:HB2	1:HG:1041:PHE:HE1	1.77	0.49
1:MG:871:ALA:HB2	1:MG:889:ILE:HD13	1.94	0.49
1:MG:1017:GLN:NE2	1:MG:1018:GLN:OE1	2.44	0.49
3:Hf:256:THR:OG1	3:Hf:257:SER:N	2.46	0.49
6:IL:121:ASP:O	6:IL:235:THR:OG1	2.30	0.49
4:JH:282:HIS:HB3	4:JH:287:VAL:HB	1.94	0.49
7:LM:170:SER:OG	7:LM:172:ASN:O	2.30	0.49
1:Mg:820:TYR:OH	1:Mg:822:GLU:OE2	2.30	0.49
3:Mf:258:SER:OG	3:Mf:260:GLN:NE2	2.41	0.49
4:WH:176:VAL:HG22	4:WH:216:GLN:HB2	1.94	0.49
3:XF:245:LYS:HE3	3:XF:257:SER:HA	1.94	0.49
3:CF:207:ARG:HH22	3:CF:240:GLY:HA3	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:BM:114:ASN:O	7:BM:134:LEU:HA	2.13	0.49
11:EC:91:ASP:HB3	11:EC:147:TRP:HE1	1.78	0.49
2:ED:158:TYR:O	2:ED:137:TYR:OH	2.30	0.49
11:MC:154:ASP:OD1	11:MC:154:ASP:N	2.45	0.49
4:DH:191:ILE:O	4:DH:231:ARG:NH1	2.46	0.49
7:DM:199:LYS:HA	7:DM:219:ALA:HB3	1.95	0.49
7:FM:279:ILE:HB	7:FM:298:VAL:HG12	1.95	0.49
4:GH:284:LEU:O	4:GH:314:ARG:NH2	2.41	0.48
6:JL:208:TYR:HB3	6:JL:211:LYS:HD3	1.95	0.48
11:CC:122:ASP:N	11:CC:122:ASP:OD1	2.45	0.48
4:KH:112:PHE:HA	4:KH:115:MET:HE3	1.95	0.48
4:LH:177:SER:HB2	4:LH:215:ILE:HG22	1.95	0.48
4:LH:234:ASN:OD1	4:LH:234:ASN:N	2.46	0.48
2:Ld:150:ASN:OD1	2:Ld:150:ASN:N	2.46	0.48
7:AM:141:GLU:OE2	7:AM:143:THR:OG1	2.31	0.48
11:EC:101:LEU:HB2	11:EC:105:ILE:HG23	1.93	0.48
4:FH:112:PHE:HA	4:FH:115:MET:HE3	1.94	0.48
4:FH:343:PRO:HA	4:FH:358:VAL:HB	1.95	0.48
1:HG:1003:ASN:HA	1:HG:1006:ILE:HD12	1.95	0.48
1:JG:969:GLY:HA2	1:JG:1005:VAL:HA	1.94	0.48
3:HF:213:GLN:HG3	4:HH:170:ARG:HH21	1.77	0.48
2:JD:29:PRO:HG2	6:JL:225:GLN:HA	1.95	0.48
7:JM:180:ASP:O	7:JM:182:LYS:NZ	2.42	0.48
1:CG:875:THR:HA	1:DG:940:ALA:HB1	1.95	0.48
6:KL:192:PHE:O	6:KL:196:ASN:ND2	2.43	0.48
7:KM:153:GLN:NE2	7:KM:172:ASN:OD1	2.43	0.48
4:LH:183:ASP:OD1	4:LH:187:ALA:N	2.44	0.48
7:LM:128:ASN:HB3	7:LM:130:ARG:HH12	1.78	0.48
2:CD:55:MET:HA	2:CD:58:VAL:HG12	1.94	0.48
1:DG:966:GLN:O	1:DG:970:ASN:ND2	2.45	0.48
4:WH:106:VAL:HA	4:WH:109:LYS:HE2	1.95	0.48
2:BD:36:ASP:OD1	2:BD:36:ASP:N	2.45	0.48
11:KC:243:ILE:HG12	11:LC:130:ARG:H	1.77	0.48
5:EK:152:ARG:HD3	4:FH:352:LYS:HB2	1.94	0.48
5:FK:122:LYS:NZ	5:FK:129:GLU:OE2	2.41	0.48
1:LG:966:GLN:O	1:LG:970:ASN:ND2	2.46	0.48
1:PG:1042:THR:OG1	1:PG:1043:GLN:OE1	2.31	0.48
11:AC:89:ASN:N	11:AC:89:ASN:OD1	2.45	0.48
1:Hg:800:ASP:OD1	1:Hg:800:ASP:N	2.35	0.48
6:HL:121:ASP:OD1	6:HL:121:ASP:N	2.46	0.48
1:BG:871:ALA:HB2	1:BG:889:ILE:HD13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Jg:800:ASP:HB2	4:KH:121:PRO:HG2	1.95	0.48
4:AH:311:MET:HG3	4:AH:341:LYS:HA	1.95	0.48
1:CG:966:GLN:O	1:CG:970:ASN:ND2	2.45	0.48
5:KK:111:LYS:HD3	5:KK:114:ILE:HD11	1.95	0.48
7:KM:123:VAL:HG13	7:KM:143:THR:HB	1.94	0.48
8:KN:72:ARG:HE	4:LH:298:SER:HG	1.59	0.48
2:Kd:150:ASN:OD1	2:Kd:150:ASN:N	2.42	0.48
5:MK:92:ASN:O	5:MK:95:SER:OG	2.31	0.48
4:VH:158:VAL:HG22	4:VH:256:VAL:HA	1.95	0.48
2:AD:130:GLU:OE2	2:AD:133:ARG:NH1	2.46	0.48
2:Ad:60:LYS:NZ	2:Ad:61:VAL:O	2.46	0.48
7:BM:124:VAL:O	7:BM:144:THR:HA	2.13	0.48
7:CM:145:ARG:HH22	7:CM:164:GLN:HG2	1.79	0.48
7:CM:240:GLN:HB3	7:CM:242:LYS:HE2	1.95	0.48
2:DD:105:ARG:HB2	2:DD:153:VAL:HG22	1.95	0.48
6:EL:226:ASN:O	6:EL:228:ARG:NE	2.42	0.48
1:HG:914:ILE:HD11	1:HG:1031:VAL:HG11	1.96	0.48
1:HG:966:GLN:O	1:HG:970:ASN:ND2	2.46	0.48
2:Fd:128:LEU:HA	2:Fd:131:ILE:HD12	1.95	0.48
1:Gg:793:GLU:O	1:Gg:796:GLN:NE2	2.45	0.48
5:GK:46:ASP:OD1	5:GK:46:ASP:N	2.45	0.48
6:HL:94:VAL:HA	6:HL:97:ILE:HG12	1.95	0.48
5:IK:44:ARG:HB2	8:IN:67:THR:HG22	1.95	0.48
4:JH:170:ARG:HD3	4:JH:245:GLN:HB3	1.95	0.48
2:KD:148:TYR:O	2:KD:152:GLN:N	2.47	0.48
7:MM:249:GLN:OE1	7:MM:267:ASN:ND2	2.45	0.48
2:Ad:148:TYR:HB2	2:Ad:153:VAL:HG12	1.95	0.48
7:BM:152:LEU:HD22	7:BM:155:LEU:HD21	1.95	0.48
11:GC:96:ASP:O	11:GC:99:SER:OG	2.31	0.48
11:KC:152:LEU:HD21	11:KC:203:ILE:HG21	1.94	0.48
11:LC:176:TRP:O	11:LC:180:THR:OG1	2.30	0.48
6:EL:44:HIS:HB2	6:EL:48:ASN:HA	1.95	0.48
8:EN:81:LEU:HD11	4:FH:355:GLN:HG3	1.96	0.48
1:KG:951:HIS:O	1:KG:955:ARG:NE	2.46	0.48
5:GK:76:ILE:HB	5:GK:182:ILE:HG23	1.96	0.48
8:GN:103:CYS:SG	8:GN:109:SER:OG	2.71	0.48
3:HF:207:ARG:NH1	3:HF:208:ILE:O	2.47	0.48
1:Hg:811:ASP:N	1:Hg:811:ASP:OD1	2.45	0.48
2:Jd:148:TYR:HB2	2:Jd:153:VAL:HG12	1.95	0.48
1:CG:931:SER:O	1:CG:1042:THR:OG1	2.30	0.48
11:CC:128:ILE:HD11	11:BC:246:ARG:HD3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Kg:791:GLN:N	1:Kg:793:GLU:OE1	2.46	0.48
4:KH:191:ILE:HG21	4:KH:213:LEU:HD21	1.94	0.48
1:Cg:824:THR:O	4:BH:231:ARG:NH2	2.46	0.48
7:MM:288:ARG:NH2	7:MM:318:GLN:O	2.42	0.48
4:XH:168:VAL:HA	4:XH:240:THR:O	2.14	0.48
4:YH:171:LEU:HD12	4:YH:241:LEU:HB3	1.95	0.48
10:AX:23:UNK:HA	10:AX:33:UNK:HA	1.94	0.48
7:BM:190:ASN:OD1	7:BM:190:ASN:N	2.46	0.48
2:Bd:84:SER:H	11:KC:268:ALA:HB3	1.77	0.48
11:GC:235:THR:OG1	11:GC:236:GLY:N	2.46	0.48
2:ED:69:ASN:OD1	2:ED:69:ASN:N	2.40	0.48
4:CH:229:ARG:HG2	4:CH:236:PRO:HB3	1.96	0.48
6:EL:118:GLU:HG3	6:EL:123:ARG:HG2	1.94	0.48
1:KG:958:SER:O	1:KG:962:SER:OG	2.30	0.48
5:GK:85:ALA:HB3	5:GK:88:SER:HB2	1.94	0.48
4:HH:229:ARG:HH22	4:XH:210:SER:HB2	1.79	0.48
3:If:245:LYS:HB2	3:If:255:LEU:HD12	1.95	0.48
4:JH:183:ASP:OD1	4:JH:187:ALA:N	2.46	0.48
2:LD:36:ASP:OD2	11:GC:193:ASN:ND2	2.47	0.48
4:LH:330:SER:OG	4:LH:332:ASP:OD1	2.32	0.48
2:CD:26:LYS:NZ	6:CL:114:ILE:O	2.46	0.48
4:WH:206:TRP:O	4:WH:208:LYS:NZ	2.39	0.48
2:AD:150:ASN:OD1	2:AD:150:ASN:N	2.45	0.48
5:BK:106:LEU:O	5:BK:111:LYS:NZ	2.42	0.48
11:HC:170:LYS:HA	11:HC:173:LYS:HE2	1.95	0.48
11:LC:34:LEU:HA	11:LC:37:MET:HG2	1.94	0.48
11:LC:154:ASP:OD1	11:LC:154:ASP:N	2.45	0.48
7:CM:307:SER:OG	3:Cf:253:ARG:NH2	2.45	0.48
8:DN:46:GLY:O	8:DN:61:ASN:ND2	2.46	0.48
2:FD:81:ALA:HB3	2:FD:128:LEU:HD11	1.96	0.48
4:FH:289:PRO:O	4:FH:292:SER:OG	2.31	0.48
5:FK:90:ARG:HD3	7:FM:292:MET:HB2	1.94	0.48
1:KG:873:LEU:HD23	1:KG:1037:LEU:HD22	1.94	0.48
8:FN:92:TYR:HD1	8:FN:94:GLN:H	1.61	0.48
11:BC:168:PRO:O	11:BC:174:LYS:NZ	2.46	0.48
7:GM:166:ASN:HA	7:GM:186:SER:HB3	1.95	0.48
8:HN:89:GLY:HA3	8:HN:104:ASN:HB2	1.96	0.48
3:IF:219:ARG:HH22	4:JH:151:PRO:HD2	1.79	0.48
3:KF:246:LEU:HB3	3:KF:255:LEU:HD12	1.95	0.48
3:LF:241:TYR:O	3:LF:258:SER:OG	2.32	0.48
4:LH:182:LEU:HB3	4:LH:186:GLY:HA2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AK:92:ASN:O	5:AK:95:SER:OG	2.31	0.48
4:VH:178:SER:HA	4:VH:213:LEU:O	2.14	0.48
7:BM:193:GLN:NE2	7:BM:195:ASP:OD2	2.47	0.48
11:FC:147:TRP:O	11:FC:151:LEU:HB2	2.14	0.48
11:MC:258:ASN:OD1	11:MC:258:ASN:N	2.45	0.48
11:LC:121:ASP:N	11:LC:124:SER:OG	2.45	0.48
11:LC:146:THR:H	11:LC:149:GLN:HE22	1.61	0.48
11:LC:154:ASP:HB2	8:DN:111:GLU:HG3	1.94	0.48
5:CK:44:ARG:HD2	5:CK:48:ALA:HB3	1.95	0.48
7:DM:284:LEU:HD22	7:DM:302:ARG:HH12	1.78	0.48
2:Ed:97:ARG:NH1	11:AC:264:ALA:O	2.46	0.48
1:MG:1006:ILE:O	1:MG:1010:THR:OG1	2.29	0.48
11:BC:234:VAL:HG12	11:BC:243:ILE:HA	1.96	0.48
7:GM:228:VAL:HG11	7:GM:231:LEU:HB2	1.96	0.48
7:GM:292:MET:N	7:GM:292:MET:SD	2.86	0.48
7:IM:289:ALA:HA	7:IM:318:GLN:HE22	1.77	0.48
6:KL:187:GLU:OE1	7:KM:268:HIS:ND1	2.47	0.48
7:KM:249:GLN:OE1	7:KM:267:ASN:ND2	2.47	0.48
10:KX:26:UNK:O	4:LH:132:GLN:NE2	2.44	0.48
4:LH:329:THR:OG1	4:LH:335:HIS:ND1	2.40	0.48
5:AK:50:ASP:HB2	8:AN:45:MET:HE3	1.96	0.48
6:ML:127:ILE:HB	6:ML:229:ILE:HB	1.95	0.48
4:VH:207:ASP:OD2	4:VH:209:THR:OG1	2.30	0.48
4:XH:313:VAL:HG23	4:XH:337:TYR:HB2	1.96	0.48
3:Bf:245:LYS:NZ	3:Bf:256:THR:O	2.47	0.48
11:EC:146:THR:HG23	11:EC:148:ARG:HB3	1.96	0.48
11:GC:110:VAL:HG13	11:GC:209:GLY:HA3	1.94	0.48
11:HC:258:ASN:ND2	11:HC:261:GLU:OE2	2.46	0.48
11:KC:218:ALA:O	11:KC:264:ARG:NH2	2.47	0.48
7:DM:215:ARG:NH1	7:DM:232:ASP:OD2	2.44	0.48
7:DM:257:ASP:OD1	7:DM:257:ASP:N	2.39	0.48
3:EF:208:ILE:HG13	3:EF:225:SER:H	1.79	0.48
1:Fg:796:GLN:O	1:Fg:799:SER:OG	2.31	0.48
1:MG:947:ARG:HH21	1:MG:1030:GLU:HB3	1.79	0.48
1:NG:1032:TYR:HD1	1:OG:941:ARG:HH22	1.60	0.48
4:HH:183:ASP:OD1	4:HH:187:ALA:N	2.46	0.48
5:HK:134:LEU:HD22	7:HM:304:TRP:HZ2	1.78	0.48
4:IH:316:ASN:N	4:IH:316:ASN:OD1	2.46	0.48
8:IN:87:TRP:O	8:IN:88:HIS:ND1	2.47	0.48
4:AH:183:ASP:OD1	4:AH:187:ALA:N	2.40	0.48
4:AH:196:LEU:HD22	4:AH:204:ILE:HD11	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CG:877:VAL:HG23	1:DG:942:THR:HG21	1.96	0.48
6:KL:55:ARG:HD2	6:KL:153:ARG:HH12	1.79	0.48
6:KL:177:HIS:ND1	7:KM:315:TYR:OH	2.39	0.48
8:KN:45:MET:HG2	8:KN:62:ASN:HD21	1.78	0.48
4:LH:320:LEU:N	4:LH:346:LEU:O	2.45	0.48
1:EG:912:MET:HB3	1:EG:944:LEU:HB2	1.96	0.48
4:XH:221:TYR:HA	4:XH:243:PRO:HG2	1.96	0.48
1:ZG:801:MET:HG2	4:BH:115:MET:HE2	1.94	0.48
8:AN:79:GLN:NE2	4:BH:355:GLN:OE1	2.39	0.48
2:Ad:141:LYS:HE3	2:Ad:141:LYS:HB3	1.73	0.48
4:BH:110:LYS:HA	4:BH:113:LYS:HG2	1.95	0.48
4:BH:316:ASN:N	4:BH:316:ASN:OD1	2.46	0.48
11:DC:79:ILE:HD11	11:DC:195:LEU:HD22	1.96	0.48
11:GC:105:ASN:ND2	11:GC:142:ILE:O	2.47	0.48
11:LC:40:SER:OG	11:LC:44:ARG:NH2	2.47	0.48
4:CH:168:VAL:HG13	4:CH:242:ILE:HD13	1.94	0.48
1:Eg:820:TYR:OH	1:Eg:822:GLU:OE1	2.29	0.48
4:FH:330:SER:OG	4:FH:332:ASP:OD1	2.30	0.48
1:NG:951:HIS:O	1:NG:955:ARG:NE	2.46	0.48
1:OG:899:LEU:HD11	1:OG:916:PHE:HB3	1.95	0.48
11:AC:255:LEU:H	11:AC:255:LEU:HG	1.48	0.48
11:BC:176:ILE:HA	11:BC:179:ILE:HG12	1.96	0.48
1:AG:910:ASP:OD1	1:AG:910:ASP:N	2.47	0.48
2:Gd:26:LYS:NZ	2:Gd:27:LYS:O	2.39	0.48
1:Bg:796:GLN:O	1:Bg:799:SER:OG	2.31	0.48
2:Id:36:ASP:OD1	2:Id:36:ASP:N	2.45	0.48
2:JD:75:ASN:HA	2:JD:79:LEU:HD22	1.96	0.48
5:KK:151:SER:OG	5:KK:152:ARG:N	2.47	0.48
3:LF:208:ILE:O	3:LF:241:TYR:OH	2.30	0.48
6:LL:44:HIS:HB2	6:LL:48:ASN:HA	1.94	0.48
3:Lf:260:GLN:NE2	3:Lf:261:VAL:O	2.47	0.48
5:MK:121:SER:OG	5:MK:122:LYS:N	2.45	0.48
4:VH:166:PRO:HG3	4:DH:151:PRO:HB2	1.96	0.48
4:WH:317:LEU:O	4:WH:337:TYR:OH	2.32	0.48
3:XF:213:GLN:O	4:XH:170:ARG:NH1	2.47	0.48
6:AL:108:ASP:OD2	6:AL:150:ASN:ND2	2.47	0.48
2:AD:122:SER:OG	11:IC:88:ARG:NH2	2.46	0.48
7:AM:210:ASP:N	7:AM:210:ASP:OD1	2.47	0.48
2:Ad:98:ILE:HG21	2:Ad:132:LEU:HD21	1.96	0.48
4:BH:117:ARG:NH1	4:CH:108:ASP:OD2	2.47	0.48
2:Cd:68:ASP:N	2:Cd:68:ASP:OD1	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:DH:324:TRP:HA	4:DH:339:MET:HG3	1.96	0.48
6:DL:170:ASP:OD2	6:DL:227:ARG:NH2	2.46	0.48
1:KG:880:ASP:OD1	1:KG:880:ASP:N	2.46	0.48
3:Ff:256:THR:OG1	3:Ff:257:SER:N	2.47	0.48
3:AF:220:ALA:HB3	3:AF:232:VAL:HG12	1.96	0.48
7:HM:202:LEU:HB2	7:HM:222:ILE:HG23	1.96	0.47
6:IL:121:ASP:OD1	6:IL:121:ASP:N	2.45	0.47
10:IX:26:UNK:O	4:KH:129:LYS:NZ	2.47	0.47
1:Jg:794:ILE:O	1:Jg:798:THR:N	2.44	0.47
4:LH:205:GLN:HB2	4:LH:214:MET:HE2	1.97	0.47
4:LH:319:ILE:HD11	4:LH:345:LEU:HB3	1.94	0.47
4:XH:179:LEU:HG	4:XH:252:VAL:HB	1.96	0.47
11:LC:102:GLU:OE2	11:LC:103:HIS:ND1	2.47	0.47
7:CM:249:GLN:NE2	7:CM:267:ASN:OD1	2.47	0.47
7:DM:167:GLY:H	7:DM:186:SER:HB3	1.79	0.47
8:DN:109:SER:OG	8:DN:112:CYS:SG	2.68	0.47
4:EH:130:LEU:HA	4:EH:133:ILE:HG22	1.96	0.47
7:EM:163:THR:HB	7:EM:183:VAL:HG12	1.96	0.47
5:FK:76:ILE:HB	5:FK:182:ILE:HG13	1.95	0.47
5:FK:131:ALA:HB3	7:FM:299:LEU:HD23	1.95	0.47
11:AC:116:THR:OG1	11:AC:128:SER:OG	2.31	0.47
11:AC:175:ILE:HA	11:AC:178:ILE:HG12	1.95	0.47
11:IC:79:ILE:HD11	11:IC:195:LEU:HD13	1.95	0.47
1:AG:1020:GLN:OE1	1:PG:1017:GLN:NE2	2.44	0.47
4:GH:148:PRO:HD2	3:WF:219:ARG:HG2	1.96	0.47
4:GH:345:LEU:HB3	4:GH:356:LEU:HB2	1.96	0.47
7:GM:284:LEU:O	7:GM:310:LYS:NZ	2.46	0.47
4:HH:313:VAL:HG22	4:HH:337:TYR:HB2	1.96	0.47
2:ID:85:VAL:HG12	2:ID:123:THR:HG22	1.96	0.47
3:IF:213:GLN:O	4:IH:170:ARG:NH2	2.47	0.47
4:IH:332:ASP:OD1	4:IH:334:THR:OG1	2.31	0.47
5:IK:92:ASN:O	5:IK:95:SER:OG	2.31	0.47
4:JH:191:ILE:HA	4:JH:230:LEU:HA	1.96	0.47
4:AH:106:VAL:HA	4:AH:109:LYS:HE2	1.96	0.47
4:KH:114:ASP:O	4:KH:118:ASN:ND2	2.48	0.47
5:KK:43:CYS:SG	5:KK:44:ARG:N	2.87	0.47
5:KK:87:GLN:HB3	5:KK:128:ARG:HH12	1.78	0.47
5:AK:85:ALA:HB3	5:AK:88:SER:HB3	1.96	0.47
3:Df:243:MET:O	3:Df:257:SER:N	2.43	0.47
7:MM:271:SER:OG	7:MM:290:ASP:OD1	2.32	0.47
4:ZH:174:GLY:N	4:ZH:217:ALA:O	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:ZH:179:LEU:O	4:ZH:212:THR:HA	2.13	0.47
4:ZH:315:THR:OG1	4:ZH:316:ASN:N	2.47	0.47
7:AM:125:THR:HG23	7:AM:145:ARG:HB2	1.97	0.47
2:Bd:87:TRP:O	2:Bd:120:SER:HA	2.14	0.47
11:EC:109:VAL:HB	11:EC:135:ALA:HB3	1.96	0.47
11:FC:109:VAL:HG13	11:FC:208:GLY:HA3	1.95	0.47
11:FC:240:ILE:O	11:GC:132:THR:OG1	2.31	0.47
11:MC:46:GLN:OE1	11:MC:49:GLN:NE2	2.47	0.47
5:CK:86:ASP:OD1	5:CK:86:ASP:N	2.45	0.47
4:DH:339:MET:HE1	4:DH:345:LEU:HD11	1.96	0.47
1:GG:1005:VAL:O	1:GG:1009:ALA:CB	2.62	0.47
6:DL:150:ASN:OD1	6:DL:153:ARG:NH2	2.44	0.47
5:FK:87:GLN:HB3	5:FK:128:ARG:HH12	1.78	0.47
1:HG:1042:THR:OG1	1:HG:1043:GLN:OE1	2.31	0.47
1:IG:966:GLN:O	1:IG:970:ASN:ND2	2.47	0.47
1:NG:886:LEU:HD23	1:OG:1040:LEU:HD12	1.97	0.47
1:OG:937:PRO:HD3	1:OG:1037:LEU:HA	1.96	0.47
8:FN:45:MET:HG2	8:FN:62:ASN:HD21	1.79	0.47
5:GK:66:LYS:HB3	5:GK:77:SER:HB3	1.97	0.47
2:HD:36:ASP:OD1	2:HD:36:ASP:N	2.46	0.47
2:Hd:36:ASP:OD1	2:Hd:36:ASP:N	2.40	0.47
3:Jf:209:ILE:O	3:Jf:225:SER:OG	2.29	0.47
4:AH:319:ILE:HD11	4:AH:345:LEU:HD12	1.96	0.47
1:CG:872:VAL:HB	1:CG:888:THR:HB	1.95	0.47
2:LD:150:ASN:OD1	2:LD:150:ASN:N	2.46	0.47
1:DG:881:GLU:OE1	1:EG:904:ASN:ND2	2.46	0.47
8:MN:89:GLY:O	8:MN:104:ASN:ND2	2.47	0.47
4:ZH:151:PRO:HA	4:ZH:248:VAL:HG13	1.97	0.47
4:BH:149:PRO:O	3:AF:219:ARG:NH2	2.46	0.47
11:DC:216:LEU:HD11	11:DC:223:PRO:HG3	1.96	0.47
11:JC:132:TYR:O	11:IC:239:GLU:HA	2.14	0.47
5:EK:78:ILE:HB	5:EK:180:VAL:HG23	1.95	0.47
1:IG:911:LYS:HA	1:IG:943:ALA:HA	1.97	0.47
7:FM:199:LYS:HA	7:FM:219:ALA:HB3	1.95	0.47
6:GL:149:ASN:HB3	6:GL:153:ARG:HH12	1.78	0.47
7:HM:128:ASN:O	7:HM:130:ARG:NH1	2.47	0.47
6:IL:210:ASP:OD1	6:IL:210:ASP:N	2.44	0.47
6:JL:125:LEU:HB2	6:JL:231:ILE:HB	1.96	0.47
1:CG:1024:ASN:OD1	1:CG:1024:ASN:N	2.44	0.47
4:LH:203:ASN:O	4:LH:216:GLN:NE2	2.47	0.47
4:WH:105:GLU:O	4:WH:109:LYS:NZ	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Dg:800:ASP:OD1	1:Dg:800:ASP:N	2.47	0.47
11:FC:103:HIS:HD1	11:FC:226:VAL:HG11	1.79	0.47
2:ED:86:ASP:N	2:ED:86:ASP:OD1	2.47	0.47
11:JC:91:ASP:HB3	11:JC:147:TRP:HE1	1.80	0.47
6:DL:94:VAL:HA	6:DL:97:ILE:HG12	1.97	0.47
6:DL:200:ALA:HB1	7:DM:230:ARG:HH21	1.77	0.47
7:DM:125:THR:HG23	7:DM:145:ARG:HB2	1.97	0.47
3:EF:254:ILE:HB	3:EF:262:ILE:HB	1.96	0.47
6:EL:150:ASN:OD1	6:EL:153:ARG:NH2	2.41	0.47
8:EN:89:GLY:O	8:EN:104:ASN:ND2	2.46	0.47
2:FD:77:TYR:OH	5:FK:130:ARG:NH1	2.48	0.47
1:Fg:807:GLN:NE2	1:Fg:811:ASP:OD2	2.48	0.47
1:LG:1024:ASN:OD1	1:LG:1024:ASN:N	2.41	0.47
5:GK:185:ARG:NH1	6:HL:216:ASP:OD1	2.47	0.47
3:IF:235:GLY:O	3:JF:266:GLN:NE2	2.48	0.47
6:JL:165:VAL:HG12	6:JL:231:ILE:HG12	1.97	0.47
4:KH:324:TRP:HB3	4:KH:339:MET:HE3	1.95	0.47
6:LL:130:ASP:N	6:LL:130:ASP:OD1	2.47	0.47
7:LM:257:ASP:N	7:LM:257:ASP:OD1	2.47	0.47
5:AK:87:GLN:HB3	5:AK:128:ARG:HH12	1.78	0.47
4:XH:292:SER:HB3	4:XH:305:TRP:HB3	1.95	0.47
3:ZF:241:TYR:O	3:ZF:257:SER:OG	2.32	0.47
4:BH:251:ARG:NH1	4:BH:253:ASP:OD1	2.47	0.47
11:GC:248:LEU:HB2	11:HC:125:ILE:HG22	1.97	0.47
6:DL:178:LYS:O	6:DL:182:SER:OG	2.30	0.47
10:DX:25:UNK:N	10:DX:71:UNK:O	2.47	0.47
8:FN:49:ASN:HB3	8:FN:59:VAL:HG23	1.96	0.47
2:Fd:72:THR:OG1	2:Fd:73:ILE:N	2.47	0.47
3:GF:210:TYR:HA	3:GF:224:GLY:HA2	1.96	0.47
5:GK:87:GLN:HB3	5:GK:128:ARG:HH12	1.79	0.47
6:GL:169:THR:HG21	6:GL:178:LYS:HB3	1.96	0.47
2:ID:111:LYS:HZ2	2:Id:120:SER:H	1.62	0.47
3:IF:219:ARG:NH1	4:JH:149:PRO:O	2.48	0.47
7:IM:275:ASP:HB3	7:IM:294:PHE:HB2	1.96	0.47
7:IM:303:GLU:OE1	7:IM:306:GLN:N	2.47	0.47
2:KD:23:MET:N	2:KD:23:MET:SD	2.88	0.47
4:MH:114:ASP:HA	4:MH:117:ARG:HH11	1.79	0.47
4:MH:157:PHE:HA	4:MH:255:ARG:HB2	1.97	0.47
6:ML:129:THR:HG22	6:ML:229:ILE:HG12	1.97	0.47
7:MM:292:MET:SD	7:MM:296:GLY:N	2.87	0.47
3:WF:207:ARG:HE	3:WF:240:GLY:HA3	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:EG:969:GLY:HA3	1:EG:1009:ALA:HB2	1.97	0.47
4:XH:220:LEU:HD23	4:XH:221:TYR:HB3	1.95	0.47
1:YG:807:GLN:NE2	1:YG:810:GLN:OE1	2.43	0.47
4:YH:198:ASP:OD1	4:YH:200:SER:OG	2.31	0.47
6:BL:53:ASP:O	6:BL:54:ARG:NE	2.47	0.47
6:BL:102:LYS:HA	6:BL:105:ILE:HD12	1.96	0.47
2:Bd:108:VAL:HG22	2:Bd:156:LEU:HB3	1.96	0.47
11:FC:146:THR:OG1	11:FC:147:TRP:N	2.45	0.47
7:CM:149:ASN:OD1	7:CM:149:ASN:N	2.44	0.47
7:EM:117:ARG:HA	7:EM:137:TYR:O	2.15	0.47
4:FH:130:LEU:HA	4:FH:133:ILE:HD12	1.97	0.47
1:IG:1006:ILE:O	1:IG:1010:THR:OG1	2.33	0.47
1:JG:966:GLN:O	1:JG:970:ASN:ND2	2.48	0.47
1:AG:872:VAL:HA	1:AG:1036:GLY:HA2	1.97	0.47
6:GL:133:PHE:HA	6:GL:140:LEU:HA	1.97	0.47
3:HF:220:ALA:HB3	3:HF:232:VAL:HG12	1.95	0.47
2:Dd:64:PRO:HD3	2:DD:67:LYS:HE3	1.97	0.47
2:Dd:73:ILE:HG22	2:Dd:75:ASN:H	1.79	0.47
5:HK:166:THR:HG22	5:HK:168:TYR:H	1.79	0.47
6:HL:44:HIS:N	6:HL:48:ASN:OD1	2.46	0.47
6:HL:49:ASN:ND2	7:HM:293:ALA:O	2.45	0.47
1:BG:958:SER:O	1:BG:962:SER:OG	2.33	0.47
7:IM:127:ASN:HB3	7:IM:147:ALA:HB3	1.96	0.47
7:IM:209:SER:OG	7:IM:210:ASP:N	2.48	0.47
7:JM:127:ASN:HB3	7:JM:147:ALA:HB3	1.96	0.47
2:Jd:92:GLU:OE2	2:Jd:158:TYR:OH	2.33	0.47
4:KH:138:GLU:HA	4:KH:141:LYS:HG2	1.97	0.47
4:KH:203:ASN:OD1	4:KH:216:GLN:NE2	2.47	0.47
7:KM:208:LYS:HE2	7:KM:227:ILE:HG12	1.95	0.47
2:LD:47:SER:O	2:LD:51:SER:OG	2.31	0.47
2:LD:148:TYR:O	2:LD:152:GLN:N	2.48	0.47
7:LM:208:LYS:HE2	7:LM:208:LYS:HB2	1.61	0.47
9:LU:127:UNK:O	6:ML:232:GLN:NE2	2.46	0.47
2:CD:32:ASN:N	2:CD:32:ASN:OD1	2.46	0.47
5:AK:113:ALA:HA	5:AK:153:ILE:O	2.15	0.47
4:MH:230:LEU:HB2	4:MH:233:LEU:HB3	1.97	0.47
4:WH:168:VAL:HA	4:WH:240:THR:O	2.15	0.47
4:ZH:284:LEU:O	4:ZH:314:ARG:NH2	2.44	0.47
1:FG:966:GLN:O	1:FG:970:ASN:ND2	2.48	0.47
11:EC:130:ARG:H	11:DC:242:ILE:HG12	1.79	0.47
11:FC:121:ASP:N	11:FC:124:SER:OG	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:GC:171:LYS:HA	11:GC:174:LYS:HE2	1.96	0.47
11:MC:117:LEU:HD12	11:MC:127:ILE:HG22	1.96	0.47
11:JC:64:LEU:HB2	11:JC:179:TYR:HB3	1.97	0.47
4:CH:319:ILE:HA	4:CH:347:VAL:HG12	1.97	0.47
5:CK:76:ILE:HB	5:CK:182:ILE:HG12	1.96	0.47
3:Cf:261:VAL:O	3:Cf:263:LYS:NZ	2.39	0.47
1:GG:951:HIS:H	1:GG:1027:THR:HG22	1.79	0.47
4:FH:189:TRP:HE1	4:FH:232:GLY:H	1.62	0.47
4:FH:296:VAL:HG13	4:FH:359:GLU:HB2	1.97	0.47
6:FL:49:ASN:ND2	7:FM:293:ALA:O	2.48	0.47
1:JG:867:ASP:H	1:JG:1041:PHE:HB2	1.78	0.47
2:GD:59:GLU:HA	2:GD:62:ILE:HG22	1.97	0.47
7:HM:158:VAL:HG22	7:HM:178:LYS:HE2	1.95	0.47
7:HM:240:GLN:HB3	7:HM:242:LYS:HE3	1.97	0.47
1:Bg:799:SER:HA	1:Bg:802:LEU:HD12	1.95	0.47
3:If:216:ILE:HD12	3:If:216:ILE:HA	1.78	0.47
1:Jg:800:ASP:OD1	1:Jg:800:ASP:N	2.31	0.47
6:JL:108:ASP:OD1	6:JL:150:ASN:ND2	2.47	0.47
5:LK:49:CYS:O	5:LK:52:THR:OG1	2.28	0.47
1:DG:1003:ASN:HA	1:DG:1006:ILE:HD12	1.97	0.47
6:ML:108:ASP:OD2	6:ML:150:ASN:ND2	2.47	0.47
4:YH:311:MET:HG2	4:YH:341:LYS:HA	1.96	0.47
4:ZH:228:VAL:HB	4:ZH:237:VAL:HB	1.96	0.47
2:Ad:36:ASP:OD1	2:Ad:36:ASP:N	2.46	0.47
4:BH:183:ASP:OD1	4:BH:187:ALA:N	2.48	0.47
1:FG:1017:GLN:NE2	1:FG:1018:GLN:OE1	2.48	0.47
1:Dg:817:THR:OG1	1:Dg:818:GLN:N	2.48	0.47
11:DC:201:ARG:HE	11:DC:201:ARG:HB2	1.57	0.47
2:ED:36:ASP:OD2	11:MC:192:ASN:ND2	2.48	0.47
2:ED:81:ALA:HB3	2:ED:128:LEU:HD11	1.96	0.47
11:LC:157:LYS:HB2	8:DN:82:MET:HE1	1.96	0.47
3:DF:216:ILE:HG22	3:DF:219:ARG:H	1.79	0.47
4:DH:182:LEU:O	4:DH:255:ARG:HA	2.15	0.47
6:DL:187:GLU:OE2	7:DM:268:HIS:ND1	2.48	0.47
7:EM:117:ARG:HB3	7:EM:137:TYR:HD2	1.79	0.47
7:EM:127:ASN:HB3	7:EM:147:ALA:HB3	1.97	0.47
1:IG:878:ASN:ND2	1:JG:910:ASP:OD2	2.48	0.47
1:JG:951:HIS:HE1	1:JG:1028:THR:HG23	1.79	0.47
1:LG:874:ASP:OD1	1:LG:874:ASP:N	2.47	0.47
1:AG:886:LEU:HD23	1:BG:1040:LEU:HD12	1.97	0.47
7:GM:235:LEU:HD23	7:GM:259:SER:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:GN:62:ASN:HA	2:HD:26:LYS:HG3	1.96	0.47
3:Gf:256:THR:OG1	3:Gf:257:SER:N	2.48	0.47
5:HK:73:ASN:N	5:HK:73:ASN:OD1	2.48	0.47
2:Hd:128:LEU:HA	2:Hd:131:ILE:HD12	1.97	0.47
1:Bg:792:GLN:O	1:Bg:795:GLN:NE2	2.42	0.47
5:JK:87:GLN:OE1	5:JK:128:ARG:NH1	2.47	0.47
6:JL:190:MET:HB2	6:JL:203:LEU:HD11	1.95	0.47
5:KK:78:ILE:HB	5:KK:180:VAL:HG23	1.97	0.47
2:Kd:82:ARG:NH2	2:Kd:126:GLU:H	2.13	0.47
2:CD:87:TRP:CD1	2:CD:89:GLY:H	2.32	0.47
2:Ld:93:GLU:HG2	11:HC:263:ARG:HA	1.96	0.47
7:MM:257:ASP:N	7:MM:257:ASP:OD1	2.47	0.47
8:AN:92:TYR:HD1	8:AN:94:GLN:H	1.63	0.47
7:BM:153:GLN:HA	7:BM:173:LEU:HG	1.96	0.47
1:FG:911:LYS:HA	1:FG:943:ALA:HA	1.96	0.47
4:CH:184:SER:HB2	4:CH:259:TYR:HE1	1.79	0.47
5:CK:38:VAL:HA	5:CK:41:LEU:HB2	1.96	0.47
1:GG:870:PHE:HD2	1:GG:891:THR:HG21	1.80	0.47
6:DL:118:GLU:OE2	6:DL:123:ARG:NE	2.43	0.47
4:FH:198:ASP:OD1	4:FH:200:SER:OG	2.32	0.47
11:IC:166:LEU:HD13	11:IC:167:PRO:HD2	1.96	0.47
4:GH:256:VAL:HG23	4:GH:258:GLY:H	1.80	0.47
5:GK:92:ASN:N	5:GK:92:ASN:OD1	2.48	0.47
7:HM:209:SER:OG	7:HM:210:ASP:N	2.48	0.47
2:ID:35:ASP:O	2:ID:38:THR:OG1	2.32	0.47
2:Id:138:GLN:HE21	2:Id:138:GLN:HB2	1.49	0.47
2:Jd:59:GLU:OE2	11:EC:213:ARG:NH2	2.48	0.47
11:CC:134:LYS:HA	11:BC:240:GLU:HG3	1.97	0.47
4:LH:124:PRO:HB3	4:YH:140:ALA:HB2	1.96	0.47
2:Ld:149:PRO:O	2:Ld:152:GLN:NE2	2.48	0.47
8:MN:62:ASN:OD1	8:MN:62:ASN:N	2.47	0.47
3:VF:222:LEU:HD11	3:VF:262:ILE:HG21	1.97	0.47
3:VF:230:LEU:HA	4:VH:165:THR:HG21	1.96	0.47
3:WF:243:MET:N	3:WF:257:SER:OG	2.45	0.47
4:ZH:328:MET:HE2	4:ZH:328:MET:HB3	1.88	0.47
4:BH:201:SER:HA	4:BH:219:LYS:HB2	1.97	0.47
7:BM:172:ASN:HD21	7:BM:174:GLN:HE22	1.63	0.47
11:FC:258:ASN:OD1	11:FC:258:ASN:N	2.44	0.47
7:DM:290:ASP:HB3	7:DM:298:VAL:HG21	1.97	0.47
6:FL:44:HIS:HB2	6:FL:48:ASN:HA	1.97	0.47
1:HG:899:LEU:HD21	1:HG:916:PHE:HB3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HG:951:HIS:O	1:HG:955:ARG:NE	2.48	0.47
1:PG:966:GLN:O	1:PG:970:ASN:ND2	2.48	0.47
11:BC:245:ASP:OD1	11:BC:245:ASP:N	2.46	0.47
7:GM:199:LYS:HA	7:GM:219:ALA:HB3	1.97	0.46
8:HN:46:GLY:HA3	8:HN:61:ASN:HB2	1.97	0.46
8:IN:66:SER:OG	8:IN:67:THR:N	2.48	0.46
2:JD:29:PRO:HG2	6:JL:225:GLN:HG2	1.97	0.46
5:KK:129:GLU:OE1	5:KK:129:GLU:N	2.48	0.46
6:KL:134:MET:HE1	6:KL:141:ASN:HA	1.97	0.46
1:Ag:816:GLU:OE2	4:ZH:200:SER:N	2.48	0.46
2:LD:149:PRO:O	2:LD:152:GLN:NE2	2.48	0.46
7:LM:173:LEU:HD21	7:LM:189:VAL:HG13	1.97	0.46
6:AL:113:ASP:OD2	6:AL:131:LYS:NZ	2.45	0.46
7:AM:190:ASN:OD1	7:AM:192:ARG:NH2	2.48	0.46
2:ED:29:PRO:HG2	6:EL:225:GLN:HA	1.98	0.46
11:KC:246:ARG:HB2	11:LC:127:ILE:HG12	1.96	0.46
4:CH:154:THR:O	4:CH:252:VAL:HA	2.15	0.46
3:DF:237:LYS:HG2	3:DF:243:MET:HG2	1.97	0.46
4:EH:230:LEU:HB2	4:EH:233:LEU:HB2	1.97	0.46
6:EL:108:ASP:OD2	6:EL:150:ASN:ND2	2.48	0.46
1:Fg:820:TYR:OH	1:Fg:822:GLU:OE2	2.33	0.46
5:FK:46:ASP:OD1	5:FK:46:ASP:N	2.48	0.46
6:FL:129:THR:OG1	6:FL:130:ASP:OD1	2.29	0.46
1:JG:1017:GLN:NE2	1:KG:1020:GLN:OE1	2.48	0.46
1:NG:873:LEU:H	1:NG:1036:GLY:HA2	1.80	0.46
7:HM:261:ALA:HB1	7:HM:263:ILE:HD11	1.97	0.46
3:JF:238:ILE:HB	3:JF:241:TYR:HB2	1.96	0.46
6:KL:54:ARG:HH21	6:KL:57:VAL:HG13	1.79	0.46
7:KM:180:ASP:O	7:KM:182:LYS:NZ	2.41	0.46
3:Kf:221:TRP:HE1	3:Kf:229:THR:HB	1.80	0.46
5:LK:87:GLN:HB3	5:LK:128:ARG:HH12	1.80	0.46
2:CD:36:ASP:OD1	2:CD:36:ASP:N	2.45	0.46
2:MD:40:LYS:NZ	11:HC:192:ASN:OD1	2.49	0.46
3:Df:234:GLU:HA	3:Df:244:VAL:HB	1.96	0.46
7:AM:271:SER:OG	7:AM:290:ASP:OD1	2.32	0.46
2:BD:82:ARG:NH2	2:BD:125:ASP:O	2.48	0.46
7:BM:129:LEU:H	7:BM:148:GLY:HA3	1.80	0.46
11:JC:106:LEU:HD12	11:JC:107:PRO:HD2	1.96	0.46
6:CL:49:ASN:OD1	6:CL:49:ASN:N	2.49	0.46
7:EM:165:ILE:HB	7:EM:185:ILE:HG23	1.96	0.46
4:FH:171:LEU:HD21	4:FH:241:LEU:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:FH:171:LEU:O	4:FH:244:GLY:N	2.49	0.46
5:FK:54:ILE:HA	5:FK:57:MET:HG2	1.97	0.46
2:Fd:82:ARG:NH2	2:Fd:126:GLU:O	2.48	0.46
11:IC:162:ASN:OD1	11:IC:162:ASN:N	2.46	0.46
3:GF:245:LYS:HE3	3:GF:257:SER:HA	1.97	0.46
6:GL:172:VAL:HG21	2:Gd:43:GLU:HG3	1.96	0.46
7:GM:168:VAL:H	7:GM:187:GLY:HA3	1.79	0.46
6:IL:94:VAL:HA	6:IL:97:ILE:HG12	1.97	0.46
4:KH:182:LEU:O	4:KH:255:ARG:HA	2.15	0.46
2:LD:87:TRP:CD1	2:LD:89:GLY:H	2.34	0.46
8:MN:89:GLY:HA3	8:MN:104:ASN:HB2	1.96	0.46
1:EG:1017:GLN:NE2	1:EG:1018:GLN:OE1	2.42	0.46
4:XH:222:ASN:OD1	4:XH:222:ASN:N	2.49	0.46
4:ZH:292:SER:HB3	4:ZH:307:SER:HB2	1.95	0.46
2:BD:81:ALA:HB3	2:BD:128:LEU:HD11	1.97	0.46
1:FG:904:ASN:OD1	1:FG:904:ASN:N	2.49	0.46
2:ED:116:PRO:HG2	2:ED:118:LEU:HD21	1.96	0.46
11:KC:62:GLU:O	11:KC:66:SER:OG	2.31	0.46
5:CK:92:ASN:O	5:CK:95:SER:OG	2.29	0.46
4:DH:201:SER:O	4:DH:218:THR:N	2.49	0.46
1:GG:872:VAL:HB	1:GG:888:THR:HB	1.97	0.46
8:DN:46:GLY:HA3	8:DN:61:ASN:HB2	1.96	0.46
3:EF:241:TYR:HB3	3:EF:256:THR:HG21	1.97	0.46
2:Fd:93:GLU:HB2	11:BC:264:ARG:HH12	1.80	0.46
8:GN:89:GLY:HA3	8:GN:104:ASN:HB2	1.96	0.46
1:BG:880:ASP:OD1	1:BG:880:ASP:N	2.47	0.46
4:IH:226:LEU:O	4:IH:238:MET:HA	2.16	0.46
3:JF:219:ARG:NH1	3:KF:269:SER:O	2.45	0.46
4:JH:162:PRO:HA	4:KH:251:ARG:HH12	1.81	0.46
5:JK:54:ILE:O	5:JK:58:THR:OG1	2.34	0.46
5:JK:72:GLN:HB3	5:JK:186:ARG:HB3	1.97	0.46
11:CC:243:ILE:HD11	11:DC:129:ASP:HB3	1.96	0.46
4:LH:263:ALA:HB1	4:LH:266:MET:HB2	1.98	0.46
1:Mg:802:LEU:O	1:Mg:806:THR:OG1	2.26	0.46
7:AM:210:ASP:HA	7:AM:229:ASN:H	1.81	0.46
3:BF:246:LEU:HB3	3:BF:255:LEU:HB2	1.97	0.46
6:BL:230:GLU:OE2	6:BL:232:GLN:NE2	2.48	0.46
7:CM:173:LEU:HB3	7:CM:191:LEU:HD13	1.98	0.46
7:CM:235:LEU:HG	7:CM:239:ALA:HB3	1.97	0.46
2:FD:59:GLU:HA	2:FD:62:ILE:HG22	1.97	0.46
1:KG:871:ALA:HA	1:KG:890:VAL:HG22	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:IC:95:ASP:O	11:IC:98:SER:OG	2.31	0.46
5:GK:66:LYS:NZ	5:GK:67:VAL:O	2.47	0.46
7:GM:275:ASP:HB3	7:GM:294:PHE:HB2	1.97	0.46
7:IM:119:GLU:HG3	7:IM:139:ALA:HB3	1.96	0.46
2:KD:158:TYR:O	2:Kd:137:TYR:OH	2.33	0.46
5:KK:92:ASN:O	5:KK:95:SER:OG	2.34	0.46
5:LK:92:ASN:O	5:LK:95:SER:OG	2.33	0.46
6:LL:129:THR:OG1	6:LL:130:ASP:OD1	2.34	0.46
7:LM:190:ASN:ND2	7:LM:208:LYS:O	2.41	0.46
7:LM:267:ASN:O	7:LM:287:THR:OG1	2.30	0.46
1:Cg:792:GLN:O	1:Cg:795:GLN:NE2	2.45	0.46
4:VH:183:ASP:OD1	4:VH:187:ALA:N	2.48	0.46
4:WH:344:VAL:HG13	4:WH:355:GLN:HE21	1.81	0.46
3:XF:221:TRP:HE3	3:XF:231:THR:HB	1.80	0.46
4:YH:292:SER:HB3	4:YH:307:SER:HB2	1.96	0.46
4:ZH:295:LEU:HD13	4:ZH:311:MET:HE1	1.97	0.46
8:AN:49:ASN:OD1	8:AN:61:ASN:ND2	2.48	0.46
5:BK:125:SER:OG	5:BK:126:VAL:N	2.46	0.46
7:BM:154:LYS:HD3	7:BM:154:LYS:HA	1.78	0.46
1:GG:886:LEU:HD23	1:HG:1040:LEU:HD12	1.96	0.46
6:DL:116:TYR:OH	6:DL:118:GLU:OE1	2.34	0.46
7:EM:209:SER:OG	7:EM:210:ASP:N	2.47	0.46
2:FD:29:PRO:HG2	6:FL:225:GLN:HG3	1.97	0.46
1:Fg:800:ASP:N	1:Fg:800:ASP:OD1	2.47	0.46
5:GK:72:GLN:HE22	6:HL:215:SER:HA	1.80	0.46
7:GM:203:SER:HA	7:GM:223:GLN:O	2.16	0.46
3:Gf:208:ILE:O	3:Gf:241:TYR:OH	2.34	0.46
3:Gf:253:ARG:O	3:Gf:253:ARG:NH1	2.48	0.46
4:HH:203:ASN:HB3	4:HH:216:GLN:HB3	1.98	0.46
6:HL:116:TYR:OH	6:HL:118:GLU:OE1	2.34	0.46
3:IF:219:ARG:HH12	4:JH:151:PRO:HD3	1.81	0.46
4:JH:203:ASN:OD1	4:JH:205:GLN:NE2	2.45	0.46
2:Kd:148:TYR:HB2	2:Kd:153:VAL:HG12	1.98	0.46
2:MD:111:LYS:NZ	2:Md:120:SER:O	2.47	0.46
4:WH:298:SER:N	4:WH:357:LYS:O	2.48	0.46
2:AD:55:MET:HE2	2:AD:55:MET:HB3	1.78	0.46
8:AN:95:LEU:HG	1:LG:923:GLY:HA2	1.97	0.46
7:BM:196:MET:HE3	7:BM:198:GLY:H	1.80	0.46
11:FC:79:ILE:HD11	11:FC:195:LEU:HD13	1.97	0.46
11:KC:220:ASN:HB2	11:KC:264:ARG:CZ	2.46	0.46
7:CM:217:LYS:HA	7:CM:236:TRP:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:DD:68:ASP:OD1	2:DD:70:THR:OG1	2.31	0.46
2:DD:87:TRP:CD1	2:DD:89:GLY:H	2.33	0.46
4:DH:135:GLU:O	4:DH:139:TYR:HB2	2.16	0.46
4:DH:189:TRP:HE1	4:DH:232:GLY:H	1.63	0.46
7:EM:278:ASP:OD2	7:EM:280:TYR:OH	2.33	0.46
2:FD:87:TRP:CD1	2:FD:89:GLY:H	2.33	0.46
1:LG:952:TYR:O	1:LG:956:TYR:HB2	2.16	0.46
4:HH:275:SER:OG	4:HH:276:ALA:N	2.49	0.46
7:JM:172:ASN:HA	7:JM:190:ASN:HD22	1.81	0.46
11:CC:107:LEU:HD12	11:CC:108:PRO:HD2	1.97	0.46
4:LH:143:ALA:O	4:MH:131:LYS:NZ	2.40	0.46
6:LL:170:ASP:N	6:LL:170:ASP:OD1	2.38	0.46
5:MK:102:ILE:HD13	5:MK:102:ILE:HA	1.85	0.46
5:MK:186:ARG:NH2	8:MN:65:TYR:O	2.49	0.46
3:Mf:256:THR:OG1	3:Mf:257:SER:N	2.49	0.46
1:EG:966:GLN:O	1:EG:970:ASN:ND2	2.49	0.46
4:XH:155:SER:OG	4:XH:255:ARG:NH1	2.49	0.46
6:AL:124:THR:HA	6:AL:231:ILE:O	2.15	0.46
4:ZH:191:ILE:HG13	4:ZH:211:ASN:HA	1.98	0.46
4:ZH:198:ASP:OD2	4:ZH:201:SER:OG	2.34	0.46
4:ZH:315:THR:O	4:ZH:334:THR:OG1	2.30	0.46
7:BM:316:ASN:OD1	7:BM:316:ASN:N	2.48	0.46
1:FG:919:MET:HG3	1:FG:930:ILE:HG23	1.98	0.46
11:GC:114:GLY:O	11:GC:131:ARG:HA	2.16	0.46
11:HC:206:PHE:HA	11:HC:209:MET:HE3	1.98	0.46
11:LC:46:GLN:O	11:LC:50:LYS:NZ	2.43	0.46
2:DD:36:ASP:N	2:DD:36:ASP:OD1	2.49	0.46
1:GG:885:ILE:O	1:GG:900:ILE:HA	2.15	0.46
5:EK:116:VAL:HG12	5:EK:182:ILE:HB	1.96	0.46
1:PG:1024:ASN:OD1	1:PG:1024:ASN:N	2.42	0.46
2:Fd:100:LYS:HE3	2:Fd:100:LYS:HB2	1.79	0.46
4:IH:172:SER:HB3	4:IH:175:PHE:HB2	1.98	0.46
3:JF:265:SER:HB3	3:JF:268:ASP:HB3	1.98	0.46
3:KF:241:TYR:O	3:KF:258:SER:OG	2.34	0.46
4:KH:339:MET:N	4:KH:339:MET:SD	2.89	0.46
6:LL:210:ASP:OD1	6:LL:210:ASP:N	2.48	0.46
4:VH:168:VAL:O	4:VH:170:ARG:NH2	2.46	0.46
1:WG:801:MET:HE3	1:WG:801:MET:HB2	1.76	0.46
3:XF:219:ARG:HD3	3:XF:233:ARG:HD2	1.97	0.46
4:XH:229:ARG:HG2	4:XH:236:PRO:HB3	1.98	0.46
4:XH:283:VAL:O	4:XH:314:ARG:NH1	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:BM:119:GLU:HG3	7:BM:139:ALA:HB3	1.97	0.46
11:JC:255:LEU:N	11:IC:237:GLY:O	2.44	0.46
11:KC:107:LEU:HD12	11:KC:108:PRO:HD2	1.98	0.46
11:LC:256:ASN:OD1	11:LC:262:TRP:NE1	2.46	0.46
4:CH:203:ASN:N	4:CH:216:GLN:O	2.49	0.46
7:CM:133:TYR:HD1	7:CM:153:GLN:H	1.62	0.46
6:GL:134:MET:HB2	6:GL:139:ARG:HB2	1.97	0.46
2:HD:118:LEU:O	11:CC:98:ASN:ND2	2.49	0.46
8:HN:95:LEU:H	8:HN:95:LEU:HG	1.46	0.46
8:HN:109:SER:OG	8:HN:111:GLU:OE2	2.31	0.46
3:IF:208:ILE:HD11	3:IF:224:GLY:HA3	1.97	0.46
7:IM:275:ASP:HA	7:IM:295:ASN:H	1.81	0.46
9:IU:127:UNK:O	6:JL:232:GLN:NE2	2.49	0.46
10:IX:70:UNK:H2	4:JH:146:GLY:HA2	1.81	0.46
2:LD:35:ASP:O	2:LD:38:THR:OG1	2.30	0.46
2:LD:120:SER:N	2:LD:138:GLN:OE1	2.49	0.46
1:Mg:818:GLN:HB3	4:MH:216:GLN:HG2	1.98	0.46
6:ML:91:VAL:HA	6:ML:94:VAL:HG12	1.98	0.46
3:VF:231:THR:OG1	3:VF:233:ARG:NH1	2.36	0.46
4:WH:319:ILE:HD11	4:WH:324:TRP:HB3	1.97	0.46
1:EG:876:SER:OG	1:FG:941:ARG:NH2	2.49	0.46
11:FC:107:PRO:HD2	11:FC:209:MET:HE1	1.98	0.46
11:HC:121:ASP:N	11:HC:121:ASP:OD1	2.49	0.46
11:LC:45:ALA:HA	11:LC:48:LYS:HE2	1.96	0.46
3:Cf:212:ILE:HG21	3:Cf:254:ILE:HG13	1.98	0.46
2:DD:107:ARG:HH21	2:DD:153:VAL:HG11	1.80	0.46
3:DF:268:ASP:OD1	4:DH:170:ARG:NH1	2.49	0.46
4:DH:196:LEU:HD21	4:DH:202:PHE:HB2	1.97	0.46
1:GG:966:GLN:O	1:GG:970:ASN:ND2	2.49	0.46
7:DM:275:ASP:HA	7:DM:295:ASN:H	1.81	0.46
3:FF:210:TYR:HB3	3:FF:222:LEU:HD23	1.98	0.46
5:FK:78:ILE:HB	5:FK:180:VAL:HG23	1.98	0.46
7:FM:201:THR:HG22	7:FM:221:LYS:HB2	1.98	0.46
2:GD:118:LEU:O	11:BC:98:ASN:ND2	2.49	0.46
8:GN:91:VAL:O	8:GN:104:ASN:ND2	2.42	0.46
5:HK:148:GLY:H	2:Hd:30:ILE:HD12	1.81	0.46
6:HL:108:ASP:OD2	6:HL:150:ASN:ND2	2.49	0.46
1:BG:951:HIS:H	1:BG:1027:THR:HG22	1.81	0.46
5:IK:45:VAL:HG12	8:IN:67:THR:HG23	1.98	0.46
6:JL:185:GLN:HG2	6:JL:229:ILE:HD11	1.97	0.46
4:KH:174:GLY:N	4:KH:217:ALA:O	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LD:158:TYR:O	2:Ld:137:TYR:OH	2.32	0.46
6:LL:163:ILE:O	6:LL:204:LYS:NZ	2.45	0.46
3:Lf:253:ARG:HG3	3:Lf:263:LYS:HD3	1.98	0.46
2:MD:69:ASN:O	2:MD:72:THR:OG1	2.33	0.46
3:WF:214:ALA:H	3:WF:221:TRP:HB2	1.81	0.46
1:EG:953:LEU:HA	1:EG:956:TYR:HB2	1.97	0.46
3:YF:246:LEU:HB3	3:YF:255:LEU:HD12	1.97	0.46
3:ZF:243:MET:N	3:ZF:243:MET:SD	2.89	0.46
7:AM:144:THR:O	7:AM:145:ARG:NE	2.48	0.46
8:AN:115:GLN:NE2	11:IC:69:GLN:OE1	2.49	0.46
6:BL:139:ARG:HH12	7:BM:319:PHE:HB2	1.80	0.46
7:BM:141:GLU:OE2	7:BM:143:THR:OG1	2.29	0.46
7:BM:210:ASP:OD1	7:BM:210:ASP:N	2.48	0.46
1:Dg:796:GLN:O	1:Dg:799:SER:OG	2.31	0.46
11:EC:181:GLU:O	11:EC:185:LYS:NZ	2.49	0.46
11:KC:80:ILE:HD11	11:KC:196:LEU:HD13	1.98	0.46
7:CM:174:GLN:NE2	7:CM:193:GLN:O	2.49	0.46
2:DD:69:ASN:OD1	2:DD:69:ASN:N	2.43	0.46
4:EH:341:LYS:HD3	4:EH:361:LEU:HD21	1.97	0.46
2:Ed:105:ARG:HB2	2:Ed:153:VAL:HG23	1.96	0.46
1:IG:946:SER:OG	1:IG:1030:GLU:O	2.25	0.46
7:FM:210:ASP:HA	7:FM:229:ASN:H	1.79	0.46
2:GD:52:MET:HE3	2:GD:52:MET:HB3	1.71	0.45
4:IH:169:ILE:HG12	4:IH:239:LEU:HD12	1.97	0.45
6:IL:129:THR:O	6:IL:133:PHE:HB2	2.16	0.45
2:JD:87:TRP:CD1	2:JD:89:GLY:H	2.34	0.45
6:JL:94:VAL:HA	6:JL:97:ILE:HG12	1.97	0.45
6:JL:121:ASP:N	6:JL:121:ASP:OD1	2.49	0.45
1:CG:886:LEU:HD21	1:DG:1040:LEU:HB2	1.98	0.45
3:KF:219:ARG:HH12	4:YH:151:PRO:HD3	1.79	0.45
3:Kf:216:ILE:HD12	3:Kf:216:ILE:HA	1.86	0.45
1:Lg:801:MET:H	1:Lg:801:MET:HG3	1.55	0.45
7:LM:217:LYS:HA	7:LM:236:TRP:HB2	1.98	0.45
2:MD:36:ASP:HA	2:MD:39:ILE:HD12	1.98	0.45
2:MD:55:MET:HA	2:MD:58:VAL:HG12	1.99	0.45
6:ML:210:ASP:OD1	6:ML:210:ASP:N	2.41	0.45
3:VF:254:ILE:HG23	3:VF:262:ILE:HB	1.97	0.45
4:VH:192:ALA:N	4:VH:229:ARG:O	2.48	0.45
4:ZH:190:PRO:HB2	4:ZH:231:ARG:HG3	1.98	0.45
2:BD:87:TRP:CD1	2:BD:89:GLY:H	2.34	0.45
11:EC:215:LEU:HA	11:EC:218:MET:HG2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:ED:31:ASN:OD1	2:ED:31:ASN:N	2.49	0.45
1:GG:873:LEU:HB3	1:GG:1036:GLY:HA2	1.97	0.45
3:Ef:238:ILE:HB	3:Ef:241:TYR:HB2	1.98	0.45
11:IC:167:PRO:O	11:IC:173:LYS:NZ	2.50	0.45
7:GM:281:TYR:CZ	7:GM:300:ASP:HA	2.52	0.45
1:BG:936:ASP:HB3	1:BG:939:THR:HB	1.98	0.45
1:Ig:800:ASP:OD1	1:Ig:800:ASP:N	2.35	0.45
5:IK:76:ILE:HB	5:IK:182:ILE:HG13	1.98	0.45
4:KH:171:LEU:O	4:KH:244:GLY:N	2.42	0.45
6:LL:184:ALA:O	6:LL:188:THR:OG1	2.32	0.45
3:Lf:216:ILE:HD12	3:Lf:216:ILE:HA	1.80	0.45
2:MD:87:TRP:CD1	2:MD:89:GLY:H	2.34	0.45
1:EG:944:LEU:HD11	1:EG:1031:VAL:HA	1.97	0.45
10:XX:20:UNK:HA	10:XX:79:UNK:HA	1.97	0.45
4:BH:191:ILE:O	4:BH:231:ARG:NH1	2.49	0.45
11:JC:258:ASN:N	11:JC:258:ASN:OD1	2.50	0.45
2:DD:124:LYS:HD3	5:DK:145:TRP:CD1	2.52	0.45
5:DK:127:LYS:HE2	5:DK:127:LYS:HB3	1.83	0.45
7:DM:269:GLN:HB3	7:DM:288:ARG:HG2	1.98	0.45
1:KG:911:LYS:HB2	1:KG:942:THR:HB	1.98	0.45
1:OG:886:LEU:HA	1:OG:899:LEU:O	2.16	0.45
2:Fd:84:SER:H	11:BC:268:ALA:HB3	1.81	0.45
3:AF:243:MET:N	3:AF:243:MET:SD	2.88	0.45
1:AG:936:ASP:OD2	1:AG:939:THR:OG1	2.35	0.45
1:AG:1017:GLN:NE2	1:AG:1018:GLN:OE1	2.49	0.45
4:GH:151:PRO:HA	4:GH:248:VAL:HG13	1.98	0.45
4:GH:301:ASP:OD1	4:GH:301:ASP:N	2.39	0.45
3:Gf:219:ARG:HG3	3:Gf:233:ARG:HH11	1.81	0.45
8:HN:89:GLY:O	8:HN:104:ASN:ND2	2.49	0.45
6:JL:113:ASP:OD1	6:JL:113:ASP:N	2.41	0.45
7:LM:254:LYS:HE2	7:LM:272:LEU:HD23	1.99	0.45
1:DG:900:ILE:HD11	1:EG:865:THR:HG22	1.98	0.45
3:MF:250:LEU:O	3:MF:253:ARG:NH1	2.50	0.45
4:MH:170:ARG:N	4:MH:249:ASP:OD2	2.48	0.45
5:MK:76:ILE:HG13	5:MK:182:ILE:HB	1.99	0.45
10:MX:70:UNK:H2	4:ZH:146:GLY:H	1.65	0.45
4:ZH:149:PRO:HB2	4:ZH:248:VAL:HG12	1.98	0.45
7:AM:117:ARG:HE	7:AM:117:ARG:HB3	1.59	0.45
2:Ad:55:MET:HE3	2:Ad:55:MET:HB3	1.85	0.45
3:Af:220:ALA:O	3:Af:231:THR:HA	2.16	0.45
2:BD:41:LEU:HD22	11:JC:199:ILE:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BF:264:PHE:HE2	4:BH:246:LYS:HB2	1.81	0.45
6:BL:130:ASP:OD1	6:BL:130:ASP:N	2.49	0.45
8:CN:39:ASP:N	8:CN:39:ASP:OD1	2.48	0.45
11:IC:31:LEU:H	11:IC:31:LEU:HG	1.47	0.45
7:GM:207:ILE:HG13	7:GM:226:GLY:HA3	1.98	0.45
2:Dd:108:VAL:HG12	2:Dd:156:LEU:HB3	1.99	0.45
8:HN:52:ASP:OD2	8:HN:55:ALA:N	2.49	0.45
2:ID:111:LYS:NZ	2:Id:120:SER:H	2.14	0.45
7:IM:278:ASP:OD1	7:IM:297:SER:OG	2.34	0.45
2:Id:82:ARG:NH2	2:Id:125:ASP:OD2	2.49	0.45
2:KD:97:ARG:HH22	5:KK:112:ILE:HB	1.82	0.45
11:CC:243:ILE:HG12	11:DC:130:ARG:H	1.82	0.45
2:CD:47:SER:O	2:CD:51:SER:OG	2.30	0.45
6:ML:113:ASP:OD1	6:ML:113:ASP:N	2.47	0.45
3:VF:214:ALA:H	3:VF:221:TRP:HB2	1.82	0.45
3:VF:256:THR:OG1	3:VF:260:GLN:O	2.33	0.45
3:XF:250:LEU:HG	3:XF:251:GLN:HG3	1.97	0.45
1:EG:1030:GLU:OE2	1:FG:941:ARG:NE	2.48	0.45
2:AD:109:LEU:HD13	2:AD:155:GLU:HG3	1.99	0.45
3:BF:207:ARG:O	3:BF:225:SER:OG	2.34	0.45
3:BF:243:MET:HE3	3:BF:243:MET:HB3	1.85	0.45
2:DD:150:ASN:O	2:DD:152:GLN:NE2	2.50	0.45
4:DH:316:ASN:N	4:DH:316:ASN:OD1	2.47	0.45
1:GG:1030:GLU:OE2	1:HG:941:ARG:NE	2.49	0.45
4:EH:183:ASP:O	4:EH:255:ARG:NH1	2.50	0.45
8:EN:62:ASN:OD1	8:EN:62:ASN:N	2.45	0.45
1:PG:937:PRO:HD3	1:PG:1037:LEU:HA	1.96	0.45
1:Gg:794:ILE:O	1:Gg:798:THR:N	2.49	0.45
7:HM:302:ARG:HD2	7:HM:309:LEU:HD11	1.97	0.45
1:BG:1042:THR:OG1	1:BG:1043:GLN:OE1	2.30	0.45
4:JH:347:VAL:HG13	4:JH:354:MET:HB3	1.99	0.45
4:AH:306:LEU:HD11	4:AH:309:GLU:HA	1.99	0.45
11:CC:122:ASP:OD1	11:CC:125:SER:OG	2.32	0.45
3:KF:219:ARG:HD2	4:YH:148:PRO:HB2	1.99	0.45
2:Ld:150:ASN:O	2:Ld:152:GLN:NE2	2.49	0.45
3:BF:234:GLU:OE1	3:BF:247:ILE:N	2.49	0.45
7:BM:209:SER:OG	7:BM:210:ASP:N	2.46	0.45
11:FC:218:MET:HE3	11:FC:264:ALA:HA	1.97	0.45
11:HC:106:LEU:HD12	11:HC:107:PRO:HD2	1.98	0.45
11:MC:242:ILE:HD11	11:AC:129:ASP:HB3	1.97	0.45
4:CH:223:TYR:HB2	4:CH:242:ILE:HG13	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:EH:214:MET:HE3	4:EH:214:MET:HB3	1.74	0.45
5:EK:102:ILE:HD12	5:EK:102:ILE:HA	1.85	0.45
11:AC:106:LEU:HD12	11:AC:107:PRO:HD2	1.98	0.45
2:GD:86:ASP:OD2	5:GK:152:ARG:NH2	2.50	0.45
2:GD:125:ASP:OD2	5:GK:138:ARG:NE	2.47	0.45
7:GM:141:GLU:OE2	7:GM:143:THR:OG1	2.28	0.45
3:Gf:243:MET:O	3:Gf:257:SER:N	2.49	0.45
2:ID:80:GLN:HG3	7:IM:304:TRP:HB3	1.99	0.45
4:IH:311:MET:HE3	4:IH:339:MET:HE3	1.98	0.45
7:JM:154:LYS:HA	7:JM:154:LYS:HD3	1.77	0.45
4:AH:316:ASN:HB3	4:AH:334:THR:HG22	1.99	0.45
3:KF:223:ILE:HB	3:KF:229:THR:HG22	1.98	0.45
7:KM:278:ASP:OD1	7:KM:297:SER:OG	2.33	0.45
5:AK:72:GLN:HE21	6:BL:215:SER:HA	1.82	0.45
5:MK:71:GLY:O	2:AD:27:LYS:NZ	2.40	0.45
3:Mf:263:LYS:HB2	3:Mf:263:LYS:HE2	1.68	0.45
3:XF:245:LYS:N	3:XF:255:LEU:O	2.48	0.45
6:AL:220:ILE:HG13	2:AD:39:ILE:HG23	1.98	0.45
8:AN:81:LEU:HD11	4:BH:355:GLN:HG3	1.98	0.45
11:JC:95:ASP:O	11:JC:98:SER:OG	2.31	0.45
4:CH:284:LEU:HD11	4:CH:330:SER:HB3	1.98	0.45
2:DD:150:ASN:OD1	2:DD:150:ASN:N	2.47	0.45
7:DM:276:ALA:H	7:DM:295:ASN:HB2	1.81	0.45
7:DM:306:GLN:HB2	7:DM:309:LEU:HB2	1.98	0.45
2:GD:34:SER:OG	2:Gd:36:ASP:OD1	2.30	0.45
7:GM:127:ASN:HB3	7:GM:147:ALA:HB3	1.98	0.45
8:GN:113:SER:OG	8:GN:114:LEU:N	2.50	0.45
2:Dd:105:ARG:HH22	2:Dd:151:SER:HB2	1.82	0.45
1:Ig:795:GLN:OE1	1:Ig:796:GLN:N	2.50	0.45
6:IL:139:ARG:HD2	7:IM:319:PHE:HD1	1.82	0.45
8:IN:84:CYS:HA	11:DC:154:ASP:HB2	1.97	0.45
2:Id:72:THR:OG1	2:Id:73:ILE:N	2.49	0.45
6:JL:127:ILE:HB	6:JL:229:ILE:HB	1.98	0.45
8:JN:62:ASN:OD1	8:JN:62:ASN:N	2.36	0.45
1:Kg:807:GLN:NE2	1:Kg:811:ASP:OD2	2.49	0.45
1:Ag:800:ASP:OD1	1:Ag:800:ASP:N	2.47	0.45
4:LH:131:LYS:HD3	4:YH:145:PRO:HD3	1.98	0.45
6:LL:109:LEU:HG	6:LL:114:ILE:HB	1.99	0.45
2:Ld:52:MET:HA	2:Ld:55:MET:HE2	1.98	0.45
5:AK:116:VAL:HB	5:AK:182:ILE:HG23	1.99	0.45
3:WF:216:ILE:HD11	3:WF:219:ARG:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:XH:127:VAL:HA	4:XH:130:LEU:HD23	1.98	0.45
7:AM:199:LYS:HA	7:AM:219:ALA:HB3	1.97	0.45
4:BH:150:LYS:HA	3:AF:219:ARG:HH21	1.81	0.45
11:FC:111:LEU:O	11:FC:132:TYR:HA	2.17	0.45
11:HC:147:TRP:O	11:HC:151:LEU:HB2	2.17	0.45
11:KC:140:HIS:ND1	11:KC:141:PHE:O	2.50	0.45
11:LC:88:ARG:HH21	2:DD:122:SER:HB2	1.81	0.45
4:CH:207:ASP:OD1	4:CH:207:ASP:N	2.35	0.45
1:JG:951:HIS:ND1	1:JG:1026:PRO:O	2.37	0.45
1:JG:962:SER:HB3	1:JG:1015:TRP:HB3	1.99	0.45
1:LG:886:LEU:HB3	1:LG:900:ILE:HG12	1.98	0.45
1:OG:966:GLN:O	1:OG:970:ASN:ND2	2.50	0.45
6:GL:192:PHE:O	6:GL:196:ASN:ND2	2.35	0.45
6:GL:216:ASP:N	5:FK:72:GLN:HE22	2.14	0.45
8:GN:96:ASN:OD1	8:GN:97:SER:N	2.49	0.45
2:Dd:147:VAL:HG22	2:Dd:154:VAL:HG12	1.99	0.45
4:HH:115:MET:HE3	4:HH:115:MET:HB3	1.80	0.45
6:HL:165:VAL:HG23	6:HL:205:ALA:HA	1.99	0.45
7:HM:119:GLU:HG3	7:HM:139:ALA:HB3	1.98	0.45
8:HN:62:ASN:OD1	8:HN:62:ASN:N	2.45	0.45
5:JK:142:GLU:OE2	6:JL:139:ARG:NH1	2.50	0.45
6:JL:187:GLU:HA	6:JL:190:MET:HG3	1.98	0.45
7:JM:127:ASN:OD1	7:JM:127:ASN:N	2.49	0.45
7:JM:174:GLN:NE2	7:JM:193:GLN:O	2.37	0.45
7:JM:189:VAL:HB	7:JM:207:ILE:HG22	1.97	0.45
4:KH:324:TRP:HA	4:KH:339:MET:HB3	1.99	0.45
4:LH:236:PRO:O	4:MH:251:ARG:NH1	2.50	0.45
3:Lf:210:TYR:HB3	3:Lf:222:LEU:HD11	1.99	0.45
7:MM:306:GLN:HB3	7:MM:309:LEU:HB2	1.99	0.45
3:VF:208:ILE:HG13	3:VF:225:SER:H	1.82	0.45
3:CF:210:TYR:HD1	3:CF:224:GLY:HA2	1.82	0.45
3:CF:226:ASN:HD21	3:CF:228:SER:HB3	1.82	0.45
4:YH:115:MET:HE2	4:YH:115:MET:HB2	1.82	0.45
8:AN:84:CYS:HB2	11:IC:154:ASP:HB3	1.99	0.45
8:BN:57:ARG:HH21	8:BN:67:THR:HA	1.82	0.45
1:FG:910:ASP:OD1	1:FG:910:ASP:N	2.48	0.45
1:FG:968:PHE:CG	1:FG:1008:LEU:HD13	2.52	0.45
11:LC:261:GLU:OE1	11:LC:261:GLU:N	2.50	0.45
7:CM:228:VAL:HG11	7:CM:231:LEU:HB2	1.99	0.45
7:CM:242:LYS:HA	7:CM:262:GLU:HG3	1.98	0.45
8:CN:86:LEU:O	8:CN:88:HIS:ND1	2.38	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:DM:271:SER:OG	7:DM:290:ASP:OD1	2.35	0.45
7:EM:159:GLY:HA2	7:EM:181:PRO:HG3	1.97	0.45
1:OG:901:GLY:HA3	1:OG:916:PHE:HA	1.99	0.45
1:PG:874:ASP:OD1	1:PG:874:ASP:N	2.50	0.45
2:Fd:36:ASP:N	2:Fd:36:ASP:OD1	2.49	0.45
2:Fd:82:ARG:NH2	2:Fd:83:ALA:O	2.48	0.45
2:GD:52:MET:HA	2:GD:55:MET:HB3	1.99	0.45
4:HH:297:VAL:HG13	4:HH:358:VAL:HG22	1.97	0.45
5:JK:81:SER:OG	5:JK:173:ASP:O	2.35	0.45
8:LN:81:LEU:HD13	8:LN:81:LEU:HA	1.84	0.45
5:MK:151:SER:OG	5:MK:152:ARG:N	2.49	0.45
3:WF:209:ILE:O	3:WF:225:SER:N	2.49	0.45
11:FC:139:HIS:ND1	11:FC:140:PHE:O	2.45	0.45
11:MC:103:HIS:CD2	11:MC:226:VAL:HG11	2.52	0.45
4:CH:183:ASP:OD1	4:CH:185:THR:OG1	2.29	0.45
6:CL:163:ILE:HG23	6:CL:233:TRP:HB3	1.98	0.45
5:DK:92:ASN:N	5:DK:92:ASN:OD1	2.49	0.45
7:EM:245:TYR:OH	3:Ef:249:SER:OG	2.30	0.45
4:FH:171:LEU:HD12	4:FH:243:PRO:HB3	1.99	0.45
1:OG:1017:GLN:HE21	1:OG:1017:GLN:HB2	1.61	0.45
11:IC:146:THR:OG1	11:IC:147:TRP:N	2.49	0.45
4:GH:169:ILE:HD12	4:GH:252:VAL:HG21	1.99	0.45
7:GM:271:SER:OG	7:GM:290:ASP:OD1	2.35	0.45
2:Gd:139:ALA:HB1	2:Gd:143:ALA:HB3	1.98	0.45
3:HF:233:ARG:NH1	3:XF:269:SER:O	2.50	0.45
4:IH:149:PRO:O	3:XF:219:ARG:NH2	2.50	0.45
2:Id:81:ALA:HB3	2:Id:128:LEU:HD11	1.99	0.45
3:JF:253:ARG:HH12	3:JF:255:LEU:HD11	1.82	0.45
2:Jd:110:GLY:HA3	2:Jd:158:TYR:HB2	1.99	0.45
6:KL:91:VAL:HA	6:KL:94:VAL:HG22	1.99	0.45
1:Ag:814:GLN:NE2	1:Ag:814:GLN:O	2.48	0.45
1:DG:1010:THR:HB	1:EG:963:SER:HB3	1.98	0.45
4:WH:330:SER:OG	4:WH:332:ASP:OD1	2.30	0.45
2:AD:59:GLU:O	2:AD:63:THR:OG1	2.31	0.45
11:EC:184:TRP:HB3	11:EC:185:LYS:HZ2	1.82	0.45
11:JC:228:HIS:HA	11:JC:246:VAL:O	2.17	0.45
11:KC:154:MET:HE2	11:KC:154:MET:HB2	1.72	0.45
11:LC:96:PHE:HA	11:LC:99:LEU:HB2	1.99	0.45
4:CH:114:ASP:HA	4:CH:117:ARG:HG2	1.99	0.45
3:DF:219:ARG:HH12	3:DF:233:ARG:HH11	1.64	0.45
1:GG:936:ASP:HB3	1:GG:939:THR:HB	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:EF:248:ASP:HB3	3:EF:253:ARG:HB2	1.99	0.45
5:EK:129:GLU:OE1	5:EK:129:GLU:N	2.50	0.45
6:EL:191:THR:HG21	7:EM:289:ALA:HB3	1.99	0.45
1:JG:898:LYS:HE3	1:JG:898:LYS:HB3	1.85	0.45
2:Fd:110:GLY:HA3	2:Fd:158:TYR:HB2	1.99	0.45
1:AG:966:GLN:O	1:AG:970:ASN:ND2	2.50	0.44
3:GF:243:MET:N	3:GF:257:SER:OG	2.46	0.44
4:GH:298:SER:OG	8:FN:72:ARG:NH1	2.50	0.44
4:JH:183:ASP:HA	4:JH:256:VAL:HG12	1.98	0.44
4:JH:221:TYR:HE2	4:KH:138:GLU:HG3	1.82	0.44
7:JM:302:ARG:HD2	7:JM:309:LEU:HD11	1.99	0.44
11:CC:190:ASP:O	11:CC:194:THR:OG1	2.35	0.44
1:DG:885:ILE:O	1:DG:900:ILE:HA	2.17	0.44
4:MH:313:VAL:HG13	4:MH:337:TYR:HB2	1.99	0.44
3:Df:253:ARG:NH2	7:DM:307:SER:OG	2.49	0.44
7:MM:144:THR:O	7:MM:145:ARG:NE	2.50	0.44
2:Md:74:PRO:HG3	2:Md:147:VAL:HG11	1.98	0.44
3:WF:250:LEU:HG	3:WF:251:GLN:HG3	1.99	0.44
4:BH:235:THR:OG1	4:CH:251:ARG:NH2	2.50	0.44
7:BM:145:ARG:HH21	7:BM:163:THR:HA	1.81	0.44
7:BM:275:ASP:HA	7:BM:295:ASN:H	1.82	0.44
11:HC:37:MET:HE2	11:HC:37:MET:HB2	1.75	0.44
11:HC:175:ILE:HA	11:HC:178:ILE:HG12	1.99	0.44
11:HC:194:ILE:O	11:HC:198:ASN:ND2	2.39	0.44
7:CM:286:LYS:O	7:CM:316:ASN:ND2	2.50	0.44
8:CN:48:ILE:H	8:CN:48:ILE:HG12	1.48	0.44
9:CU:129:UNK:N	6:DL:232:GLN:OE1	2.50	0.44
4:DH:198:ASP:OD1	4:DH:200:SER:OG	2.34	0.44
1:Eg:810:GLN:H	1:Eg:810:GLN:HG3	1.63	0.44
4:EH:154:THR:HG23	4:EH:252:VAL:HG13	1.99	0.44
5:EK:99:LEU:HD12	5:EK:99:LEU:HA	1.80	0.44
2:Ed:110:GLY:HA3	2:Ed:158:TYR:HB2	1.99	0.44
1:HG:919:MET:HG3	1:HG:930:ILE:HG23	1.98	0.44
1:JG:886:LEU:HD23	1:KG:1040:LEU:HD12	1.99	0.44
1:LG:938:ASN:HA	11:IC:55:ARG:HH21	1.82	0.44
1:OG:898:LYS:NZ	1:PG:865:THR:O	2.47	0.44
4:GH:173:GLN:HB2	4:GH:220:LEU:HA	1.98	0.44
6:GL:54:ARG:HE	6:GL:57:VAL:HG22	1.83	0.44
7:GM:159:GLY:HA2	7:GM:181:PRO:HG3	1.99	0.44
2:Gd:139:ALA:O	2:Gd:142:LYS:NZ	2.44	0.44
6:HL:127:ILE:HB	6:HL:229:ILE:HB	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:HM:141:GLU:OE2	7:HM:143:THR:OG1	2.32	0.44
3:Hf:243:MET:O	3:Hf:257:SER:N	2.46	0.44
5:IK:74:TYR:HE2	5:IK:186:ARG:HB2	1.82	0.44
10:JX:21:UNK:O	10:JX:78:UNK:N	2.50	0.44
2:KD:92:GLU:OE2	2:KD:158:TYR:OH	2.36	0.44
11:CC:260:SER:HA	11:CC:263:TRP:CE2	2.53	0.44
5:KK:54:ILE:HD11	8:KN:44:LYS:HB3	1.99	0.44
7:LM:240:GLN:HB3	7:LM:242:LYS:HE3	1.98	0.44
3:MF:265:SER:HB3	3:MF:268:ASP:HB3	1.99	0.44
6:ML:220:ILE:H	6:ML:220:ILE:HG13	1.55	0.44
6:AL:94:VAL:HA	6:AL:97:ILE:HG12	2.00	0.44
4:YH:208:LYS:HD3	4:YH:208:LYS:HA	1.80	0.44
2:BD:42:ALA:HB2	2:Bd:41:LEU:HD22	2.00	0.44
2:BD:161:ILE:HD12	2:BD:161:ILE:HA	1.86	0.44
4:BH:169:ILE:HB	4:BH:241:LEU:HG	1.99	0.44
1:FG:898:LYS:HZ2	1:FG:920:SER:HB3	1.82	0.44
11:EC:153:MET:HE2	11:EC:153:MET:HB2	1.70	0.44
11:FC:101:LEU:HB2	11:FC:105:ILE:HG13	1.98	0.44
4:DH:191:ILE:HG12	4:DH:211:ASN:HA	1.99	0.44
6:DL:139:ARG:NE	7:DM:319:PHE:H	2.15	0.44
1:Fg:792:GLN:O	1:Fg:795:GLN:NE2	2.39	0.44
1:KG:885:ILE:HG13	1:KG:916:PHE:HE1	1.83	0.44
4:GH:230:LEU:HD12	4:GH:233:LEU:HD12	1.99	0.44
2:ID:85:VAL:HG23	5:IK:153:ILE:HG13	2.00	0.44
7:IM:122:GLY:O	7:IM:142:GLY:HA2	2.18	0.44
4:AH:131:LYS:NZ	4:ZH:143:ALA:O	2.47	0.44
4:AH:339:MET:HE3	4:AH:339:MET:HB2	1.77	0.44
7:LM:201:THR:HG22	7:LM:221:LYS:HB2	2.00	0.44
2:CD:41:LEU:HD22	11:KC:200:ILE:HD12	1.99	0.44
4:MH:183:ASP:OD1	4:MH:186:GLY:N	2.50	0.44
7:MM:278:ASP:OD1	7:MM:297:SER:OG	2.35	0.44
7:MM:278:ASP:OD2	7:MM:280:TYR:OH	2.27	0.44
2:Md:95:THR:HA	2:Md:98:ILE:HG22	1.99	0.44
4:WH:324:TRP:O	11:MC:248:ARG:NH2	2.38	0.44
3:CF:263:LYS:NZ	3:CF:264:PHE:O	2.48	0.44
3:ZF:209:ILE:O	3:ZF:225:SER:N	2.50	0.44
2:AD:111:LYS:NZ	2:Ad:120:SER:O	2.41	0.44
2:AD:121:ILE:HD13	2:AD:121:ILE:HA	1.88	0.44
4:ZH:123:ASN:OD1	4:ZH:126:GLN:NE2	2.45	0.44
7:AM:190:ASN:HB3	7:AM:192:ARG:HH21	1.82	0.44
4:BH:184:SER:OG	4:BH:256:VAL:O	2.29	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:DC:172:GLU:HA	11:DC:175:ILE:HG12	1.98	0.44
11:MC:115:ASN:N	11:MC:129:ASP:O	2.48	0.44
11:MC:116:THR:HB	11:MC:128:SER:HB3	2.00	0.44
4:CH:128:VAL:O	4:CH:132:GLN:NE2	2.50	0.44
2:Ed:121:ILE:HD13	2:Ed:121:ILE:HA	1.88	0.44
2:FD:93:GLU:OE2	2:FD:97:ARG:NE	2.49	0.44
2:FD:107:ARG:HE	2:FD:155:GLU:HG3	1.83	0.44
6:FL:165:VAL:HG23	6:FL:205:ALA:HA	1.99	0.44
1:JG:968:PHE:O	1:JG:972:PHE:HB2	2.18	0.44
11:AC:168:LYS:HE2	11:AC:168:LYS:HB2	1.70	0.44
2:Fd:29:PRO:HB2	2:Fd:32:ASN:HB2	1.99	0.44
11:IC:116:THR:HB	11:IC:128:SER:HB3	1.99	0.44
1:AG:922:PRO:HB3	1:BG:864:LYS:HE2	1.99	0.44
3:GF:254:ILE:HB	3:GF:262:ILE:HB	2.00	0.44
3:Gf:236:SER:O	3:Gf:243:MET:HA	2.17	0.44
2:HD:79:LEU:HA	2:HD:128:LEU:HD12	2.00	0.44
2:ID:82:ARG:HH21	2:ID:126:GLU:HA	1.82	0.44
4:IH:140:ALA:HB2	4:JH:124:PRO:HB3	1.99	0.44
4:IH:293:ARG:NH2	4:IH:361:LEU:O	2.50	0.44
4:JH:171:LEU:HB2	4:JH:243:PRO:HA	2.00	0.44
4:JH:273:PRO:HD3	11:DC:248:ARG:HH21	1.82	0.44
5:JK:92:ASN:O	5:JK:95:SER:OG	2.34	0.44
6:KL:193:LEU:HD13	6:KL:193:LEU:HA	1.86	0.44
2:LD:131:ILE:HD13	2:LD:131:ILE:HA	1.88	0.44
3:LF:219:ARG:NH1	4:MH:148:PRO:O	2.38	0.44
3:Lf:222:LEU:HB3	3:Lf:230:LEU:HB2	1.99	0.44
5:AK:71:GLY:O	2:BD:27:LYS:NZ	2.41	0.44
5:MK:81:SER:OG	5:MK:173:ASP:O	2.35	0.44
6:ML:203:LEU:HD12	6:ML:203:LEU:HA	1.85	0.44
4:BH:130:LEU:HA	4:BH:133:ILE:HG12	2.00	0.44
5:BK:120:SER:N	5:BK:160:GLY:O	2.43	0.44
4:CH:233:LEU:HD22	4:CH:235:THR:H	1.82	0.44
1:Eg:820:TYR:OH	4:EH:207:ASP:OD2	2.35	0.44
2:Ed:26:LYS:HZ3	2:Ed:26:LYS:HG2	1.63	0.44
1:HG:968:PHE:CG	1:HG:1008:LEU:HD13	2.53	0.44
1:LG:899:LEU:HD13	1:LG:919:MET:HG2	1.98	0.44
1:NG:886:LEU:HB3	1:NG:900:ILE:HG23	2.00	0.44
4:HH:230:LEU:HD12	4:HH:233:LEU:HD12	1.99	0.44
6:HL:169:THR:OG1	6:HL:170:ASP:N	2.45	0.44
7:HM:276:ALA:H	7:HM:295:ASN:HB2	1.83	0.44
1:BG:1010:THR:HB	1:CG:963:SER:HB3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CG:876:SER:OG	1:CG:1031:VAL:O	2.35	0.44
3:KF:211:TYR:N	3:KF:223:ILE:O	2.47	0.44
1:Ag:797:ARG:HE	4:CH:111:ALA:HB2	1.83	0.44
6:ML:49:ASN:ND2	7:MM:293:ALA:O	2.47	0.44
3:VF:241:TYR:HB3	3:VF:256:THR:HG21	2.00	0.44
4:YH:204:ILE:HG12	4:YH:215:ILE:HD12	1.99	0.44
3:Af:216:ILE:HD12	3:Af:216:ILE:HA	1.86	0.44
1:FG:944:LEU:HD11	1:FG:1031:VAL:HG12	1.99	0.44
3:Bf:226:ASN:OD1	3:Bf:226:ASN:N	2.50	0.44
11:EC:114:ARG:HG2	11:EC:130:ARG:HG2	2.00	0.44
11:FC:249:ILE:O	11:GC:124:GLN:NE2	2.50	0.44
11:LC:82:GLN:HA	11:LC:85:LYS:HZ3	1.83	0.44
7:CM:169:SER:OG	7:CM:188:PHE:N	2.48	0.44
4:DH:203:ASN:ND2	4:DH:205:GLN:OE1	2.44	0.44
1:Eg:795:GLN:H	1:Eg:795:GLN:HG3	1.52	0.44
7:EM:238:PHE:N	7:EM:258:LYS:O	2.44	0.44
3:FF:216:ILE:HD11	3:FF:219:ARG:HB2	2.00	0.44
1:JG:885:ILE:HG13	1:JG:916:PHE:HE1	1.82	0.44
1:MG:920:SER:HB2	1:NG:865:THR:HB	2.00	0.44
11:AC:97:ASN:HB3	11:AC:144:PRO:HG3	2.00	0.44
11:AC:215:LEU:HD12	11:AC:218:MET:HB3	1.99	0.44
7:HM:149:ASN:OD1	7:HM:149:ASN:N	2.50	0.44
1:Bg:807:GLN:OE1	1:Bg:810:GLN:NE2	2.49	0.44
7:IM:285:SER:OG	7:IM:287:THR:O	2.35	0.44
8:IN:58:LEU:HB2	8:IN:66:SER:HB3	1.99	0.44
2:Id:76:ALA:HB3	2:Id:79:LEU:HD23	1.99	0.44
11:CC:229:HIS:HB3	11:CC:248:LEU:HB3	2.00	0.44
2:LD:114:SER:HB2	11:HC:117:LEU:HB2	2.00	0.44
2:LD:162:TYR:HB3	11:GC:248:LEU:HD21	1.99	0.44
3:LF:258:SER:OG	3:LF:260:GLN:OE1	2.34	0.44
7:LM:129:LEU:HD13	7:LM:129:LEU:HA	1.90	0.44
7:LM:154:LYS:HD3	7:LM:154:LYS:HA	1.87	0.44
2:CD:131:ILE:HD13	2:CD:131:ILE:HA	1.88	0.44
4:MH:200:SER:N	1:ZG:816:GLU:OE2	2.51	0.44
4:MH:238:MET:HB2	4:ZH:250:TYR:CE2	2.53	0.44
6:ML:170:ASP:N	6:ML:170:ASP:OD1	2.41	0.44
3:WF:258:SER:OG	3:WF:260:GLN:OE1	2.32	0.44
6:AL:44:HIS:N	6:AL:48:ASN:OD1	2.50	0.44
4:BH:166:PRO:HA	4:BH:167:PRO:HD3	1.92	0.44
8:BN:39:ASP:OD1	8:BN:39:ASP:N	2.51	0.44
2:Bd:72:THR:OG1	2:Bd:73:ILE:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:EC:115:ASN:N	11:EC:129:ASP:O	2.44	0.44
11:EC:129:ASP:HB3	11:DC:242:ILE:HD11	1.99	0.44
4:CH:288:PRO:HB3	4:CH:305:TRP:CE2	2.52	0.44
2:DD:107:ARG:HD2	2:DD:155:GLU:HG3	1.98	0.44
5:FK:92:ASN:O	5:FK:95:SER:OG	2.34	0.44
6:FL:91:VAL:HA	6:FL:94:VAL:HG12	1.99	0.44
11:AC:91:ASP:OD1	11:AC:91:ASP:N	2.48	0.44
4:GH:206:TRP:HZ3	4:GH:208:LYS:HZ2	1.64	0.44
4:HH:330:SER:OG	4:HH:334:THR:N	2.43	0.44
3:Jf:218:GLY:H	3:Jf:247:ILE:HD11	1.83	0.44
4:AH:238:MET:SD	4:BH:178:SER:OG	2.74	0.44
4:AH:330:SER:OG	4:AH:334:THR:OG1	2.29	0.44
8:KN:89:GLY:HA3	8:KN:104:ASN:HB2	1.98	0.44
2:CD:87:TRP:CD1	2:CD:94:LEU:HD22	2.53	0.44
2:MD:87:TRP:CD2	2:MD:94:LEU:HD13	2.53	0.44
8:MN:109:SER:O	8:MN:113:SER:OG	2.34	0.44
2:Md:69:ASN:OD1	2:Md:69:ASN:N	2.40	0.44
1:EG:951:HIS:H	1:EG:1027:THR:HG22	1.82	0.44
11:EC:75:ARG:HH11	11:EC:188:ILE:HG23	1.83	0.44
2:ED:118:LEU:O	11:MC:97:ASN:ND2	2.51	0.44
11:JC:109:VAL:HG11	11:JC:136:LYS:HE3	2.00	0.44
2:Cd:72:THR:OG1	2:Cd:73:ILE:N	2.50	0.44
1:HG:910:ASP:OD1	1:HG:910:ASP:N	2.49	0.44
1:NG:1017:GLN:NE2	1:NG:1018:GLN:OE1	2.46	0.44
11:AC:114:ARG:HG2	11:AC:130:ARG:HG2	1.99	0.44
11:IC:59:LEU:O	11:IC:62:THR:OG1	2.35	0.44
2:GD:98:ILE:HD12	2:GD:98:ILE:HA	1.80	0.44
2:GD:135:ILE:HA	2:GD:135:ILE:HD13	1.85	0.44
2:Gd:78:ASN:N	2:Gd:78:ASN:OD1	2.51	0.44
3:Hf:255:LEU:HD13	3:Hf:261:VAL:HG22	1.99	0.44
1:Bg:800:ASP:O	1:Bg:803:THR:OG1	2.33	0.44
4:IH:192:ALA:H	4:IH:230:LEU:HA	1.82	0.44
4:IH:242:ILE:HG13	4:IH:245:GLN:HE22	1.83	0.44
5:IK:66:LYS:NZ	5:IK:67:VAL:O	2.51	0.44
8:IN:103:CYS:N	8:IN:107:TYR:O	2.46	0.44
4:JH:345:LEU:HB2	4:JH:356:LEU:HB2	1.99	0.44
7:LM:199:LYS:HA	7:LM:219:ALA:HB3	2.00	0.44
2:CD:148:TYR:O	2:CD:152:GLN:N	2.50	0.44
1:Cg:808:LEU:O	1:Cg:812:TRP:NE1	2.50	0.44
5:MK:49:CYS:O	5:MK:52:THR:OG1	2.29	0.44
4:WH:171:LEU:O	4:WH:244:GLY:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:XH:246:LYS:HE2	4:XH:246:LYS:HB3	1.88	0.44
1:YG:795:GLN:HE21	1:YG:795:GLN:HB2	1.61	0.44
4:ZH:106:VAL:HA	4:ZH:109:LYS:HE2	2.00	0.44
2:BD:149:PRO:O	2:BD:152:GLN:NE2	2.50	0.44
11:EC:240:ILE:O	11:EC:241:HIS:ND1	2.51	0.44
11:FC:148:ARG:NH2	11:FC:149:GLN:HB3	2.32	0.44
11:FC:240:ILE:HG12	11:GC:256:LEU:HD13	2.00	0.44
2:ED:36:ASP:HA	2:ED:39:ILE:HD12	1.99	0.44
11:KC:185:TRP:HZ3	11:LC:30:SER:HB3	1.83	0.44
6:DL:129:THR:O	6:DL:133:PHE:HB2	2.18	0.44
4:EH:332:ASP:OD2	4:EH:334:THR:OG1	2.36	0.44
7:EM:134:LEU:HD12	7:EM:152:LEU:HB3	2.00	0.44
7:EM:149:ASN:OD1	7:EM:149:ASN:N	2.45	0.44
2:Ed:107:ARG:HD2	2:Ed:155:GLU:HG3	2.00	0.44
2:FD:107:ARG:HH21	2:FD:155:GLU:HG3	1.82	0.44
11:AC:64:LEU:HD22	11:AC:179:TYR:HB3	1.99	0.44
2:GD:75:ASN:N	2:GD:75:ASN:OD1	2.50	0.44
2:HD:87:TRP:CE2	2:HD:94:LEU:HB2	2.53	0.44
3:Hf:247:ILE:HG22	3:Hf:254:ILE:HD12	1.99	0.44
1:BG:946:SER:OG	1:BG:1030:GLU:O	2.32	0.44
4:IH:283:VAL:HG21	4:IH:312:TYR:HD2	1.83	0.44
6:IL:130:ASP:OD1	6:IL:130:ASP:N	2.50	0.44
7:IM:138:LEU:HD11	7:IM:142:GLY:HA3	1.99	0.44
7:IM:193:GLN:HG3	7:IM:213:THR:HB	1.99	0.44
8:IN:86:LEU:HD12	8:IN:86:LEU:HA	1.87	0.44
6:JL:55:ARG:H	6:JL:55:ARG:CZ	2.31	0.44
7:JM:172:ASN:OD1	7:JM:190:ASN:ND2	2.51	0.44
11:CC:218:ALA:O	11:CC:264:ARG:NE	2.51	0.44
2:LD:55:MET:HG2	11:GC:211:ILE:HD11	2.00	0.44
3:Df:216:ILE:HD12	3:Df:216:ILE:HA	1.90	0.44
1:VG:800:ASP:O	1:VG:803:THR:OG1	2.34	0.44
3:YF:245:LYS:HE3	3:YF:257:SER:HA	1.99	0.44
6:AL:113:ASP:OD1	6:AL:113:ASP:N	2.51	0.44
6:AL:208:TYR:HA	6:AL:211:LYS:HZ3	1.83	0.44
2:BD:150:ASN:OD1	2:BD:150:ASN:N	2.50	0.44
4:BH:189:TRP:HE1	4:BH:232:GLY:H	1.66	0.44
4:BH:330:SER:OG	4:BH:334:THR:N	2.48	0.44
11:EC:226:VAL:HA	11:EC:249:ILE:HA	2.00	0.44
4:CH:321:SER:OG	4:CH:346:LEU:N	2.51	0.44
6:CL:116:TYR:OH	6:CL:118:GLU:OE1	2.30	0.44
7:EM:136:LEU:HD23	7:EM:152:LEU:HD13	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:FH:106:VAL:HA	4:FH:109:LYS:HE2	2.00	0.44
6:FL:219:ILE:HG23	6:FL:222:GLY:H	1.83	0.44
1:HG:898:LYS:HD3	1:IG:864:LYS:HE3	1.99	0.44
7:FM:292:MET:HE1	7:FM:298:VAL:HG22	1.99	0.44
11:IC:244:ASP:OD1	11:IC:244:ASP:N	2.51	0.44
3:AF:255:LEU:HD23	3:AF:261:VAL:HG22	2.00	0.44
1:AG:869:MET:HB2	1:AG:1041:PHE:HE1	1.83	0.43
1:AG:898:LYS:HE2	1:BG:867:ASP:HB3	2.00	0.43
4:GH:123:ASN:OD1	4:GH:123:ASN:N	2.51	0.43
5:GK:115:THR:HG22	5:GK:155:PHE:HB2	2.00	0.43
2:Dd:91:ILE:HD11	2:Dd:119:ILE:HG23	1.99	0.43
2:Dd:111:LYS:HE2	2:Dd:111:LYS:HB3	1.86	0.43
2:Dd:142:LYS:H	2:Dd:142:LYS:NZ	2.15	0.43
2:KD:44:ALA:O	2:KD:47:SER:OG	2.28	0.43
5:LK:117:THR:HA	5:LK:157:GLN:O	2.18	0.43
8:LN:45:MET:HG3	8:LN:60:CYS:HB3	2.00	0.43
2:CD:60:LYS:HD3	2:Cd:58:VAL:HG21	2.00	0.43
4:WH:107:ILE:HG23	1:Eg:794:ILE:HD13	1.99	0.43
4:WH:113:LYS:HD3	4:WH:113:LYS:HA	1.83	0.43
11:DC:102:GLU:HG2	11:DC:103:HIS:HD2	1.83	0.43
11:GC:176:ILE:HA	11:GC:179:ILE:HG12	2.00	0.43
2:ED:62:ILE:HG23	2:ED:63:THR:HG22	2.00	0.43
11:JC:123:GLN:HG2	11:IC:249:ILE:HD12	2.00	0.43
4:CH:132:GLN:HE21	4:CH:132:GLN:HB2	1.50	0.43
2:DD:31:ASN:OD1	2:DD:31:ASN:N	2.49	0.43
5:DK:70:VAL:HG13	6:EL:214:ILE:HD11	2.00	0.43
6:DL:193:LEU:HD13	6:DL:193:LEU:HA	1.85	0.43
11:AC:98:SER:HB2	2:Fd:52:MET:HE2	2.00	0.43
7:FM:117:ARG:HE	7:FM:117:ARG:HB3	1.60	0.43
3:Ff:216:ILE:HD12	3:Ff:216:ILE:HA	1.84	0.43
1:AG:899:LEU:HD11	1:AG:916:PHE:HB3	1.99	0.43
5:GK:49:CYS:O	5:GK:52:THR:OG1	2.28	0.43
2:Dd:79:LEU:O	2:Dd:127:SER:OG	2.28	0.43
4:HH:171:LEU:O	4:HH:244:GLY:N	2.47	0.43
5:IK:110:ARG:HG2	5:IK:187:ALA:HB3	2.00	0.43
2:JD:155:GLU:OE2	2:JD:157:ARG:NE	2.43	0.43
3:JF:241:TYR:HB3	3:JF:256:THR:HG21	1.99	0.43
3:Jf:219:ARG:HA	3:Jf:232:VAL:O	2.18	0.43
2:KD:150:ASN:OD1	2:KD:150:ASN:N	2.52	0.43
11:CC:246:ARG:HE	11:CC:246:ARG:HB3	1.55	0.43
4:KH:329:THR:OG1	11:FC:114:ARG:O	2.29	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:LH:295:LEU:HD11	4:LH:306:LEU:HB2	2.00	0.43
7:LM:191:LEU:HB3	7:LM:212:LEU:HD21	2.00	0.43
3:Df:241:TYR:HD2	3:Df:256:THR:HG21	1.83	0.43
7:MM:156:GLU:OE1	7:MM:178:LYS:NZ	2.47	0.43
4:VH:321:SER:HB3	4:VH:346:LEU:HD12	2.00	0.43
6:AL:129:THR:OG1	6:AL:130:ASP:OD1	2.35	0.43
8:AN:87:TRP:O	8:AN:88:HIS:ND1	2.51	0.43
2:BD:38:THR:HA	2:BD:41:LEU:HB2	2.00	0.43
11:JC:101:LEU:HB2	11:JC:105:ILE:HG23	2.00	0.43
11:LC:118:ASN:ND2	11:LC:119:LEU:O	2.51	0.43
5:CK:53:ILE:HA	5:CK:56:MET:HE2	2.00	0.43
8:CN:105:ASP:OD1	8:CN:105:ASP:N	2.49	0.43
2:Cd:100:LYS:HE3	2:Cd:100:LYS:HB2	1.89	0.43
4:DH:191:ILE:HG23	4:DH:228:VAL:HG13	1.99	0.43
6:DL:53:ASP:O	6:DL:54:ARG:NE	2.49	0.43
6:DL:109:LEU:HD13	6:DL:109:LEU:HA	1.89	0.43
4:EH:106:VAL:HA	4:EH:109:LYS:HE2	1.99	0.43
6:EL:183:GLN:HE21	7:EM:268:HIS:CE1	2.36	0.43
7:FM:263:ILE:O	7:FM:281:TYR:HA	2.18	0.43
11:IC:111:LEU:HD23	11:IC:111:LEU:HA	1.86	0.43
5:GK:166:THR:HG22	5:GK:168:TYR:H	1.83	0.43
3:HF:212:ILE:HB	3:HF:264:PHE:HD2	1.84	0.43
4:HH:107:ILE:H	4:HH:107:ILE:HG13	1.58	0.43
2:Hd:136:ASP:OD2	2:Hd:145:ILE:N	2.50	0.43
7:IM:125:THR:HG23	7:IM:145:ARG:HB2	1.99	0.43
2:Id:89:GLY:HA2	2:Id:118:LEU:HG	2.00	0.43
3:JF:220:ALA:O	3:JF:231:THR:HA	2.18	0.43
5:JK:40:LYS:HE3	5:JK:40:LYS:HB3	1.93	0.43
2:KD:30:ILE:O	6:KL:131:LYS:NZ	2.44	0.43
4:LH:304:ALA:HA	4:LH:312:TYR:O	2.18	0.43
2:Ld:92:GLU:OE2	2:Ld:158:TYR:OH	2.34	0.43
3:Mf:246:LEU:HB3	3:Mf:255:LEU:HD21	1.99	0.43
1:VG:791:GLN:HB3	1:VG:794:ILE:HG13	2.00	0.43
4:VH:283:VAL:HG22	4:VH:289:PRO:HD3	1.99	0.43
3:WF:219:ARG:HD2	3:WF:233:ARG:HB3	1.99	0.43
1:XG:801:MET:HE3	1:XG:801:MET:HB2	1.85	0.43
3:YF:236:SER:O	3:YF:244:VAL:N	2.50	0.43
2:AD:60:LYS:O	2:AD:60:LYS:NZ	2.46	0.43
2:BD:97:ARG:HH12	5:BK:112:ILE:HG12	1.83	0.43
11:MC:127:ILE:HG12	11:LC:245:ARG:HB2	2.00	0.43
11:JC:97:ASN:OD1	11:JC:97:ASN:N	2.41	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CM:307:SER:HG	3:Cf:253:ARG:HH22	1.62	0.43
3:Cf:216:ILE:HD12	3:Cf:216:ILE:HA	1.77	0.43
1:GG:899:LEU:HA	1:GG:918:THR:O	2.19	0.43
6:DL:139:ARG:HA	6:DL:139:ARG:HD2	1.74	0.43
2:Ed:107:ARG:O	2:Ed:155:GLU:HA	2.18	0.43
1:HG:951:HIS:HB2	1:HG:1027:THR:HG22	2.01	0.43
1:AG:876:SER:HB3	1:BG:941:ARG:HG2	2.01	0.43
5:GK:50:ASP:OD1	5:GK:50:ASP:N	2.50	0.43
8:GN:63:GLY:HA3	2:HD:27:LYS:HB2	2.00	0.43
4:HH:166:PRO:HG3	4:XH:151:PRO:HB2	2.00	0.43
1:CG:880:ASP:OD1	1:CG:880:ASP:N	2.47	0.43
11:CC:114:GLY:O	11:CC:131:ARG:HA	2.19	0.43
2:Kd:81:ALA:HB3	2:Kd:128:LEU:HD13	2.01	0.43
4:LH:329:THR:HA	4:LH:334:THR:O	2.19	0.43
5:AK:39:PRO:HG2	5:AK:40:LYS:HD3	2.01	0.43
3:MF:230:LEU:HA	4:MH:165:THR:HG21	2.01	0.43
1:Mg:800:ASP:OD1	1:Mg:800:ASP:N	2.41	0.43
7:MM:209:SER:OG	7:MM:210:ASP:N	2.51	0.43
3:VF:244:VAL:HG13	3:VF:254:ILE:HD11	2.00	0.43
3:ZF:207:ARG:NH1	3:ZF:208:ILE:O	2.51	0.43
4:ZH:195:ASP:OD1	4:ZH:195:ASP:N	2.51	0.43
7:BM:276:ALA:H	7:BM:295:ASN:HB2	1.84	0.43
7:BM:300:ASP:OD1	7:BM:302:ARG:NE	2.46	0.43
11:GC:165:THR:OG1	11:GC:166:LEU:N	2.51	0.43
11:JC:147:TRP:HB2	11:JC:151:LEU:HD23	2.00	0.43
11:LC:103:HIS:HA	2:DD:162:TYR:HE1	1.83	0.43
3:Cf:209:ILE:HD12	3:Cf:209:ILE:HA	1.88	0.43
4:DH:321:SER:OG	4:DH:346:LEU:N	2.50	0.43
4:EH:120:TYR:HD1	4:EH:122:LEU:HD21	1.83	0.43
6:FL:169:THR:OG1	6:FL:170:ASP:N	2.51	0.43
1:HG:952:TYR:HA	1:HG:955:ARG:HE	1.83	0.43
1:IG:968:PHE:CG	1:IG:1008:LEU:HD13	2.53	0.43
1:JG:899:LEU:HB2	1:JG:919:MET:HG2	2.00	0.43
6:GL:230:GLU:OE2	6:GL:232:GLN:NE2	2.48	0.43
5:HK:66:LYS:HB3	5:HK:77:SER:HB3	2.00	0.43
7:HM:199:LYS:HA	7:HM:219:ALA:HB3	1.99	0.43
3:Hf:216:ILE:HD12	3:Hf:216:ILE:HA	1.87	0.43
1:Ig:810:GLN:H	1:Ig:810:GLN:HG3	1.59	0.43
7:IM:120:GLY:H	7:IM:140:ASN:HB2	1.83	0.43
7:JM:274:THR:HA	7:JM:293:ALA:HB3	2.01	0.43
2:KD:108:VAL:HG12	2:KD:156:LEU:HB3	1.98	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:KH:117:ARG:NH1	4:KH:118:ASN:OD1	2.45	0.43
2:LD:36:ASP:HA	2:LD:39:ILE:HD12	2.01	0.43
2:LD:85:VAL:HA	5:LK:152:ARG:O	2.18	0.43
8:LN:78:LEU:O	8:LN:79:GLN:NE2	2.51	0.43
2:CD:27:LYS:HB2	8:BN:63:GLY:HA3	2.00	0.43
6:ML:139:ARG:HH21	7:MM:317:LYS:HG2	1.83	0.43
3:VF:207:ARG:HH12	3:VF:210:TYR:H	1.66	0.43
1:EG:1006:ILE:O	1:EG:1010:THR:OG1	2.33	0.43
7:AM:149:ASN:OD1	7:AM:149:ASN:N	2.51	0.43
7:BM:215:ARG:CZ	7:BM:234:GLU:HB3	2.49	0.43
11:FC:130:ARG:NH1	11:FC:132:TYR:OH	2.52	0.43
11:MC:106:LEU:HD12	11:MC:107:PRO:HD2	2.00	0.43
2:DD:124:LYS:HE2	2:DD:124:LYS:HB3	1.89	0.43
4:DH:187:ALA:HB2	4:DH:264:LYS:HB2	2.00	0.43
5:DK:45:VAL:HG12	5:DK:48:ALA:HB2	2.01	0.43
4:EH:203:ASN:HB3	4:EH:216:GLN:HB3	2.00	0.43
3:FF:213:GLN:O	4:FH:170:ARG:NH1	2.52	0.43
5:FK:120:SER:N	5:FK:160:GLY:O	2.45	0.43
11:IC:106:LEU:HD12	11:IC:107:PRO:HD2	2.00	0.43
11:IC:259:SER:HA	11:IC:262:TRP:CE2	2.54	0.43
7:GM:229:ASN:N	7:GM:229:ASN:OD1	2.52	0.43
4:HH:207:ASP:HB2	4:HH:210:SER:HB3	2.00	0.43
4:IH:339:MET:HE1	4:IH:345:LEU:HD11	2.00	0.43
2:JD:35:ASP:O	2:JD:38:THR:OG1	2.35	0.43
4:JH:170:ARG:N	4:JH:249:ASP:OD2	2.51	0.43
5:JK:57:MET:O	5:JK:61:ASN:ND2	2.48	0.43
4:AH:330:SER:OG	4:AH:332:ASP:OD1	2.30	0.43
11:CC:176:ILE:HA	11:CC:179:ILE:HG12	1.99	0.43
3:KF:216:ILE:HD11	3:KF:221:TRP:HE1	1.83	0.43
6:LL:165:VAL:HG12	6:LL:231:ILE:HG13	2.00	0.43
7:LM:203:SER:HA	7:LM:223:GLN:O	2.17	0.43
5:AK:183:THR:HG21	9:AU:123:UNK:HA	2.00	0.43
3:Mf:209:ILE:O	3:Mf:225:SER:OG	2.34	0.43
4:YH:337:TYR:HB3	4:YH:339:MET:HE1	1.99	0.43
4:BH:289:PRO:O	4:BH:292:SER:OG	2.27	0.43
4:BH:319:ILE:H	4:BH:319:ILE:HG12	1.68	0.43
7:BM:308:ASP:OD1	7:BM:308:ASP:N	2.51	0.43
11:DC:230:ASP:OD1	11:DC:230:ASP:N	2.52	0.43
2:ED:130:GLU:HA	2:ED:133:ARG:HD2	2.00	0.43
11:LC:144:PRO:HA	11:LC:145:PRO:HD3	1.93	0.43
6:CL:191:THR:HG21	7:CM:289:ALA:HB3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:DF:210:TYR:HB3	3:DF:222:LEU:HD12	2.01	0.43
7:DM:153:GLN:HA	7:DM:173:LEU:HA	2.00	0.43
2:Ed:111:LYS:HE2	2:Ed:111:LYS:HB3	1.78	0.43
1:NG:899:LEU:HD13	1:NG:919:MET:HG2	2.01	0.43
1:NG:931:SER:O	1:NG:1042:THR:OG1	2.36	0.43
1:PG:931:SER:O	1:PG:1042:THR:OG1	2.37	0.43
1:AG:1040:LEU:HB2	1:PG:886:LEU:HD21	2.00	0.43
2:GD:145:ILE:HD13	2:GD:145:ILE:HA	1.87	0.43
3:GF:243:MET:HE2	3:GF:243:MET:HB2	1.80	0.43
1:Hg:797:ARG:HD2	1:Hg:797:ARG:HA	1.75	0.43
5:HK:68:ALA:HB3	5:HK:75:LEU:HB2	2.01	0.43
7:HM:180:ASP:O	7:HM:182:LYS:NZ	2.43	0.43
6:JL:219:ILE:HD12	6:JL:219:ILE:HA	1.83	0.43
7:JM:172:ASN:OD1	7:JM:192:ARG:NH1	2.51	0.43
2:KD:59:GLU:OE2	2:KD:63:THR:OG1	2.33	0.43
2:KD:149:PRO:O	2:KD:152:GLN:NE2	2.52	0.43
1:CG:871:ALA:HB1	1:CG:887:ALA:HB1	2.01	0.43
2:Kd:98:ILE:HG23	2:Kd:128:LEU:HD23	2.01	0.43
2:LD:77:TYR:HE1	7:LM:304:TRP:HE3	1.65	0.43
6:LL:178:LYS:O	6:LL:182:SER:OG	2.30	0.43
2:Md:149:PRO:O	2:Md:152:GLN:NE2	2.47	0.43
2:AD:42:ALA:HB2	2:Ad:41:LEU:HD22	2.01	0.43
2:AD:47:SER:O	2:AD:51:SER:OG	2.35	0.43
11:FC:218:MET:HB3	11:FC:220:MET:HG2	2.00	0.43
2:ED:131:ILE:HD13	2:ED:131:ILE:HA	1.86	0.43
11:HC:116:THR:HB	11:HC:128:SER:HB3	1.99	0.43
7:EM:124:VAL:HG23	7:EM:144:THR:HG23	1.99	0.43
3:FF:246:LEU:HB3	3:FF:255:LEU:HD12	2.00	0.43
1:HG:1010:THR:HG21	1:IG:967:GLY:HA3	1.99	0.43
2:HD:52:MET:HE2	2:HD:52:MET:HB3	1.64	0.43
5:HK:49:CYS:O	5:HK:52:THR:OG1	2.27	0.43
1:BG:966:GLN:HE22	1:BG:1013:LYS:HE2	1.84	0.43
8:JN:39:ASP:OD1	8:JN:39:ASP:N	2.49	0.43
7:KM:127:ASN:OD1	7:KM:127:ASN:N	2.52	0.43
7:KM:216:ALA:HB3	7:KM:235:LEU:HD12	2.00	0.43
4:LH:138:GLU:HA	4:LH:141:LYS:HG2	1.99	0.43
2:CD:82:ARG:HE	5:CK:138:ARG:HH21	1.66	0.43
6:ML:52:PRO:HB2	6:ML:54:ARG:HH12	1.83	0.43
6:AL:121:ASP:OD1	6:AL:121:ASP:N	2.46	0.43
3:BF:220:ALA:HB3	3:BF:232:VAL:HG23	2.00	0.43
5:BK:76:ILE:HB	5:BK:182:ILE:HG12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:BN:84:CYS:SG	8:BN:85:CYS:N	2.92	0.43
11:FC:153:MET:HE2	11:FC:153:MET:HB2	1.72	0.43
11:HC:139:HIS:ND1	11:HC:140:PHE:O	2.44	0.43
11:LC:150:TYR:O	11:LC:198:ASN:ND2	2.49	0.43
1:GG:1003:ASN:HA	1:GG:1006:ILE:HD12	1.99	0.43
7:DM:278:ASP:OD1	7:DM:297:SER:OG	2.36	0.43
1:HG:962:SER:HB3	1:HG:1015:TRP:HB3	2.00	0.43
3:Ff:212:ILE:HG21	3:Ff:254:ILE:HD13	2.00	0.43
3:GF:209:ILE:O	3:GF:225:SER:N	2.52	0.43
5:IK:123:TYR:HD2	5:IK:124:VAL:HG23	1.83	0.43
4:VH:348:SER:HA	4:VH:352:LYS:O	2.19	0.43
4:XH:166:PRO:HA	4:XH:167:PRO:HD3	1.88	0.43
6:AL:209:GLY:H	6:AL:211:LYS:HZ3	1.66	0.43
4:YH:279:LEU:HD11	4:YH:289:PRO:HB3	2.01	0.43
11:MC:218:MET:HB3	11:MC:220:MET:HG2	2.01	0.43
11:KC:143:THR:HG22	11:KC:144:THR:HG23	1.99	0.43
11:LC:169:THR:OG1	11:LC:172:GLU:OE1	2.35	0.43
5:CK:59:ASP:O	5:CK:63:LYS:HB2	2.19	0.43
3:Cf:233:ARG:O	3:Cf:236:SER:OG	2.37	0.43
5:DK:99:LEU:HD12	5:DK:99:LEU:HA	1.88	0.43
8:DN:89:GLY:HA3	8:DN:104:ASN:HB2	1.99	0.43
5:EK:115:THR:HG23	5:EK:155:PHE:HB2	2.01	0.43
3:Ef:216:ILE:HD12	3:Ef:216:ILE:HA	1.83	0.43
4:FH:132:GLN:O	4:FH:136:THR:OG1	2.32	0.43
4:FH:253:ASP:HB3	4:FH:255:ARG:HH22	1.83	0.43
1:IG:869:MET:HB2	1:IG:1041:PHE:HE1	1.84	0.43
1:IG:1015:TRP:NE1	1:JG:956:TYR:OH	2.52	0.43
11:IC:261:GLU:OE1	11:IC:261:GLU:N	2.52	0.43
3:AF:253:ARG:HA	3:AF:263:LYS:HG2	2.01	0.43
1:AG:900:ILE:HG13	1:AG:918:THR:HB	2.00	0.43
2:GD:142:LYS:O	2:GD:159:ALA:CB	2.67	0.43
2:Gd:97:ARG:HH12	11:CC:267:VAL:HB	1.81	0.43
4:HH:307:SER:OG	4:HH:308:ASN:N	2.52	0.43
5:HK:117:THR:HA	5:HK:157:GLN:O	2.19	0.43
5:HK:162:ASP:OD1	5:HK:162:ASP:N	2.52	0.43
7:JM:131:THR:HG23	7:JM:151:GLY:H	1.84	0.43
5:KK:138:ARG:HB3	7:KM:319:PHE:HE2	1.82	0.43
3:Kf:238:ILE:HG13	3:Kf:241:TYR:HB2	2.01	0.43
2:LD:44:ALA:O	2:LD:47:SER:OG	2.34	0.43
3:LF:241:TYR:HB3	3:LF:256:THR:HG21	2.01	0.43
8:LN:89:GLY:O	8:LN:104:ASN:ND2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CD:42:ALA:HB2	2:Cd:41:LEU:HD22	2.00	0.43
1:DG:969:GLY:HA2	1:DG:1005:VAL:HA	2.00	0.43
4:MH:123:ASN:HB3	4:MH:126:GLN:HB2	2.00	0.43
4:MH:185:THR:OG1	4:MH:264:LYS:NZ	2.52	0.43
4:MH:283:VAL:HG11	4:MH:312:TYR:HB3	2.01	0.43
3:Df:243:MET:N	3:Df:257:SER:OG	2.43	0.43
4:VH:324:TRP:HA	4:VH:339:MET:HG3	2.00	0.43
2:AD:87:TRP:CD1	2:AD:89:GLY:H	2.37	0.43
2:Ad:111:LYS:HE2	2:Ad:111:LYS:HB2	1.75	0.43
3:BF:208:ILE:HG22	3:BF:224:GLY:HA3	2.00	0.43
5:BK:68:ALA:HB3	5:BK:75:LEU:HB3	2.01	0.43
1:FG:1003:ASN:HA	1:FG:1006:ILE:HD12	2.01	0.43
4:EH:264:LYS:HA	4:EH:264:LYS:HD2	1.83	0.43
5:EK:111:LYS:HD3	5:EK:114:ILE:HD11	1.99	0.43
7:EM:254:LYS:HB2	7:EM:254:LYS:HE3	1.85	0.43
7:EM:301:MET:HE2	7:EM:301:MET:HB2	1.83	0.43
8:EN:52:ASP:OD1	8:EN:55:ALA:N	2.49	0.43
1:HG:867:ASP:OD1	1:HG:867:ASP:N	2.50	0.43
1:KG:869:MET:HE3	1:KG:869:MET:HB2	1.89	0.43
1:LG:862:ILE:HD13	1:LG:1046:THR:HA	2.00	0.43
7:FM:275:ASP:N	7:FM:275:ASP:OD1	2.51	0.43
8:FN:111:GLU:OE1	8:FN:111:GLU:N	2.51	0.43
5:GK:125:SER:HG	5:GK:128:ARG:H	1.65	0.42
6:GL:173:GLY:O	6:GL:178:LYS:NZ	2.52	0.42
2:HD:150:ASN:OD1	2:HD:150:ASN:N	2.52	0.42
3:HF:208:ILE:HD11	3:HF:224:GLY:HA3	2.01	0.42
2:Dd:31:ASN:OD1	2:Dd:31:ASN:N	2.39	0.42
1:Bg:816:GLU:OE2	4:AH:200:SER:N	2.52	0.42
1:BG:876:SER:OG	1:BG:1031:VAL:O	2.36	0.42
2:JD:67:LYS:HE3	2:JD:67:LYS:HB3	1.76	0.42
4:JH:332:ASP:OD1	4:JH:332:ASP:N	2.53	0.42
7:KM:153:GLN:HE22	7:KM:174:GLN:HB2	1.84	0.42
8:KN:89:GLY:O	8:KN:104:ASN:ND2	2.51	0.42
1:Lg:819:VAL:HG12	4:YH:199:PRO:HG3	2.01	0.42
5:LK:111:LYS:HG3	5:LK:151:SER:HB2	2.01	0.42
7:MM:263:ILE:HD11	7:MM:265:ALA:HB2	2.01	0.42
4:VH:321:SER:O	11:JC:227:SER:OG	2.30	0.42
4:WH:148:PRO:HD2	3:FF:218:GLY:HA3	2.01	0.42
4:WH:278:ASP:OD1	4:WH:278:ASP:N	2.52	0.42
4:XH:170:ARG:HA	4:XH:242:ILE:O	2.19	0.42
7:AM:228:VAL:HB	7:AM:231:LEU:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Ad:98:ILE:HD13	2:Ad:98:ILE:HA	1.90	0.42
4:BH:311:MET:HG3	4:BH:339:MET:HG3	2.01	0.42
11:HC:261:GLU:N	11:HC:261:GLU:OE1	2.52	0.42
4:CH:330:SER:OG	4:CH:334:THR:OG1	2.31	0.42
5:CK:144:LEU:HD13	5:CK:144:LEU:HA	1.89	0.42
3:DF:241:TYR:HB3	3:DF:256:THR:HG21	2.00	0.42
4:DH:161:SER:O	4:DH:164:SER:OG	2.30	0.42
3:EF:213:GLN:OE1	3:EF:213:GLN:N	2.52	0.42
4:EH:154:THR:O	4:EH:252:VAL:HA	2.19	0.42
1:KG:884:PRO:HG3	1:LG:1042:THR:HG22	2.01	0.42
1:KG:968:PHE:CG	1:KG:1008:LEU:HD13	2.54	0.42
1:Gg:794:ILE:HD13	4:XH:107:ILE:HG23	2.01	0.42
4:GH:304:ALA:HB2	4:GH:313:VAL:HG23	2.01	0.42
5:GK:127:LYS:HB2	5:GK:127:LYS:HE3	1.83	0.42
5:GK:129:GLU:HA	5:GK:132:LEU:HB3	2.00	0.42
2:Gd:74:PRO:HG3	2:Gd:147:VAL:HG11	2.01	0.42
5:HK:78:ILE:HB	5:HK:180:VAL:HG13	2.00	0.42
2:JD:150:ASN:OD1	2:JD:150:ASN:N	2.52	0.42
6:JL:54:ARG:HD2	6:JL:54:ARG:HA	1.86	0.42
6:JL:170:ASP:OD2	2:Jd:40:LYS:NZ	2.46	0.42
2:KD:82:ARG:NE	2:KD:125:ASP:OD1	2.40	0.42
8:KN:39:ASP:N	8:KN:39:ASP:OD1	2.52	0.42
2:Kd:89:GLY:N	2:Kd:119:ILE:O	2.44	0.42
4:LH:231:ARG:H	4:LH:231:ARG:HG3	1.43	0.42
7:LM:275:ASP:N	7:LM:275:ASP:OD1	2.52	0.42
2:CD:121:ILE:HD13	2:CD:121:ILE:HA	1.89	0.42
1:DG:962:SER:HB3	1:DG:1015:TRP:HB3	2.02	0.42
5:AK:40:LYS:HE2	5:AK:40:LYS:HB2	1.74	0.42
7:MM:158:VAL:HA	7:MM:178:LYS:HG3	2.00	0.42
4:WH:146:GLY:O	10:FX:70:UNK:N	2.44	0.42
1:EG:910:ASP:OD1	1:EG:910:ASP:N	2.40	0.42
6:AL:219:ILE:HD12	6:AL:219:ILE:HA	1.89	0.42
4:BH:179:LEU:O	4:BH:212:THR:HA	2.20	0.42
11:KC:244:ASP:N	11:KC:244:ASP:OD1	2.51	0.42
7:CM:206:TRP:HZ3	3:Cf:214:ALA:HB3	1.84	0.42
7:CM:303:GLU:OE1	7:CM:305:GLY:N	2.43	0.42
1:MG:1024:ASN:OD1	1:MG:1024:ASN:N	2.36	0.42
1:NG:876:SER:OG	1:OG:941:ARG:NH2	2.51	0.42
1:OG:867:ASP:OD1	1:OG:867:ASP:N	2.53	0.42
7:FM:280:TYR:HE1	7:FM:299:LEU:HD13	1.83	0.42
2:GD:150:ASN:OD1	2:GD:150:ASN:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:HH:166:PRO:HA	4:HH:167:PRO:HD3	1.92	0.42
4:IH:250:TYR:HB3	4:XH:238:MET:HG3	2.01	0.42
7:IM:127:ASN:N	7:IM:127:ASN:OD1	2.52	0.42
7:JM:311:ASP:OD1	7:JM:312:PHE:N	2.46	0.42
3:Jf:238:ILE:O	3:Jf:242:GLY:N	2.52	0.42
3:Jf:243:MET:N	3:Jf:257:SER:OG	2.52	0.42
2:LD:26:LYS:O	6:LL:115:GLN:NE2	2.48	0.42
4:LH:117:ARG:HH22	4:LH:121:PRO:HB3	1.85	0.42
6:ML:199:ALA:HB3	6:ML:202:ARG:HD3	2.01	0.42
7:MM:275:ASP:HA	7:MM:295:ASN:H	1.84	0.42
4:WH:151:PRO:HA	4:WH:248:VAL:HG13	2.02	0.42
1:XG:798:THR:O	1:XG:802:LEU:HB2	2.19	0.42
4:YH:130:LEU:HA	4:YH:133:ILE:HG22	2.01	0.42
4:BH:207:ASP:OD1	4:BH:210:SER:OG	2.36	0.42
6:BL:94:VAL:HA	6:BL:97:ILE:HG12	2.01	0.42
1:FG:1006:ILE:O	1:FG:1010:THR:OG1	2.36	0.42
11:DC:259:SER:HA	11:DC:262:TRP:CE2	2.55	0.42
11:MC:222:SER:N	11:MC:254:GLU:O	2.45	0.42
6:CL:169:THR:OG1	6:CL:170:ASP:N	2.51	0.42
10:CX:23:UNK:HA	10:CX:33:UNK:HA	2.00	0.42
1:GG:1003:ASN:HA	1:GG:1006:ILE:HB	2.01	0.42
7:DM:274:THR:OG1	7:DM:275:ASP:N	2.53	0.42
5:FK:159:LEU:HA	5:FK:159:LEU:HD13	1.87	0.42
6:FL:124:THR:HG22	6:FL:232:GLN:HG2	2.01	0.42
1:LG:900:ILE:HB	1:LG:918:THR:HB	2.01	0.42
2:Fd:64:PRO:HG2	2:Fd:67:LYS:HG2	2.00	0.42
2:Fd:82:ARG:CZ	2:Fd:83:ALA:H	2.32	0.42
2:Fd:148:TYR:HB2	2:Fd:153:VAL:HG12	2.02	0.42
4:GH:166:PRO:HA	4:GH:167:PRO:HD3	1.90	0.42
3:HF:265:SER:HB3	3:HF:268:ASP:HB3	2.01	0.42
4:HH:275:SER:HA	11:CC:127:ARG:HD3	2.01	0.42
3:Hf:219:ARG:HH22	3:Hf:233:ARG:HB3	1.83	0.42
2:ID:122:SER:OG	11:DC:88:ARG:NH2	2.43	0.42
7:IM:154:LYS:HD3	7:IM:154:LYS:HA	1.90	0.42
6:JL:59:ARG:HA	6:JL:59:ARG:HD2	1.86	0.42
1:CG:1003:ASN:HA	1:CG:1006:ILE:HB	2.01	0.42
4:LH:130:LEU:HA	4:LH:133:ILE:HG22	2.02	0.42
6:ML:150:ASN:OD1	6:ML:153:ARG:NH2	2.37	0.42
10:MX:21:UNK:N	10:MX:78:UNK:O	2.52	0.42
4:VH:181:PHE:HE1	4:VH:254:LEU:HD12	1.85	0.42
2:Ad:35:ASP:O	2:Ad:38:THR:OG1	2.32	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:BK:66:LYS:HB3	5:BK:77:SER:HB3	1.99	0.42
7:BM:212:LEU:HD13	7:BM:212:LEU:HA	1.86	0.42
2:ED:36:ASP:OD1	2:ED:36:ASP:N	2.52	0.42
11:JC:202:ILE:HD12	11:JC:202:ILE:HA	1.90	0.42
6:CL:136:SER:O	6:CL:136:SER:OG	2.36	0.42
6:CL:193:LEU:HD13	6:CL:193:LEU:HA	1.86	0.42
6:DL:190:MET:HE2	6:DL:190:MET:HB2	1.81	0.42
2:FD:52:MET:HE2	2:FD:52:MET:HB3	1.88	0.42
5:FK:133:THR:HG21	5:FK:160:GLY:H	1.84	0.42
1:JG:1019:ALA:HA	1:JG:1022:LEU:HG	2.01	0.42
1:PG:904:ASN:OD1	1:PG:904:ASN:N	2.52	0.42
7:FM:275:ASP:HA	7:FM:295:ASN:H	1.83	0.42
1:AG:968:PHE:CG	1:AG:1008:LEU:HD13	2.55	0.42
3:GF:207:ARG:HB2	3:GF:208:ILE:H	1.63	0.42
4:GH:311:MET:HG3	4:GH:341:LYS:HA	2.01	0.42
2:Gd:92:GLU:H	2:Gd:92:GLU:HG2	1.69	0.42
2:Gd:127:SER:HB3	2:Gd:130:GLU:HG2	2.02	0.42
1:Hg:800:ASP:O	1:Hg:803:THR:OG1	2.32	0.42
5:HK:87:GLN:HB3	5:HK:128:ARG:HH12	1.84	0.42
6:HL:109:LEU:HD13	6:HL:109:LEU:HA	1.85	0.42
8:HN:78:LEU:HD12	8:HN:78:LEU:HA	1.91	0.42
1:BG:969:GLY:HA3	1:BG:1009:ALA:HB2	2.01	0.42
6:IL:102:LYS:HE3	6:IL:102:LYS:HB2	1.90	0.42
3:If:219:ARG:HH11	3:If:233:ARG:HH11	1.66	0.42
1:Jg:798:THR:HG23	4:YH:115:MET:HB3	2.01	0.42
4:JH:225:ASN:ND2	4:KH:176:VAL:O	2.51	0.42
4:JH:273:PRO:O	11:EC:126:ARG:NH1	2.42	0.42
1:CG:885:ILE:O	1:CG:900:ILE:HA	2.20	0.42
4:LH:277:ASN:HD21	4:LH:279:LEU:HD23	1.85	0.42
2:MD:73:ILE:HD13	2:MD:133:ARG:HG3	2.01	0.42
5:MK:163:LYS:HD2	5:MK:163:LYS:HA	1.78	0.42
6:ML:138:PRO:HB2	6:ML:188:THR:HG21	2.02	0.42
4:VH:108:ASP:OD1	4:VH:108:ASP:N	2.52	0.42
4:YH:222:ASN:OD1	4:YH:222:ASN:N	2.37	0.42
3:ZF:236:SER:OG	3:ZF:237:LYS:N	2.51	0.42
2:AD:81:ALA:HB3	2:AD:128:LEU:HD11	2.01	0.42
3:BF:263:LYS:HD3	3:BF:263:LYS:HA	1.82	0.42
6:BL:139:ARG:HH12	7:BM:319:PHE:H	1.65	0.42
11:EC:185:LYS:HZ3	11:EC:185:LYS:HG2	1.76	0.42
11:GC:234:VAL:HG12	11:GC:243:ILE:HA	2.01	0.42
11:JC:168:LYS:HE2	11:JC:168:LYS:HB2	1.71	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:LC:214:LYS:HE3	11:LC:214:LYS:HB3	1.89	0.42
5:CK:90:ARG:HH21	5:CK:92:ASN:HA	1.83	0.42
2:DD:123:THR:OG1	2:DD:124:LYS:N	2.51	0.42
7:EM:199:LYS:HA	7:EM:219:ALA:O	2.20	0.42
1:HG:1006:ILE:HD13	1:IG:968:PHE:HA	2.01	0.42
1:NG:1025:THR:HA	1:NG:1026:PRO:HD3	1.91	0.42
11:BC:269:LYS:HD2	11:BC:269:LYS:HA	1.86	0.42
1:AG:1025:THR:HA	1:AG:1026:PRO:HD3	1.92	0.42
4:GH:255:ARG:HE	4:GH:255:ARG:HB3	1.74	0.42
6:GL:102:LYS:HE3	6:GL:102:LYS:HB2	1.89	0.42
2:Dd:105:ARG:HB2	2:Dd:153:VAL:HG23	2.02	0.42
4:HH:253:ASP:OD1	4:HH:253:ASP:N	2.52	0.42
7:HM:275:ASP:HA	7:HM:295:ASN:H	1.85	0.42
5:IK:107:LYS:HE2	5:IK:107:LYS:HB3	1.84	0.42
6:JL:44:HIS:N	6:JL:48:ASN:OD1	2.44	0.42
10:JX:24:UNK:O	10:JX:32:UNK:N	2.53	0.42
2:Jd:32:ASN:HD22	2:Jd:32:ASN:HA	1.72	0.42
2:LD:68:ASP:OD1	2:LD:137:TYR:OH	2.35	0.42
5:LK:104:ALA:O	5:LK:108:GLN:NE2	2.41	0.42
5:AK:152:ARG:H	5:AK:152:ARG:HG2	1.67	0.42
3:MF:219:ARG:HG2	4:ZH:148:PRO:HD2	2.00	0.42
1:Cg:818:GLN:NE2	4:CH:205:GLN:OE1	2.53	0.42
5:MK:118:SER:HB3	5:MK:180:VAL:HG12	2.01	0.42
7:MM:129:LEU:HD13	7:MM:129:LEU:HA	1.94	0.42
3:VF:269:SER:O	3:CF:233:ARG:NH2	2.53	0.42
1:XG:817:THR:OG1	1:XG:818:GLN:N	2.53	0.42
4:YH:133:ILE:HD12	4:YH:133:ILE:HA	1.91	0.42
11:MC:125:ILE:HD12	11:LC:247:LEU:HD11	2.01	0.42
11:LC:220:MET:HE3	11:LC:220:MET:HB3	1.82	0.42
4:CH:283:VAL:HG22	4:CH:289:PRO:HD3	2.02	0.42
7:CM:214:ILE:O	7:CM:215:ARG:NH1	2.52	0.42
7:DM:146:LEU:HD23	7:DM:165:ILE:HG12	2.01	0.42
2:Ed:29:PRO:HB2	2:Ed:32:ASN:HB2	2.02	0.42
3:Ef:247:ILE:HA	3:Ef:254:ILE:HG13	2.01	0.42
2:GD:87:TRP:CD1	2:GD:89:GLY:H	2.38	0.42
1:Gg:804:ALA:HB3	4:HH:122:LEU:HD21	2.02	0.42
2:HD:36:ASP:HA	2:HD:39:ILE:HD12	2.02	0.42
3:HF:213:GLN:HB2	3:HF:223:ILE:HG22	2.01	0.42
2:ID:47:SER:O	2:ID:51:SER:OG	2.36	0.42
4:IH:166:PRO:HA	4:IH:167:PRO:HD3	1.86	0.42
4:IH:313:VAL:HG23	4:IH:337:TYR:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:IM:210:ASP:OD2	7:IM:211:THR:OG1	2.37	0.42
5:JK:66:LYS:HB3	5:JK:77:SER:HB3	2.02	0.42
3:Jf:256:THR:OG1	3:Jf:257:SER:N	2.52	0.42
2:LD:147:VAL:HG22	2:LD:154:VAL:HG22	2.01	0.42
4:LH:170:ARG:HB3	4:LH:245:GLN:HB2	2.00	0.42
4:LH:238:MET:HE3	4:LH:238:MET:HB2	1.72	0.42
4:VH:148:PRO:HB2	3:CF:219:ARG:HG3	2.00	0.42
1:EG:937:PRO:HD3	1:EG:1037:LEU:HA	2.01	0.42
1:YG:797:ARG:HH12	1:YG:801:MET:HE2	1.85	0.42
4:BH:219:LYS:HD2	4:BH:219:LYS:HA	1.85	0.42
3:Bf:219:ARG:HH21	3:Bf:233:ARG:HH22	1.67	0.42
11:HC:249:ILE:HD12	11:IC:123:GLN:HG2	2.01	0.42
4:CH:178:SER:HA	4:CH:213:LEU:O	2.20	0.42
2:Cd:142:LYS:H	2:Cd:142:LYS:HZ3	1.67	0.42
4:DH:132:GLN:O	4:DH:136:THR:OG1	2.34	0.42
3:FF:207:ARG:HB2	3:FF:208:ILE:H	1.66	0.42
5:FK:163:LYS:HD2	5:FK:163:LYS:HA	1.87	0.42
1:JG:919:MET:HB3	1:JG:928:ILE:HG13	2.02	0.42
3:Ff:241:TYR:O	3:Ff:256:THR:OG1	2.38	0.42
11:IC:110:LEU:HD23	11:IC:212:TYR:HB2	2.01	0.42
1:AG:911:LYS:HE3	1:AG:913:VAL:HB	2.01	0.42
7:HM:183:VAL:O	7:HM:202:LEU:HA	2.20	0.42
7:IM:153:GLN:HE22	7:IM:154:LYS:HE2	1.85	0.42
8:IN:95:LEU:H	8:IN:95:LEU:HG	1.70	0.42
2:JD:87:TRP:CD1	2:JD:94:LEU:HD22	2.55	0.42
6:JL:141:ASN:HD21	6:JL:143:ILE:HB	1.85	0.42
6:KL:126:ILE:HD13	6:KL:126:ILE:HA	1.92	0.42
7:KM:254:LYS:HB2	7:KM:254:LYS:HE3	1.85	0.42
3:LF:222:LEU:O	3:LF:229:THR:HA	2.20	0.42
5:MK:90:ARG:HD3	7:MM:292:MET:HE3	2.00	0.42
7:MM:208:LYS:HA	7:MM:208:LYS:HD3	1.70	0.42
3:XF:238:ILE:HG23	3:XF:241:TYR:HB2	2.00	0.42
7:AM:217:LYS:HB2	7:AM:217:LYS:HE2	1.87	0.42
7:AM:263:ILE:HG22	7:AM:265:ALA:H	1.83	0.42
7:AM:279:ILE:HB	7:AM:298:VAL:HG22	2.00	0.42
7:AM:284:LEU:HD23	7:AM:310:LYS:HE3	2.01	0.42
2:BD:158:TYR:O	2:Bd:137:TYR:OH	2.32	0.42
4:BH:173:GLN:HA	4:BH:217:ALA:HB3	2.01	0.42
8:BN:76:MET:SD	8:BN:76:MET:N	2.93	0.42
11:LC:49:GLN:H	11:LC:49:GLN:HG2	1.55	0.42
6:CL:170:ASP:N	6:CL:170:ASP:OD1	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:EH:151:PRO:HA	4:EH:248:VAL:HG13	2.01	0.42
7:EM:154:LYS:HA	7:EM:154:LYS:HD3	1.86	0.42
2:FD:161:ILE:HD12	2:FD:161:ILE:HA	1.88	0.42
7:FM:151:GLY:HA2	7:FM:168:VAL:HG13	2.01	0.42
11:BC:163:ASN:OD1	11:BC:163:ASN:N	2.52	0.42
11:IC:57:MET:SD	11:IC:57:MET:N	2.83	0.42
5:IK:56:MET:HE2	5:IK:105:PHE:HB2	2.01	0.42
1:CG:916:PHE:HD1	1:CG:916:PHE:HA	1.68	0.42
11:CC:262:GLU:N	11:CC:262:GLU:OE1	2.53	0.42
1:Lg:801:MET:HE2	1:Lg:801:MET:HB2	1.81	0.42
4:LH:173:GLN:HA	4:LH:217:ALA:HB3	2.01	0.42
6:LL:131:LYS:HD2	6:LL:131:LYS:HA	1.92	0.42
4:MH:130:LEU:HA	4:MH:133:ILE:HG12	2.01	0.42
5:MK:57:MET:HE3	5:MK:57:MET:HB3	1.90	0.42
6:ML:109:LEU:HD13	6:ML:109:LEU:HA	1.84	0.42
7:AM:280:TYR:HE1	7:AM:299:LEU:HD23	1.84	0.42
1:FG:872:VAL:HG23	1:FG:890:VAL:HG21	2.01	0.42
1:FG:969:GLY:HA3	1:FG:1009:ALA:N	2.35	0.42
11:HC:146:THR:H	11:HC:149:GLN:HE22	1.66	0.42
3:Cf:260:GLN:HE21	3:Cf:260:GLN:HB3	1.64	0.42
5:EK:107:LYS:HE2	5:EK:107:LYS:HB2	1.83	0.42
1:JG:899:LEU:HD13	1:JG:919:MET:HG2	2.01	0.42
1:MG:947:ARG:NH2	1:MG:1030:GLU:OE1	2.51	0.42
1:NG:879:SER:HG	1:NG:1029:VAL:H	1.67	0.42
8:FN:48:ILE:H	8:FN:48:ILE:HG12	1.68	0.42
4:GH:208:LYS:NZ	1:Hg:822:GLU:O	2.50	0.42
6:GL:47:TYR:OH	6:GL:142:GLU:OE1	2.37	0.42
7:HM:153:GLN:HA	7:HM:173:LEU:HA	2.00	0.42
1:BG:1005:VAL:O	1:BG:1009:ALA:HB2	2.19	0.42
2:Id:71:LEU:HD12	2:Id:136:ASP:HB2	2.02	0.42
4:JH:196:LEU:HD11	4:JH:202:PHE:HB2	2.02	0.42
2:Jd:86:ASP:HA	2:Jd:121:ILE:O	2.19	0.42
7:KM:284:LEU:HD13	7:KM:302:ARG:HH12	1.85	0.42
2:Kd:160:LYS:HE3	2:Kd:160:LYS:HB2	1.89	0.42
1:Lg:795:GLN:O	1:Lg:798:THR:OG1	2.36	0.42
7:LM:275:ASP:HA	7:LM:295:ASN:H	1.85	0.42
2:CD:60:LYS:HB2	2:CD:60:LYS:HE2	1.84	0.42
2:CD:73:ILE:O	2:CD:133:ARG:NH2	2.40	0.42
1:DG:1031:VAL:O	1:EG:941:ARG:NH2	2.53	0.42
3:MF:207:ARG:NH1	3:MF:240:GLY:O	2.53	0.42
1:Mg:814:GLN:O	1:Mg:814:GLN:NE2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:MH:191:ILE:HB	4:MH:206:TRP:HE1	1.85	0.42
7:MM:199:LYS:HG3	7:MM:219:ALA:HB3	2.02	0.42
4:XH:321:SER:OG	4:XH:346:LEU:N	2.53	0.42
4:YH:154:THR:O	4:YH:252:VAL:HA	2.20	0.42
4:ZH:292:SER:HB2	4:ZH:305:TRP:HB3	2.02	0.42
4:ZH:341:LYS:HE3	4:ZH:341:LYS:HB2	1.86	0.42
2:Ad:41:LEU:HD13	2:Ad:41:LEU:HA	1.94	0.42
6:BL:124:THR:HG22	6:BL:232:GLN:HG2	2.01	0.42
11:EC:117:LEU:HD13	11:EC:127:ILE:HG22	2.02	0.42
11:FC:221:VAL:HG12	11:FC:255:LEU:HD23	2.02	0.42
11:HC:121:ASP:OD1	11:HC:124:SER:OG	2.32	0.42
11:KC:246:ARG:HD3	11:LC:127:ILE:HD11	2.02	0.42
11:LC:106:LEU:HD12	11:LC:107:PRO:HD2	2.02	0.42
4:CH:151:PRO:HA	4:CH:248:VAL:HG13	2.02	0.42
3:DF:208:ILE:HG23	3:DF:225:SER:H	1.85	0.42
5:DK:76:ILE:HB	5:DK:182:ILE:HG12	2.02	0.42
4:EH:127:VAL:HG12	4:EH:131:LYS:HE2	2.01	0.42
8:EN:87:TRP:O	8:EN:88:HIS:ND1	2.53	0.42
6:FL:60:VAL:HG11	6:FL:93:LEU:HD22	2.02	0.42
1:IG:919:MET:HG3	1:IG:930:ILE:HG23	2.01	0.42
1:IG:937:PRO:HD3	1:IG:1037:LEU:HA	2.02	0.42
1:MG:972:PHE:HD1	1:MG:972:PHE:HA	1.67	0.42
7:FM:190:ASN:HA	7:FM:209:SER:HB2	2.02	0.42
7:FM:292:MET:HE1	7:FM:298:VAL:H	1.85	0.42
8:GN:86:LEU:HB3	8:GN:87:TRP:HE3	1.85	0.41
2:Dd:29:PRO:HG3	5:DK:146:SER:HB2	2.02	0.41
2:Dd:58:VAL:HG11	2:DD:59:GLU:HG3	2.02	0.41
5:HK:65:ILE:HG12	5:HK:78:ILE:HG12	2.02	0.41
7:IM:146:LEU:HD13	7:IM:146:LEU:HA	1.88	0.41
2:Id:79:LEU:HD13	2:Id:79:LEU:HA	1.90	0.41
3:If:212:ILE:HG12	3:If:262:ILE:HG22	2.02	0.41
2:KD:77:TYR:HE1	7:KM:304:TRP:HE3	1.66	0.41
3:LF:220:ALA:O	3:LF:231:THR:HA	2.19	0.41
4:LH:132:GLN:O	4:LH:136:THR:OG1	2.32	0.41
4:LH:195:ASP:OD2	4:MH:216:GLN:NE2	2.52	0.41
2:CD:36:ASP:HA	2:CD:39:ILE:HD12	2.02	0.41
2:MD:119:ILE:HD13	2:MD:119:ILE:HA	1.92	0.41
4:MH:166:PRO:HG3	4:ZH:151:PRO:HB2	2.02	0.41
5:MK:55:LYS:NZ	5:MK:59:ASP:OD2	2.43	0.41
7:MM:218:LYS:HE2	7:MM:218:LYS:HB2	1.87	0.41
4:VH:221:TYR:HE2	4:DH:138:GLU:HG3	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:YH:109:LYS:HE2	4:YH:109:LYS:HB2	1.82	0.41
2:AD:72:THR:OG1	2:AD:73:ILE:N	2.53	0.41
7:AM:181:PRO:HB2	7:AM:183:VAL:HG13	2.02	0.41
2:BD:130:GLU:HA	2:BD:133:ARG:HB2	2.02	0.41
7:BM:204:LEU:HD22	7:BM:204:LEU:HA	1.84	0.41
11:EC:75:ARG:HG3	11:EC:79:ILE:HD13	2.01	0.41
11:DC:106:LEU:HD12	11:DC:107:PRO:HD2	2.02	0.41
11:HC:255:LEU:H	11:HC:255:LEU:HG	1.45	0.41
11:MC:44:ARG:HE	11:MC:44:ARG:HB3	1.71	0.41
11:JC:240:ILE:O	11:KC:132:THR:OG1	2.33	0.41
11:KC:116:ASN:N	11:KC:130:ASP:O	2.40	0.41
7:CM:210:ASP:O	7:CM:230:ARG:N	2.47	0.41
1:MG:1019:ALA:O	1:MG:1023:PHE:HB2	2.20	0.41
1:NG:876:SER:OG	1:NG:877:VAL:N	2.50	0.41
1:OG:869:MET:HB2	1:OG:1041:PHE:HE1	1.85	0.41
1:OG:935:ILE:HG22	1:OG:942:THR:HG22	2.01	0.41
7:FM:160:ASN:OD1	7:FM:160:ASN:N	2.53	0.41
2:GD:161:ILE:HD12	2:GD:161:ILE:HA	1.89	0.41
3:GF:233:ARG:HA	3:GF:233:ARG:HD2	1.77	0.41
2:HD:107:ARG:HE	2:HD:153:VAL:HG11	1.85	0.41
4:HH:191:ILE:HG13	4:HH:211:ASN:HA	2.02	0.41
5:HK:99:LEU:HA	5:HK:102:ILE:HD12	2.01	0.41
3:Hf:211:TYR:N	3:Hf:223:ILE:O	2.45	0.41
6:IL:125:LEU:HD13	6:IL:125:LEU:HA	1.97	0.41
6:IL:171:ASN:OD1	6:IL:217:ASN:ND2	2.52	0.41
4:JH:221:TYR:CE2	4:KH:138:GLU:HG3	2.55	0.41
7:JM:192:ARG:HE	7:JM:192:ARG:HB2	1.52	0.41
4:AH:257:GLN:HE21	4:AH:257:GLN:HB3	1.66	0.41
4:AH:275:SER:OG	4:AH:276:ALA:N	2.53	0.41
2:KD:84:SER:HA	2:KD:124:LYS:HA	2.01	0.41
11:CC:148:TRP:HB2	11:CC:152:LEU:HD23	2.01	0.41
5:KK:172:GLY:O	5:KK:175:SER:OG	2.32	0.41
6:KL:165:VAL:HG23	6:KL:205:ALA:HA	2.01	0.41
6:KL:214:ILE:HD13	6:KL:214:ILE:HA	1.89	0.41
8:KN:92:TYR:HD1	8:KN:94:GLN:H	1.66	0.41
3:Kf:233:ARG:O	3:Kf:236:SER:OG	2.38	0.41
1:Lg:817:THR:OG1	1:Lg:818:GLN:N	2.53	0.41
7:LM:233:VAL:HG13	7:LM:253:VAL:HA	2.02	0.41
3:Df:233:ARG:HA	3:Df:233:ARG:HD3	1.66	0.41
7:MM:166:ASN:HA	7:MM:186:SER:HB3	2.01	0.41
4:VH:126:GLN:HA	4:VH:129:LYS:HG2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:VH:131:LYS:NZ	4:CH:143:ALA:O	2.40	0.41
8:AN:58:LEU:HD13	8:AN:68:CYS:HB2	2.03	0.41
2:BD:94:LEU:HA	2:BD:94:LEU:HD12	1.86	0.41
5:BK:99:LEU:HD12	5:BK:99:LEU:HA	1.92	0.41
11:EC:243:ASP:N	11:EC:243:ASP:OD1	2.51	0.41
11:FC:245:ARG:HB2	11:GC:128:ILE:HG13	2.03	0.41
11:MC:110:LEU:HD12	11:MC:212:TYR:HA	2.00	0.41
7:CM:275:ASP:HA	7:CM:295:ASN:H	1.85	0.41
11:IC:176:TRP:O	11:IC:180:THR:OG1	2.34	0.41
2:GD:147:VAL:HG12	2:GD:154:VAL:HG22	2.01	0.41
3:Gf:222:LEU:HB2	3:Gf:230:LEU:HB3	2.01	0.41
2:Dd:100:LYS:O	2:Dd:100:LYS:NZ	2.39	0.41
3:Hf:214:ALA:H	3:Hf:221:TRP:HB3	1.84	0.41
4:AH:110:LYS:HZ2	1:Mg:794:ILE:HD13	1.84	0.41
4:AH:191:ILE:HG23	4:AH:228:VAL:HG13	2.02	0.41
2:Kd:79:LEU:HD12	2:Kd:79:LEU:HA	1.89	0.41
1:DG:936:ASP:OD2	1:DG:939:THR:OG1	2.32	0.41
1:Mg:795:GLN:OE1	1:Mg:796:GLN:N	2.53	0.41
4:MH:208:LYS:HG3	4:MH:209:THR:HG23	2.02	0.41
4:VH:284:LEU:HD21	4:VH:330:SER:HB3	2.02	0.41
1:EG:867:ASP:H	1:EG:1041:PHE:HB2	1.86	0.41
4:XH:229:ARG:HE	4:XH:229:ARG:HB3	1.65	0.41
6:AL:190:MET:HA	6:AL:193:LEU:HD23	2.01	0.41
7:AM:300:ASP:OD1	7:AM:302:ARG:NE	2.53	0.41
6:BL:136:SER:O	7:BM:314:ARG:NH1	2.53	0.41
11:FC:108:PRO:HD3	11:FC:138:ALA:HB2	2.01	0.41
11:JC:60:LYS:HB3	11:JC:61:GLU:H	1.56	0.41
3:Cf:218:GLY:H	3:Cf:247:ILE:HG21	1.86	0.41
2:DD:27:LYS:HA	2:DD:28:PRO:HD3	1.89	0.41
5:EK:122:LYS:NZ	5:EK:125:SER:O	2.40	0.41
6:EL:94:VAL:HA	6:EL:97:ILE:HG12	2.02	0.41
5:FK:116:VAL:HG22	5:FK:182:ILE:HG22	2.01	0.41
6:FL:230:GLU:OE2	6:FL:232:GLN:NE2	2.52	0.41
1:MG:951:HIS:O	1:MG:955:ARG:NE	2.52	0.41
7:FM:131:THR:HG22	7:FM:150:ILE:HG12	2.02	0.41
3:Ff:248:ASP:OD1	3:Ff:251:GLN:N	2.43	0.41
3:AF:209:ILE:O	3:AF:225:SER:N	2.52	0.41
1:AG:948:THR:HG22	1:AG:1029:VAL:HG12	2.02	0.41
6:GL:166:ALA:HB3	6:GL:230:GLU:HG2	2.03	0.41
2:Dd:150:ASN:OD1	2:Dd:150:ASN:N	2.51	0.41
7:HM:242:LYS:HA	7:HM:262:GLU:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:HM:302:ARG:HH11	7:HM:309:LEU:HD11	1.86	0.41
6:IL:53:ASP:N	6:IL:53:ASP:OD1	2.53	0.41
6:IL:148:LEU:HD13	6:IL:148:LEU:HA	1.83	0.41
7:IM:191:LEU:HD21	7:IM:194:LEU:HD12	2.02	0.41
3:If:256:THR:OG1	3:If:257:SER:N	2.53	0.41
4:JH:201:SER:OG	4:JH:222:ASN:ND2	2.46	0.41
4:JH:204:ILE:HD11	4:JH:213:LEU:HD22	2.02	0.41
7:JM:247:ARG:HH21	3:Jf:213:GLN:HA	1.85	0.41
4:AH:149:PRO:HB2	4:AH:248:VAL:HG12	2.02	0.41
7:KM:141:GLU:OE2	7:KM:143:THR:OG1	2.31	0.41
8:KN:99:GLY:O	8:KN:113:SER:OG	2.35	0.41
1:Ag:810:GLN:H	1:Ag:810:GLN:HG3	1.66	0.41
2:MD:130:GLU:OE2	2:MD:133:ARG:NH1	2.53	0.41
4:MH:311:MET:HG3	4:MH:341:LYS:HA	2.01	0.41
4:VH:303:ARG:O	4:VH:313:VAL:HA	2.20	0.41
4:WH:166:PRO:HA	4:WH:167:PRO:HD3	1.94	0.41
3:Af:233:ARG:O	3:Af:236:SER:OG	2.32	0.41
1:FG:862:ILE:HD13	1:FG:1046:THR:HA	2.02	0.41
2:Bd:26:LYS:HB2	2:Bd:26:LYS:HE3	1.88	0.41
2:Bd:105:ARG:H	2:Bd:105:ARG:HG2	1.64	0.41
2:ED:26:LYS:HG2	8:DN:62:ASN:HB3	2.03	0.41
7:CM:292:MET:HE1	7:CM:298:VAL:HB	2.02	0.41
2:DD:135:ILE:HD13	2:DD:135:ILE:HA	1.88	0.41
1:GG:899:LEU:HD21	1:GG:916:PHE:HB3	2.03	0.41
4:EH:171:LEU:HB2	4:EH:243:PRO:HA	2.02	0.41
1:JG:900:ILE:HD11	1:KG:865:THR:HG22	2.01	0.41
1:JG:1015:TRP:NE1	1:KG:956:TYR:OH	2.53	0.41
1:MG:905:LEU:HD23	1:MG:905:LEU:HA	1.89	0.41
1:MG:916:PHE:HD1	1:MG:916:PHE:HA	1.76	0.41
1:NG:910:ASP:OD1	1:NG:910:ASP:N	2.46	0.41
7:FM:117:ARG:HA	7:FM:137:TYR:O	2.21	0.41
2:Gd:100:LYS:HB2	2:Gd:100:LYS:HE3	1.78	0.41
4:HH:122:LEU:H	4:HH:122:LEU:HG	1.69	0.41
4:HH:229:ARG:HB2	4:HH:236:PRO:HB3	2.03	0.41
7:HM:146:LEU:HD13	7:HM:146:LEU:HA	1.91	0.41
5:IK:91:LEU:HA	5:IK:91:LEU:HD13	1.84	0.41
7:JM:228:VAL:HG11	7:JM:231:LEU:HB2	2.01	0.41
7:KM:288:ARG:HH22	7:KM:318:GLN:H	1.69	0.41
8:KN:76:MET:HB3	8:KN:78:LEU:HD23	2.02	0.41
2:Kd:64:PRO:HG2	2:Kd:67:LYS:HG2	2.02	0.41
3:Kf:226:ASN:N	3:Kf:226:ASN:OD1	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LD:39:ILE:HG23	6:LL:220:ILE:HG13	2.01	0.41
4:LH:178:SER:OG	4:YH:238:MET:SD	2.76	0.41
2:Ld:135:ILE:HD13	2:Ld:135:ILE:HA	1.86	0.41
1:DG:872:VAL:HG23	1:DG:890:VAL:HG21	2.03	0.41
2:MD:36:ASP:OD2	11:HC:75:ARG:NH2	2.52	0.41
7:MM:267:ASN:HA	7:MM:286:LYS:H	1.85	0.41
4:WH:108:ASP:OD1	4:WH:108:ASP:N	2.53	0.41
3:ZF:245:LYS:HG3	3:ZF:257:SER:HA	2.03	0.41
2:AD:137:TYR:CZ	2:Ad:57:LYS:HG3	2.56	0.41
4:ZH:158:VAL:HG22	4:ZH:256:VAL:HA	2.01	0.41
4:ZH:321:SER:HB3	4:ZH:346:LEU:HD22	2.03	0.41
4:BH:156:GLN:O	4:BH:254:LEU:HA	2.20	0.41
7:BM:254:LYS:HE2	7:BM:272:LEU:HD23	2.02	0.41
8:BN:49:ASN:HD21	8:BN:61:ASN:HA	1.86	0.41
11:EC:88:ARG:HD2	11:EC:88:ARG:HA	1.84	0.41
11:EC:242:ILE:HD11	11:FC:129:ASP:HB3	2.02	0.41
11:MC:146:THR:N	11:MC:149:GLN:HE22	2.15	0.41
11:KC:76:ARG:HD2	11:KC:76:ARG:HA	1.86	0.41
4:CH:173:GLN:HG3	4:CH:220:LEU:HD23	2.02	0.41
6:CL:94:VAL:HA	6:CL:97:ILE:HG22	2.01	0.41
4:DH:152:THR:OG1	4:DH:249:ASP:OD1	2.35	0.41
6:DL:126:ILE:HD13	6:DL:126:ILE:HA	1.89	0.41
4:EH:332:ASP:OD1	4:EH:332:ASP:N	2.51	0.41
4:FH:196:LEU:HD11	4:FH:202:PHE:HB2	2.02	0.41
4:FH:219:LYS:HD2	4:FH:219:LYS:HA	1.71	0.41
1:OG:898:LYS:NZ	1:OG:920:SER:HB3	2.35	0.41
1:PG:865:THR:OG1	1:PG:1044:ASP:OD2	2.31	0.41
2:GD:52:MET:HG3	2:Gd:48:VAL:HG23	2.02	0.41
2:GD:82:ARG:NH2	7:GM:311:ASP:OD2	2.53	0.41
4:GH:183:ASP:OD1	4:GH:187:ALA:N	2.53	0.41
4:GH:295:LEU:HD23	4:GH:295:LEU:HA	1.92	0.41
6:GL:193:LEU:HA	6:GL:193:LEU:HD13	1.84	0.41
3:Gf:216:ILE:HD12	3:Gf:216:ILE:HA	1.82	0.41
5:IK:129:GLU:OE1	5:IK:129:GLU:N	2.54	0.41
2:JD:145:ILE:HD11	2:JD:156:LEU:HD12	2.01	0.41
11:CC:61:LYS:HB2	11:CC:61:LYS:HE3	1.83	0.41
5:KK:91:LEU:HA	5:KK:91:LEU:HD12	1.77	0.41
7:KM:198:GLY:O	7:KM:219:ALA:HB3	2.20	0.41
2:LD:62:ILE:HD12	2:LD:62:ILE:HA	1.82	0.41
5:LK:67:VAL:HA	5:LK:76:ILE:HG22	2.02	0.41
5:LK:106:LEU:HD23	5:LK:106:LEU:HA	1.91	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:AK:120:SER:OG	5:AK:121:SER:N	2.53	0.41
2:MD:68:ASP:OD2	2:MD:70:THR:OG1	2.29	0.41
4:VH:170:ARG:HA	4:VH:242:ILE:O	2.20	0.41
1:XG:810:GLN:HE21	1:XG:810:GLN:HB2	1.59	0.41
1:EG:867:ASP:O	1:EG:1040:LEU:HA	2.20	0.41
4:ZH:156:GLN:O	4:ZH:254:LEU:HA	2.21	0.41
2:BD:55:MET:HA	2:BD:58:VAL:HG12	2.03	0.41
4:BH:266:MET:O	4:BH:268:THR:N	2.49	0.41
5:BK:122:LYS:H	5:BK:122:LYS:HG3	1.61	0.41
11:LC:117:LEU:HB2	11:LC:127:ILE:HG22	2.03	0.41
4:CH:176:VAL:HG22	4:CH:216:GLN:HB2	2.02	0.41
7:CM:123:VAL:HG22	7:CM:143:THR:HB	2.03	0.41
7:CM:137:TYR:HA	7:CM:156:GLU:O	2.21	0.41
2:Cd:36:ASP:N	2:Cd:36:ASP:OD1	2.49	0.41
1:GG:931:SER:H	1:GG:1043:GLN:NE2	2.19	0.41
5:DK:116:VAL:HG23	5:DK:156:THR:HA	2.02	0.41
7:DM:249:GLN:OE1	7:DM:267:ASN:ND2	2.54	0.41
4:EH:160:LEU:H	4:EH:160:LEU:HG	1.70	0.41
4:EH:174:GLY:N	4:EH:217:ALA:O	2.45	0.41
6:EL:113:ASP:OD1	6:EL:113:ASP:N	2.36	0.41
6:EL:145:TYR:HA	6:EL:148:LEU:HD13	2.02	0.41
7:EM:275:ASP:OD1	7:EM:275:ASP:N	2.49	0.41
4:FH:249:ASP:OD1	4:FH:249:ASP:N	2.54	0.41
6:FL:138:PRO:HD3	7:FM:314:ARG:HH12	1.84	0.41
11:AC:170:LYS:HA	11:AC:173:LYS:HE2	2.02	0.41
4:HH:173:GLN:NE2	4:HH:218:THR:O	2.49	0.41
1:Bg:794:ILE:O	1:Bg:798:THR:N	2.51	0.41
1:BG:1011:VAL:HG12	1:CG:963:SER:HB2	2.03	0.41
5:IK:49:CYS:O	5:IK:52:THR:OG1	2.25	0.41
5:IK:170:LEU:HD13	5:IK:170:LEU:HA	1.90	0.41
7:JM:149:ASN:OD1	7:JM:149:ASN:N	2.45	0.41
11:CC:116:ASN:N	11:CC:130:ASP:O	2.50	0.41
11:CC:130:ASP:N	11:BC:244:ASP:OD1	2.40	0.41
3:KF:219:ARG:HE	3:KF:219:ARG:HB3	1.66	0.41
4:KH:166:PRO:HA	4:KH:167:PRO:HD3	1.92	0.41
5:KK:115:THR:HB	5:KK:183:THR:HG23	2.01	0.41
6:KL:109:LEU:HD12	6:KL:109:LEU:HA	1.94	0.41
7:KM:235:LEU:HD23	7:KM:259:SER:HB2	2.02	0.41
8:KN:49:ASN:ND2	8:KN:60:CYS:O	2.54	0.41
4:LH:145:PRO:HG3	4:MH:131:LYS:HE2	2.03	0.41
5:LK:166:THR:HG22	5:LK:168:TYR:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CD:87:TRP:CD2	2:CD:94:LEU:HD13	2.56	0.41
2:MD:111:LYS:NZ	2:MD:120:SER:H	2.18	0.41
1:VG:801:MET:HB2	4:DH:122:LEU:HD21	2.02	0.41
4:XH:157:PHE:HZ	4:XH:257:GLN:HE21	1.69	0.41
7:AM:255:THR:HB	7:AM:259:SER:HB2	2.03	0.41
3:BF:241:TYR:O	3:BF:258:SER:OG	2.39	0.41
4:BH:150:LYS:H	4:BH:247:ALA:HA	1.84	0.41
5:BK:92:ASN:OD1	5:BK:92:ASN:N	2.52	0.41
2:Bd:128:LEU:HA	2:Bd:131:ILE:HB	2.03	0.41
11:EC:75:ARG:HD3	11:EC:188:ILE:HG12	2.03	0.41
11:FC:170:LYS:H	11:FC:170:LYS:HG3	1.64	0.41
11:DC:261:GLU:OE1	11:DC:261:GLU:N	2.53	0.41
10:CX:13:UNK:O	10:CX:17:UNK:CB	2.69	0.41
6:DL:104:LYS:HD2	6:DL:104:LYS:HA	1.92	0.41
3:Ef:233:ARG:H	3:Ef:233:ARG:HG2	1.72	0.41
4:FH:210:SER:OG	4:FH:211:ASN:N	2.53	0.41
6:FL:47:TYR:OH	6:FL:142:GLU:OE1	2.31	0.41
1:OG:1025:THR:HA	1:OG:1026:PRO:HD3	1.88	0.41
2:HD:83:ALA:HA	5:HK:154:ILE:O	2.21	0.41
5:HK:127:LYS:HE2	5:HK:127:LYS:HB2	1.90	0.41
5:HK:159:LEU:HD13	5:HK:159:LEU:HA	1.87	0.41
6:HL:170:ASP:HA	6:HL:226:ASN:HD22	1.85	0.41
7:HM:262:GLU:HG3	7:HM:282:TYR:HE2	1.85	0.41
4:IH:294:ARG:HH22	11:DC:194:ILE:HD13	1.85	0.41
6:JL:91:VAL:HA	6:JL:94:VAL:HG22	2.03	0.41
7:JM:199:LYS:HA	7:JM:219:ALA:HB3	2.03	0.41
7:JM:312:PHE:HB3	7:JM:316:ASN:HB3	2.03	0.41
4:AH:322:PRO:HG2	4:AH:339:MET:HE1	2.02	0.41
11:CC:76:ARG:HA	11:CC:76:ARG:HD2	1.83	0.41
11:CC:79:ILE:O	11:CC:83:GLN:NE2	2.54	0.41
3:KF:208:ILE:HD11	3:KF:224:GLY:HA3	2.02	0.41
6:KL:155:LEU:HD22	6:KL:155:LEU:HA	1.92	0.41
7:KM:205:TYR:HD1	7:KM:205:TYR:HA	1.70	0.41
2:LD:83:ALA:HA	5:LK:154:ILE:O	2.20	0.41
1:DG:931:SER:O	1:DG:1042:THR:OG1	2.38	0.41
6:ML:52:PRO:O	6:ML:54:ARG:NH1	2.54	0.41
4:VH:179:LEU:O	4:VH:212:THR:HA	2.20	0.41
4:WH:238:MET:HE3	4:WH:238:MET:HB2	1.82	0.41
4:XH:310:LYS:HD3	4:XH:310:LYS:HA	1.90	0.41
2:AD:52:MET:HE3	2:AD:52:MET:HB3	1.86	0.41
5:BK:111:LYS:HD3	5:BK:114:ILE:HD11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Bf:210:TYR:HA	3:Bf:224:GLY:HA2	2.03	0.41
3:Bf:253:ARG:HB3	3:Bf:263:LYS:HG3	2.02	0.41
2:Cd:135:ILE:HD13	2:Cd:135:ILE:HA	1.89	0.41
4:DH:157:PHE:HD1	4:DH:255:ARG:HB2	1.85	0.41
7:DM:181:PRO:HB2	7:DM:183:VAL:HG13	2.03	0.41
1:JG:952:TYR:HA	1:JG:955:ARG:HE	1.86	0.41
1:MG:869:MET:HE3	1:MG:869:MET:HB2	1.95	0.41
1:MG:879:SER:OG	1:MG:1029:VAL:O	2.34	0.41
7:FM:303:GLU:HG2	7:FM:305:GLY:H	1.86	0.41
11:BC:147:THR:OG1	11:BC:148:TRP:N	2.53	0.41
11:IC:78:ILE:HD13	11:IC:78:ILE:HA	1.94	0.41
1:Gg:802:LEU:HA	4:XH:115:MET:HE3	2.02	0.41
1:Gg:806:THR:HA	1:Gg:809:VAL:HG12	2.03	0.41
4:GH:183:ASP:OD1	4:GH:186:GLY:N	2.54	0.41
4:GH:203:ASN:HB3	4:GH:216:GLN:HG2	2.03	0.41
6:GL:98:TYR:O	6:GL:101:SER:OG	2.33	0.41
7:GM:278:ASP:OD2	7:GM:280:TYR:OH	2.33	0.41
7:GM:299:LEU:HD12	7:GM:299:LEU:HA	1.83	0.41
2:HD:87:TRP:CD1	2:HD:94:LEU:HD22	2.55	0.41
3:HF:233:ARG:NH1	3:XF:269:SER:OG	2.53	0.41
2:Dd:34:SER:O	2:Dd:34:SER:OG	2.39	0.41
2:Dd:72:THR:OG1	2:Dd:73:ILE:N	2.53	0.41
2:Dd:142:LYS:HE2	2:Dd:142:LYS:HB2	1.90	0.41
5:HK:63:LYS:HA	5:HK:63:LYS:HD3	1.90	0.41
6:HL:203:LEU:HD13	6:HL:203:LEU:HA	1.87	0.41
7:HM:254:LYS:HE2	7:HM:272:LEU:HD23	2.02	0.41
7:HM:278:ASP:OD2	7:HM:280:TYR:OH	2.33	0.41
1:BG:966:GLN:O	1:BG:970:ASN:ND2	2.53	0.41
1:BG:1024:ASN:OD1	1:BG:1024:ASN:N	2.37	0.41
2:ID:114:SER:HA	11:EC:115:ASN:HD21	1.84	0.41
2:JD:124:LYS:HE2	5:JK:145:TRP:CD1	2.56	0.41
4:JH:324:TRP:HB3	4:JH:339:MET:HE2	2.03	0.41
5:JK:133:THR:HB	5:JK:158:GLY:HA3	2.03	0.41
7:JM:194:LEU:HD23	7:JM:194:LEU:HA	1.89	0.41
8:JN:48:ILE:HD12	8:JN:58:LEU:HD13	2.01	0.41
4:AH:140:ALA:HB2	4:BH:124:PRO:HB3	2.03	0.41
2:KD:82:ARG:NH2	2:KD:125:ASP:O	2.50	0.41
11:CC:92:ASP:N	11:CC:92:ASP:OD1	2.47	0.41
4:KH:198:ASP:OD1	4:KH:200:SER:OG	2.33	0.41
6:KL:124:THR:HA	6:KL:231:ILE:O	2.21	0.41
7:KM:204:LEU:HD22	7:KM:207:ILE:HG23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:KN:55:ALA:HB2	6:LL:219:ILE:HD12	2.01	0.41
8:KN:81:LEU:HD23	8:KN:81:LEU:HA	1.89	0.41
4:LH:138:GLU:HB3	4:YH:221:TYR:HE2	1.86	0.41
5:LK:110:ARG:HE	5:LK:110:ARG:HB2	1.68	0.41
7:LM:127:ASN:ND2	7:LM:128:ASN:OD1	2.53	0.41
8:LN:95:LEU:H	8:LN:95:LEU:HG	1.69	0.41
1:Mg:798:THR:HA	1:Mg:801:MET:HE2	2.03	0.41
4:MH:223:TYR:HB2	4:MH:242:ILE:HG12	2.02	0.41
5:MK:173:ASP:N	5:MK:173:ASP:OD1	2.54	0.41
3:Df:247:ILE:HG22	3:Df:254:ILE:HD12	2.02	0.41
6:ML:125:LEU:HA	6:ML:125:LEU:HD13	1.88	0.41
7:MM:263:ILE:O	7:MM:281:TYR:HA	2.21	0.41
7:MM:303:GLU:OE2	7:MM:306:GLN:NE2	2.54	0.41
3:Mf:216:ILE:HD12	3:Mf:216:ILE:HA	1.85	0.41
4:VH:182:LEU:HB2	4:VH:255:ARG:HD2	2.02	0.41
4:VH:284:LEU:HD13	4:VH:328:MET:HG3	2.02	0.41
4:VH:310:LYS:HE2	4:VH:310:LYS:HB2	1.90	0.41
1:WG:800:ASP:O	1:WG:803:THR:OG1	2.33	0.41
4:WH:124:PRO:HB3	4:FH:140:ALA:HB2	2.03	0.41
1:YG:810:GLN:HE21	1:YG:810:GLN:HB2	1.60	0.41
7:AM:121:ALA:HA	7:AM:141:GLU:HB3	2.03	0.41
7:AM:215:ARG:NE	7:AM:234:GLU:HB3	2.36	0.41
8:AN:85:CYS:HB2	8:AN:91:VAL:HG22	2.03	0.41
3:BF:223:ILE:HB	3:BF:229:THR:HG22	2.02	0.41
4:BH:238:MET:HB2	4:BH:238:MET:HE3	1.77	0.41
4:BH:282:HIS:HB3	4:BH:287:VAL:HG13	2.02	0.41
8:BN:52:ASP:O	8:BN:56:GLY:N	2.54	0.41
1:FG:886:LEU:HG	1:GG:1040:LEU:HD12	2.03	0.41
11:EC:106:LEU:HD12	11:EC:107:PRO:HD2	2.03	0.41
11:EC:233:VAL:HA	11:EC:242:ILE:HA	2.03	0.41
11:EC:261:GLU:N	11:EC:261:GLU:OE1	2.54	0.41
11:DC:46:GLN:HA	11:DC:49:GLN:HE21	1.85	0.41
11:DC:91:ASP:OD1	11:DC:147:TRP:NE1	2.39	0.41
11:GC:62:GLU:HA	11:GC:65:LEU:HD12	2.03	0.41
11:MC:144:PRO:HA	11:MC:145:PRO:HD3	1.90	0.41
11:MC:220:MET:O	11:MC:256:ASN:ND2	2.53	0.41
11:MC:226:VAL:HG23	11:MC:249:ILE:HG12	2.02	0.41
11:JC:90:LEU:HD12	11:JC:90:LEU:HA	1.92	0.41
11:JC:261:GLU:OE1	11:JC:261:GLU:N	2.54	0.41
6:CL:142:GLU:N	6:CL:142:GLU:OE1	2.54	0.41
6:CL:168:PHE:HB2	6:CL:228:ARG:HG2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:DH:295:LEU:HD23	4:DH:295:LEU:HA	1.93	0.41
1:GG:878:ASN:ND2	1:HG:910:ASP:OD2	2.54	0.41
1:GG:1013:LYS:HB2	1:GG:1013:LYS:HE3	1.87	0.41
6:DL:161:SER:H	6:DL:202:ARG:NH2	2.19	0.41
6:DL:210:ASP:OD1	6:DL:210:ASP:N	2.44	0.41
7:DM:317:LYS:HB2	7:DM:317:LYS:HE3	1.77	0.41
5:EK:49:CYS:O	5:EK:52:THR:OG1	2.29	0.41
5:EK:83:LEU:HD23	5:EK:83:LEU:HA	1.91	0.41
7:EM:215:ARG:NE	7:EM:234:GLU:HB3	2.36	0.41
2:FD:27:LYS:HD3	2:FD:27:LYS:HA	1.86	0.41
1:HG:886:LEU:HA	1:HG:899:LEU:O	2.20	0.41
1:HG:916:PHE:HD1	1:HG:916:PHE:HA	1.70	0.41
1:KG:911:LYS:HB2	1:KG:911:LYS:HE3	1.85	0.41
1:LG:916:PHE:HD1	1:LG:916:PHE:HA	1.77	0.41
1:LG:944:LEU:HD11	1:LG:1031:VAL:HA	2.03	0.41
1:NG:999:SER:OG	1:NG:1000:THR:N	2.53	0.41
1:OG:1042:THR:OG1	1:OG:1043:GLN:OE1	2.32	0.41
11:IC:114:ARG:HG2	11:IC:130:ARG:HG2	2.02	0.41
4:GH:145:PRO:HB3	4:HH:132:GLN:HG2	2.02	0.41
4:GH:306:LEU:HD11	4:GH:309:GLU:HA	2.02	0.41
7:HM:196:MET:HE2	7:HM:200:GLY:HA3	2.02	0.41
4:IH:147:THR:HG21	4:IH:246:LYS:HE2	2.03	0.41
7:IM:205:TYR:HB3	7:IM:206:TRP:CD1	2.55	0.41
3:If:241:TYR:O	3:If:256:THR:OG1	2.34	0.41
5:JK:174:ARG:HD3	5:JK:174:ARG:HA	1.96	0.41
7:JM:306:GLN:OE1	7:JM:307:SER:N	2.53	0.41
10:JX:21:UNK:N	10:JX:78:UNK:O	2.54	0.41
4:AH:115:MET:HG2	1:Mg:801:MET:HE3	2.03	0.41
2:KD:55:MET:O	11:FC:214:LYS:NZ	2.52	0.41
2:KD:136:ASP:OD2	2:KD:145:ILE:N	2.49	0.41
6:KL:94:VAL:HA	6:KL:97:ILE:HG12	2.02	0.41
7:KM:144:THR:HB	7:KM:163:THR:HG23	2.02	0.41
7:KM:235:LEU:HG	7:KM:239:ALA:HB3	2.03	0.41
3:Kf:208:ILE:O	3:Kf:241:TYR:OH	2.39	0.41
2:LD:93:GLU:H	2:LD:93:GLU:HG3	1.63	0.41
8:LN:105:ASP:N	8:LN:105:ASP:OD1	2.51	0.41
2:CD:155:GLU:OE2	2:CD:157:ARG:NH2	2.45	0.41
1:DG:871:ALA:HA	1:DG:890:VAL:HG22	2.03	0.41
1:Mg:816:GLU:H	1:Mg:816:GLU:HG2	1.73	0.41
4:XH:125:GLU:H	4:XH:125:GLU:HG3	1.67	0.41
4:XH:126:GLN:HG3	4:XH:129:LYS:HZ3	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Af:238:ILE:HD12	3:Af:239:PRO:HD2	2.03	0.41
2:BD:160:LYS:HD2	2:BD:160:LYS:HA	1.76	0.41
5:BK:59:ASP:OD1	5:BK:62:LYS:NZ	2.53	0.41
1:FG:1019:ALA:HA	1:FG:1022:LEU:HG	2.03	0.41
2:Bd:141:LYS:HE2	2:Bd:141:LYS:HB2	1.96	0.41
11:EC:185:LYS:HA	11:EC:185:LYS:HD3	1.83	0.41
2:ED:44:ALA:O	2:ED:47:SER:OG	2.35	0.41
7:CM:315:TYR:O	7:CM:318:GLN:NE2	2.54	0.41
2:DD:116:PRO:HG2	2:DD:118:LEU:HD21	2.03	0.41
7:DM:267:ASN:HA	7:DM:286:LYS:HB2	2.03	0.41
7:EM:218:LYS:HE2	7:EM:218:LYS:HB2	1.81	0.41
3:FF:214:ALA:HB3	3:FF:221:TRP:HB2	2.02	0.41
1:IG:889:ILE:HB	1:IG:897:SER:HB2	2.03	0.41
1:KG:936:ASP:HB3	1:KG:939:THR:HB	2.03	0.41
6:GL:150:ASN:OD1	6:GL:153:ARG:NH2	2.36	0.40
8:GN:49:ASN:OD1	8:GN:49:ASN:N	2.52	0.40
8:GN:66:SER:OG	8:GN:67:THR:N	2.52	0.40
2:Hd:108:VAL:HG22	2:Hd:156:LEU:HB3	2.03	0.40
2:ID:60:LYS:O	2:ID:60:LYS:NZ	2.42	0.40
2:JD:87:TRP:CD2	2:JD:94:LEU:HD13	2.56	0.40
4:JH:189:TRP:CD1	4:JH:261:PRO:HD3	2.56	0.40
11:CC:152:LEU:HD21	11:CC:203:ILE:HG21	2.03	0.40
4:KH:129:LYS:HA	4:KH:129:LYS:HD3	1.85	0.40
6:LL:129:THR:O	6:LL:133:PHE:HB2	2.21	0.40
1:DG:1005:VAL:O	1:DG:1009:ALA:CB	2.69	0.40
4:MH:191:ILE:O	4:MH:231:ARG:NH2	2.40	0.40
1:VG:813:LYS:HA	1:VG:813:LYS:HD3	1.80	0.40
4:YH:289:PRO:O	4:YH:292:SER:OG	2.34	0.40
4:ZH:304:ALA:HA	4:ZH:312:TYR:O	2.21	0.40
3:Af:243:MET:O	3:Af:257:SER:N	2.53	0.40
5:BK:87:GLN:N	5:BK:173:ASP:OD2	2.55	0.40
1:FG:952:TYR:HA	1:FG:955:ARG:HE	1.85	0.40
1:FG:966:GLN:HG2	1:FG:1013:LYS:HG3	2.02	0.40
2:DD:147:VAL:HG22	2:DD:154:VAL:HG13	2.02	0.40
8:DN:78:LEU:H	4:EH:354:MET:HE1	1.86	0.40
4:EH:171:LEU:O	4:EH:244:GLY:N	2.47	0.40
7:EM:212:LEU:HD13	7:EM:212:LEU:HA	1.89	0.40
7:EM:279:ILE:HB	7:EM:298:VAL:HG22	2.03	0.40
1:HG:882:PRO:HB3	1:HG:902:SER:HB2	2.03	0.40
1:PG:1003:ASN:HA	1:PG:1006:ILE:HD12	2.04	0.40
11:AC:210:ILE:HD13	11:AC:210:ILE:HA	1.93	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:BC:89:ARG:HA	11:BC:89:ARG:HD2	1.83	0.40
1:AG:947:ARG:NH2	1:AG:1030:GLU:HB3	2.36	0.40
4:GH:250:TYR:HD1	4:GH:250:TYR:HA	1.74	0.40
7:GM:128:ASN:O	7:GM:130:ARG:NH1	2.52	0.40
1:Hg:810:GLN:NE2	1:Hg:811:ASP:OD1	2.55	0.40
6:HL:44:HIS:ND1	6:HL:48:ASN:OD1	2.42	0.40
4:IH:180:VAL:HG13	4:IH:253:ASP:HA	2.04	0.40
2:KD:47:SER:O	2:KD:51:SER:OG	2.37	0.40
11:CC:110:VAL:HG13	11:CC:209:GLY:HA3	2.04	0.40
4:KH:219:LYS:HD2	4:KH:219:LYS:HA	1.82	0.40
4:KH:328:MET:HE1	11:FC:116:THR:HG22	2.03	0.40
6:KL:169:THR:OG1	6:KL:170:ASP:OD1	2.40	0.40
7:KM:218:LYS:HB2	7:KM:218:LYS:HE2	1.93	0.40
2:Kd:149:PRO:O	2:Kd:152:GLN:NE2	2.43	0.40
4:MH:154:THR:HB	4:MH:156:GLN:HE22	1.86	0.40
6:ML:97:ILE:HD12	6:ML:97:ILE:HA	1.90	0.40
7:MM:191:LEU:HG	7:MM:212:LEU:HD21	2.04	0.40
3:CF:216:ILE:HG12	3:CF:221:TRP:HZ3	1.86	0.40
4:ZH:207:ASP:O	4:ZH:210:SER:OG	2.37	0.40
3:BF:253:ARG:HH12	3:BF:255:LEU:HD11	1.85	0.40
4:BH:306:LEU:HD11	4:BH:309:GLU:HA	2.02	0.40
11:DC:214:LYS:HZ1	11:DC:218:MET:HG3	1.86	0.40
2:ED:105:ARG:HB2	2:ED:153:VAL:HG22	2.04	0.40
11:KC:122:ASP:OD1	11:KC:125:SER:OG	2.31	0.40
7:CM:212:LEU:HD13	7:CM:212:LEU:HA	1.86	0.40
3:Cf:238:ILE:HG23	3:Cf:241:TYR:HB2	2.04	0.40
7:DM:121:ALA:HA	7:DM:141:GLU:HB3	2.04	0.40
4:EH:149:PRO:HB2	4:EH:248:VAL:HG12	2.03	0.40
7:EM:126:GLY:O	7:EM:146:LEU:HA	2.20	0.40
7:EM:174:GLN:NE2	7:EM:193:GLN:O	2.48	0.40
2:Ed:150:ASN:OD1	2:Ed:150:ASN:N	2.53	0.40
6:FL:124:THR:HA	6:FL:231:ILE:O	2.21	0.40
1:HG:878:ASN:H	1:IG:942:THR:HG1	1.67	0.40
1:MG:904:ASN:OD1	1:MG:904:ASN:N	2.55	0.40
1:NG:1017:GLN:HE21	1:NG:1017:GLN:HB2	1.67	0.40
1:OG:944:LEU:HD11	1:OG:1031:VAL:HG12	2.03	0.40
11:IC:157:LYS:HA	11:IC:158:PRO:HD3	1.96	0.40
1:AG:886:LEU:HB3	1:AG:900:ILE:HG23	2.02	0.40
8:GN:72:ARG:NE	4:HH:298:SER:OG	2.48	0.40
2:Dd:139:ALA:O	2:Dd:142:LYS:NZ	2.41	0.40
4:HH:115:MET:HG3	1:WG:801:MET:HB3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:HM:277:SER:O	7:HM:297:SER:OG	2.39	0.40
4:IH:255:ARG:HE	4:IH:255:ARG:HB2	1.56	0.40
2:JD:24:LYS:HE3	2:JD:24:LYS:HB3	1.94	0.40
5:KK:144:LEU:HD13	5:KK:144:LEU:HA	1.89	0.40
7:KM:199:LYS:HA	7:KM:219:ALA:HB3	2.03	0.40
7:KM:308:ASP:N	7:KM:308:ASP:OD1	2.54	0.40
5:AK:154:ILE:HD11	2:AD:84:SER:HB3	2.03	0.40
2:MD:62:ILE:HD12	2:MD:62:ILE:HA	1.93	0.40
2:Md:36:ASP:HA	2:Md:39:ILE:HD12	2.03	0.40
3:WF:247:ILE:HG12	3:WF:254:ILE:HG23	2.03	0.40
4:WH:109:LYS:HE2	4:WH:109:LYS:HB2	1.87	0.40
4:WH:304:ALA:HA	4:WH:312:TYR:O	2.21	0.40
2:Bd:41:LEU:HD13	2:Bd:41:LEU:HA	1.96	0.40
11:EC:88:ARG:O	11:EC:92:ALA:HB2	2.21	0.40
11:DC:153:MET:HE2	11:DC:153:MET:HB2	1.94	0.40
6:CL:155:LEU:HD22	6:CL:155:LEU:HA	1.90	0.40
8:CN:52:ASP:O	8:CN:56:GLY:N	2.54	0.40
6:DL:229:ILE:HD13	6:DL:229:ILE:HA	1.90	0.40
6:EL:102:LYS:HA	6:EL:105:ILE:HD12	2.03	0.40
2:FD:80:GLN:HG3	7:FM:304:TRP:CD1	2.57	0.40
6:FL:54:ARG:HD2	6:FL:54:ARG:HA	1.89	0.40
1:KG:1006:ILE:HD13	1:LG:968:PHE:HA	2.04	0.40
4:GH:225:ASN:ND2	4:HH:176:VAL:O	2.55	0.40
7:GM:210:ASP:OD1	7:GM:210:ASP:N	2.53	0.40
7:GM:303:GLU:CD	7:GM:305:GLY:H	2.30	0.40
3:HF:208:ILE:HG13	3:HF:225:SER:H	1.85	0.40
7:HM:204:LEU:HD13	7:HM:204:LEU:HA	1.91	0.40
7:HM:257:ASP:OD1	7:HM:257:ASP:N	2.53	0.40
2:Hd:98:ILE:HD13	2:Hd:98:ILE:HA	1.92	0.40
1:BG:920:SER:HB2	1:CG:865:THR:HB	2.02	0.40
2:ID:55:MET:HA	2:ID:58:VAL:HG22	2.04	0.40
5:IK:138:ARG:HH21	7:IM:319:PHE:HA	1.86	0.40
2:JD:82:ARG:HB2	5:JK:156:THR:HG23	2.04	0.40
2:JD:160:LYS:HA	2:JD:160:LYS:HD2	1.80	0.40
4:JH:166:PRO:HA	4:JH:167:PRO:HD3	1.99	0.40
7:KM:306:GLN:HB2	7:KM:309:LEU:HB2	2.02	0.40
2:Kd:87:TRP:HZ2	2:Kd:90:PRO:HD2	1.85	0.40
1:Cg:792:GLN:NE2	1:Cg:793:GLU:OE2	2.54	0.40
4:MH:150:LYS:H	4:MH:247:ALA:HA	1.85	0.40
5:MK:54:ILE:O	5:MK:58:THR:OG1	2.37	0.40
4:VH:278:ASP:N	4:VH:278:ASP:OD1	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:YF:222:LEU:O	3:YF:229:THR:HA	2.21	0.40
1:YG:817:THR:OG1	1:YG:818:GLN:N	2.54	0.40
2:AD:98:ILE:HD13	2:AD:98:ILE:HA	1.86	0.40
1:ZG:813:LYS:HA	1:ZG:813:LYS:HD3	1.79	0.40
4:BH:321:SER:OG	4:BH:346:LEU:N	2.53	0.40
1:FG:1003:ASN:HA	1:FG:1006:ILE:HB	2.03	0.40
2:Bd:97:ARG:HE	2:Bd:97:ARG:HB3	1.41	0.40
11:EC:170:LYS:H	11:EC:170:LYS:HG3	1.54	0.40
11:FC:77:LYS:HB3	11:FC:77:LYS:HE2	1.92	0.40
11:FC:102:GLU:HG2	11:FC:103:HIS:CD2	2.56	0.40
11:GC:62:GLU:H	11:GC:62:GLU:HG2	1.64	0.40
11:GC:104:HIS:CD2	11:GC:227:VAL:HG11	2.56	0.40
11:MC:127:ILE:HD11	11:LC:245:ARG:HD3	2.03	0.40
2:DD:121:ILE:HD13	2:DD:121:ILE:HA	1.91	0.40
2:DD:134:ASP:HA	2:DD:137:TYR:HB2	2.04	0.40
4:DH:345:LEU:HD13	4:DH:345:LEU:HA	1.87	0.40
2:Ed:141:LYS:HD2	2:Ed:141:LYS:HA	1.81	0.40
2:FD:148:TYR:HA	2:FD:149:PRO:HD3	1.93	0.40
5:FK:54:ILE:O	5:FK:58:THR:OG1	2.35	0.40
1:JG:925:GLU:H	1:JG:925:GLU:HG2	1.67	0.40
1:MG:969:GLY:HA3	1:MG:1009:ALA:HB2	2.03	0.40
1:OG:1032:TYR:HD1	1:PG:941:ARG:HH22	1.70	0.40
7:GM:177:LEU:HD12	7:GM:177:LEU:HA	1.95	0.40
7:GM:262:GLU:HA	7:GM:280:TYR:O	2.22	0.40
2:HD:162:TYR:O	11:CC:246:ARG:NH1	2.54	0.40
1:Bg:819:VAL:HG23	4:AH:196:LEU:HB3	2.04	0.40
6:IL:115:GLN:HB2	6:IL:126:ILE:HB	2.04	0.40
3:JF:207:ARG:HB2	3:JF:208:ILE:H	1.71	0.40
4:AH:152:THR:O	4:AH:249:ASP:HA	2.22	0.40
2:KD:92:GLU:OE1	2:KD:92:GLU:N	2.52	0.40
1:CG:962:SER:HB3	1:CG:1015:TRP:HB3	2.03	0.40
6:KL:190:MET:HE2	6:KL:190:MET:HB3	1.89	0.40
2:Kd:82:ARG:NH2	2:Kd:83:ALA:H	2.19	0.40
2:Kd:83:ALA:HB1	11:GC:268:ALA:H	1.86	0.40
5:LK:127:LYS:H	5:LK:127:LYS:HG2	1.56	0.40
8:LN:52:ASP:OD1	8:LN:54:SER:OG	2.37	0.40
1:DG:873:LEU:HD23	1:DG:1037:LEU:HD22	2.03	0.40
7:MM:127:ASN:OD1	7:MM:127:ASN:N	2.53	0.40
3:VF:207:ARG:HB2	3:VF:208:ILE:H	1.76	0.40
1:EG:898:LYS:HE3	1:EG:898:LYS:HB3	1.97	0.40
6:AL:138:PRO:HB2	6:AL:188:THR:HG21	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:ZG:809:VAL:HA	1:ZG:812:TRP:CD1	2.57	0.40
4:ZH:253:ASP:OD1	4:ZH:253:ASP:N	2.54	0.40
3:Af:219:ARG:HG3	3:Af:233:ARG:HD3	2.03	0.40
11:FC:194:ILE:HD13	11:FC:194:ILE:HA	1.88	0.40
11:MC:146:THR:O	11:MC:149:GLN:NE2	2.55	0.40
7:CM:127:ASN:HA	7:CM:147:ALA:HB3	2.03	0.40
7:CM:159:GLY:HA3	7:CM:179:GLY:HA3	2.03	0.40
5:DK:73:ASN:HA	5:DK:185:ARG:HA	2.02	0.40
6:DL:116:TYR:HA	6:DL:125:LEU:HD12	2.03	0.40
7:DM:254:LYS:HD3	7:DM:272:LEU:HB3	2.04	0.40
8:DN:86:LEU:HD22	8:DN:86:LEU:HA	1.89	0.40
8:DN:87:TRP:O	8:DN:88:HIS:ND1	2.55	0.40
5:EK:50:ASP:HA	5:EK:53:ILE:HD12	2.03	0.40
8:EN:114:LEU:H	8:EN:114:LEU:HG	1.71	0.40
2:FD:62:ILE:HG23	2:FD:63:THR:HG23	2.03	0.40
4:FH:275:SER:O	11:AC:118:ASN:ND2	2.54	0.40
5:FK:144:LEU:HD13	5:FK:144:LEU:HA	1.91	0.40
1:KG:871:ALA:HB2	1:KG:889:ILE:HD13	2.03	0.40
1:PG:886:LEU:HB3	1:PG:900:ILE:HG12	2.03	0.40
11:AC:115:ASN:N	11:AC:129:ASP:O	2.43	0.40
3:AF:219:ARG:HB2	3:AF:219:ARG:HH11	1.86	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%)	32 (100%)	0	0	100	100
1	BG	161/1048 (15%)	156 (97%)	5 (3%)	0	100	100
1	Bg	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CG	161/1048 (15%)	151 (94%)	10 (6%)	0	100	100
1	Cg	32/1048 (3%)	32 (100%)	0	0	100	100
1	DG	161/1048 (15%)	155 (96%)	6 (4%)	0	100	100
1	Dg	32/1048 (3%)	32 (100%)	0	0	100	100
1	EG	161/1048 (15%)	157 (98%)	4 (2%)	0	100	100
1	Eg	32/1048 (3%)	32 (100%)	0	0	100	100
1	FG	161/1048 (15%)	152 (94%)	9 (6%)	0	100	100
1	Fg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	GG	161/1048 (15%)	152 (94%)	9 (6%)	0	100	100
1	Gg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	HG	161/1048 (15%)	150 (93%)	11 (7%)	0	100	100
1	Hg	32/1048 (3%)	29 (91%)	3 (9%)	0	100	100
1	IG	161/1048 (15%)	152 (94%)	9 (6%)	0	100	100
1	Ig	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	JG	161/1048 (15%)	152 (94%)	9 (6%)	0	100	100
1	Jg	32/1048 (3%)	32 (100%)	0	0	100	100
1	KG	161/1048 (15%)	151 (94%)	10 (6%)	0	100	100
1	Kg	32/1048 (3%)	32 (100%)	0	0	100	100
1	LG	161/1048 (15%)	153 (95%)	8 (5%)	0	100	100
1	Lg	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	MG	161/1048 (15%)	158 (98%)	3 (2%)	0	100	100
1	Mg	32/1048 (3%)	32 (100%)	0	0	100	100
1	NG	161/1048 (15%)	154 (96%)	7 (4%)	0	100	100
1	OG	161/1048 (15%)	150 (93%)	11 (7%)	0	100	100
1	PG	161/1048 (15%)	153 (95%)	8 (5%)	0	100	100
1	VG	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	WG	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	XG	32/1048 (3%)	32 (100%)	0	0	100	100
1	YG	32/1048 (3%)	32 (100%)	0	0	100	100
1	ZG	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
2	AD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	Ad	135/163 (83%)	131 (97%)	4 (3%)	0	100	100
2	BD	138/163 (85%)	130 (94%)	8 (6%)	0	100	100
2	Bd	135/163 (83%)	132 (98%)	3 (2%)	0	100	100
2	CD	138/163 (85%)	129 (94%)	9 (6%)	0	100	100
2	Cd	135/163 (83%)	132 (98%)	3 (2%)	0	100	100
2	DD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
2	Dd	135/163 (83%)	130 (96%)	5 (4%)	0	100	100
2	ED	138/163 (85%)	135 (98%)	3 (2%)	0	100	100
2	Ed	135/163 (83%)	125 (93%)	10 (7%)	0	100	100
2	FD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
2	Fd	135/163 (83%)	127 (94%)	8 (6%)	0	100	100
2	GD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
2	Gd	135/163 (83%)	125 (93%)	10 (7%)	0	100	100
2	HD	138/163 (85%)	133 (96%)	5 (4%)	0	100	100
2	Hd	135/163 (83%)	127 (94%)	8 (6%)	0	100	100
2	ID	138/163 (85%)	129 (94%)	9 (6%)	0	100	100
2	Id	135/163 (83%)	127 (94%)	8 (6%)	0	100	100
2	JD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
2	Jd	135/163 (83%)	131 (97%)	4 (3%)	0	100	100
2	KD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
2	Kd	135/163 (83%)	129 (96%)	6 (4%)	0	100	100
2	LD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
2	Ld	135/163 (83%)	131 (97%)	4 (3%)	0	100	100
2	MD	138/163 (85%)	130 (94%)	8 (6%)	0	100	100
2	Md	135/163 (83%)	129 (96%)	6 (4%)	0	100	100
3	AF	61/269 (23%)	55 (90%)	6 (10%)	0	100	100
3	Af	57/269 (21%)	56 (98%)	1 (2%)	0	100	100
3	BF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
3	Bf	57/269 (21%)	55 (96%)	2 (4%)	0	100	100
3	CF	61/269 (23%)	55 (90%)	6 (10%)	0	100	100
3	Cf	57/269 (21%)	51 (90%)	6 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	DF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
3	Df	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
3	EF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
3	Ef	57/269 (21%)	55 (96%)	2 (4%)	0	100	100
3	FF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
3	Ff	57/269 (21%)	55 (96%)	2 (4%)	0	100	100
3	GF	61/269 (23%)	56 (92%)	5 (8%)	0	100	100
3	Gf	57/269 (21%)	50 (88%)	7 (12%)	0	100	100
3	HF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
3	Hf	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
3	IF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
3	If	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
3	JF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
3	Jf	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
3	KF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
3	Kf	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
3	LF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
3	Lf	57/269 (21%)	55 (96%)	2 (4%)	0	100	100
3	MF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
3	Mf	57/269 (21%)	55 (96%)	2 (4%)	0	100	100
3	VF	61/269 (23%)	55 (90%)	6 (10%)	0	100	100
3	WF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
3	XF	61/269 (23%)	56 (92%)	5 (8%)	0	100	100
3	YF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
3	ZF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
4	AH	256/361 (71%)	242 (94%)	14 (6%)	0	100	100
4	BH	256/361 (71%)	243 (95%)	13 (5%)	0	100	100
4	CH	256/361 (71%)	241 (94%)	15 (6%)	0	100	100
4	DH	256/361 (71%)	237 (93%)	19 (7%)	0	100	100
4	EH	256/361 (71%)	246 (96%)	10 (4%)	0	100	100
4	FH	256/361 (71%)	248 (97%)	8 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	GH	256/361 (71%)	237 (93%)	19 (7%)	0	100	100
4	HH	256/361 (71%)	240 (94%)	16 (6%)	0	100	100
4	IH	256/361 (71%)	244 (95%)	12 (5%)	0	100	100
4	JH	256/361 (71%)	239 (93%)	17 (7%)	0	100	100
4	KH	256/361 (71%)	238 (93%)	18 (7%)	0	100	100
4	LH	256/361 (71%)	238 (93%)	18 (7%)	0	100	100
4	MH	256/361 (71%)	235 (92%)	21 (8%)	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%)	229 (96%)	10 (4%)	0	100	100
4	YH	239/361 (66%)	222 (93%)	17 (7%)	0	100	100
4	ZH	239/361 (66%)	229 (96%)	10 (4%)	0	100	100
5	AK	149/189 (79%)	144 (97%)	5 (3%)	0	100	100
5	BK	149/189 (79%)	140 (94%)	9 (6%)	0	100	100
5	CK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
5	DK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
5	EK	149/189 (79%)	142 (95%)	7 (5%)	0	100	100
5	FK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
5	GK	149/189 (79%)	141 (95%)	8 (5%)	0	100	100
5	HK	149/189 (79%)	144 (97%)	5 (3%)	0	100	100
5	IK	149/189 (79%)	140 (94%)	9 (6%)	0	100	100
5	JK	149/189 (79%)	142 (95%)	7 (5%)	0	100	100
5	KK	149/189 (79%)	137 (92%)	12 (8%)	0	100	100
5	LK	149/189 (79%)	141 (95%)	8 (5%)	0	100	100
5	MK	149/189 (79%)	144 (97%)	5 (3%)	0	100	100
6	AL	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
6	BL	169/249 (68%)	163 (96%)	6 (4%)	0	100	100
6	CL	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
6	DL	169/249 (68%)	160 (95%)	9 (5%)	0	100	100
6	EL	169/249 (68%)	160 (95%)	9 (5%)	0	100	100
6	FL	169/249 (68%)	161 (95%)	8 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	GL	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
6	HL	169/249 (68%)	163 (96%)	6 (4%)	0	100	100
6	IL	169/249 (68%)	163 (96%)	6 (4%)	0	100	100
6	JL	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
6	KL	169/249 (68%)	163 (96%)	6 (4%)	0	100	100
6	LL	169/249 (68%)	159 (94%)	10 (6%)	0	100	100
6	ML	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
7	AM	206/320 (64%)	187 (91%)	19 (9%)	0	100	100
7	BM	206/320 (64%)	183 (89%)	23 (11%)	0	100	100
7	CM	206/320 (64%)	185 (90%)	21 (10%)	0	100	100
7	DM	206/320 (64%)	193 (94%)	13 (6%)	0	100	100
7	EM	206/320 (64%)	191 (93%)	15 (7%)	0	100	100
7	FM	206/320 (64%)	188 (91%)	18 (9%)	0	100	100
7	GM	206/320 (64%)	186 (90%)	20 (10%)	0	100	100
7	HM	206/320 (64%)	186 (90%)	20 (10%)	0	100	100
7	IM	206/320 (64%)	188 (91%)	18 (9%)	0	100	100
7	JM	206/320 (64%)	183 (89%)	23 (11%)	0	100	100
7	KM	206/320 (64%)	191 (93%)	15 (7%)	0	100	100
7	LM	206/320 (64%)	186 (90%)	20 (10%)	0	100	100
7	MM	206/320 (64%)	181 (88%)	25 (12%)	0	100	100
8	AN	76/124 (61%)	72 (95%)	4 (5%)	0	100	100
8	BN	76/124 (61%)	72 (95%)	4 (5%)	0	100	100
8	CN	76/124 (61%)	69 (91%)	7 (9%)	0	100	100
8	DN	76/124 (61%)	68 (90%)	8 (10%)	0	100	100
8	EN	76/124 (61%)	69 (91%)	7 (9%)	0	100	100
8	FN	76/124 (61%)	67 (88%)	9 (12%)	0	100	100
8	GN	76/124 (61%)	71 (93%)	5 (7%)	0	100	100
8	HN	76/124 (61%)	71 (93%)	5 (7%)	0	100	100
8	IN	76/124 (61%)	68 (90%)	8 (10%)	0	100	100
8	JN	76/124 (61%)	67 (88%)	9 (12%)	0	100	100
8	KN	76/124 (61%)	69 (91%)	7 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	195 (94%)	12 (6%)	0	100	100
11	BC	207/303 (68%)	198 (96%)	9 (4%)	0	100	100
11	CC	207/303 (68%)	197 (95%)	10 (5%)	0	100	100
11	DC	241/303 (80%)	225 (93%)	16 (7%)	0	100	100
11	EC	207/303 (68%)	193 (93%)	14 (7%)	0	100	100
11	FC	207/303 (68%)	192 (93%)	15 (7%)	0	100	100
11	GC	207/303 (68%)	188 (91%)	19 (9%)	0	100	100
11	HC	241/303 (80%)	227 (94%)	14 (6%)	0	100	100
11	IC	241/303 (80%)	230 (95%)	11 (5%)	0	100	100
11	JC	207/303 (68%)	196 (95%)	11 (5%)	0	100	100
11	KC	207/303 (68%)	195 (94%)	12 (6%)	0	100	100
11	LC	241/303 (80%)	230 (95%)	11 (5%)	0	100	100
11	MC	241/303 (80%)	226 (94%)	15 (6%)	0	100	100
All	All	23724/70112 (34%)	22355 (94%)	1369 (6%)	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%)	110 (82%)	25 (18%)	1	9
1	Ag	31/765 (4%)	26 (84%)	5 (16%)	2	12
1	BG	135/765 (18%)	116 (86%)	19 (14%)	3	15
1	Bg	31/765 (4%)	25 (81%)	6 (19%)	1	8
1	CG	135/765 (18%)	116 (86%)	19 (14%)	3	15
1	Cg	31/765 (4%)	27 (87%)	4 (13%)	4	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	DG	135/765 (18%)	114 (84%)	21 (16%)	2	13
1	Dg	31/765 (4%)	21 (68%)	10 (32%)	0	2
1	EG	135/765 (18%)	116 (86%)	19 (14%)	3	15
1	Eg	31/765 (4%)	27 (87%)	4 (13%)	4	17
1	FG	135/765 (18%)	114 (84%)	21 (16%)	2	13
1	Fg	31/765 (4%)	27 (87%)	4 (13%)	4	17
1	GG	135/765 (18%)	111 (82%)	24 (18%)	2	10
1	Gg	31/765 (4%)	26 (84%)	5 (16%)	2	12
1	HG	135/765 (18%)	111 (82%)	24 (18%)	2	10
1	Hg	31/765 (4%)	29 (94%)	2 (6%)	15	37
1	IG	135/765 (18%)	112 (83%)	23 (17%)	2	11
1	Ig	31/765 (4%)	23 (74%)	8 (26%)	0	4
1	JG	135/765 (18%)	113 (84%)	22 (16%)	2	12
1	Jg	31/765 (4%)	23 (74%)	8 (26%)	0	4
1	KG	135/765 (18%)	115 (85%)	20 (15%)	3	14
1	Kg	31/765 (4%)	24 (77%)	7 (23%)	1	6
1	LG	135/765 (18%)	114 (84%)	21 (16%)	2	13
1	Lg	31/765 (4%)	23 (74%)	8 (26%)	0	4
1	MG	135/765 (18%)	118 (87%)	17 (13%)	4	17
1	Mg	31/765 (4%)	24 (77%)	7 (23%)	1	6
1	NG	135/765 (18%)	113 (84%)	22 (16%)	2	12
1	OG	135/765 (18%)	111 (82%)	24 (18%)	2	10
1	PG	135/765 (18%)	116 (86%)	19 (14%)	3	15
1	VG	31/765 (4%)	27 (87%)	4 (13%)	4	17
1	WG	31/765 (4%)	26 (84%)	5 (16%)	2	12
1	XG	31/765 (4%)	24 (77%)	7 (23%)	1	6
1	YG	31/765 (4%)	25 (81%)	6 (19%)	1	8
1	ZG	31/765 (4%)	24 (77%)	7 (23%)	1	6
2	AD	121/139 (87%)	100 (83%)	21 (17%)	2	11
2	Ad	118/139 (85%)	99 (84%)	19 (16%)	2	12
2	BD	121/139 (87%)	105 (87%)	16 (13%)	4	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	Bd	118/139 (85%)	106 (90%)	12 (10%)	7	23
2	CD	121/139 (87%)	102 (84%)	19 (16%)	2	12
2	Cd	118/139 (85%)	104 (88%)	14 (12%)	5	19
2	DD	121/139 (87%)	105 (87%)	16 (13%)	4	16
2	Dd	118/139 (85%)	100 (85%)	18 (15%)	3	13
2	ED	121/139 (87%)	105 (87%)	16 (13%)	4	16
2	Ed	118/139 (85%)	103 (87%)	15 (13%)	4	17
2	FD	121/139 (87%)	104 (86%)	17 (14%)	3	15
2	Fd	118/139 (85%)	99 (84%)	19 (16%)	2	12
2	GD	121/139 (87%)	103 (85%)	18 (15%)	3	14
2	Gd	118/139 (85%)	101 (86%)	17 (14%)	3	14
2	HD	121/139 (87%)	107 (88%)	14 (12%)	5	19
2	Hd	118/139 (85%)	100 (85%)	18 (15%)	3	13
2	ID	121/139 (87%)	108 (89%)	13 (11%)	6	22
2	Id	118/139 (85%)	103 (87%)	15 (13%)	4	17
2	JD	121/139 (87%)	105 (87%)	16 (13%)	4	16
2	Jd	118/139 (85%)	97 (82%)	21 (18%)	2	10
2	KD	121/139 (87%)	107 (88%)	14 (12%)	5	19
2	Kd	118/139 (85%)	101 (86%)	17 (14%)	3	14
2	LD	121/139 (87%)	104 (86%)	17 (14%)	3	15
2	Ld	118/139 (85%)	100 (85%)	18 (15%)	3	13
2	MD	121/139 (87%)	102 (84%)	19 (16%)	2	12
2	Md	118/139 (85%)	106 (90%)	12 (10%)	7	23
3	AF	53/237 (22%)	48 (91%)	5 (9%)	8	26
3	Af	49/237 (21%)	43 (88%)	6 (12%)	5	18
3	BF	53/237 (22%)	46 (87%)	7 (13%)	4	16
3	Bf	49/237 (21%)	39 (80%)	10 (20%)	1	7
3	CF	53/237 (22%)	48 (91%)	5 (9%)	8	26
3	Cf	49/237 (21%)	40 (82%)	9 (18%)	1	10
3	DF	53/237 (22%)	47 (89%)	6 (11%)	5	20
3	Df	49/237 (21%)	44 (90%)	5 (10%)	7	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	EF	53/237 (22%)	48 (91%)	5 (9%)	8	26
3	Ef	49/237 (21%)	38 (78%)	11 (22%)	1	6
3	FF	53/237 (22%)	45 (85%)	8 (15%)	3	13
3	Ff	49/237 (21%)	44 (90%)	5 (10%)	7	23
3	GF	53/237 (22%)	49 (92%)	4 (8%)	12	33
3	Gf	49/237 (21%)	43 (88%)	6 (12%)	5	18
3	HF	53/237 (22%)	45 (85%)	8 (15%)	3	13
3	Hf	49/237 (21%)	39 (80%)	10 (20%)	1	7
3	IF	53/237 (22%)	47 (89%)	6 (11%)	5	20
3	If	49/237 (21%)	39 (80%)	10 (20%)	1	7
3	JF	53/237 (22%)	48 (91%)	5 (9%)	8	26
3	Jf	49/237 (21%)	45 (92%)	4 (8%)	10	31
3	KF	53/237 (22%)	43 (81%)	10 (19%)	1	9
3	Kf	49/237 (21%)	41 (84%)	8 (16%)	2	12
3	LF	53/237 (22%)	46 (87%)	7 (13%)	4	16
3	Lf	49/237 (21%)	41 (84%)	8 (16%)	2	12
3	MF	53/237 (22%)	49 (92%)	4 (8%)	12	33
3	Mf	49/237 (21%)	44 (90%)	5 (10%)	7	23
3	VF	53/237 (22%)	43 (81%)	10 (19%)	1	9
3	WF	53/237 (22%)	50 (94%)	3 (6%)	18	40
3	XF	53/237 (22%)	48 (91%)	5 (9%)	8	26
3	YF	53/237 (22%)	46 (87%)	7 (13%)	4	16
3	ZF	53/237 (22%)	47 (89%)	6 (11%)	5	20
4	AH	220/300 (73%)	199 (90%)	21 (10%)	8	25
4	BH	220/300 (73%)	194 (88%)	26 (12%)	5	19
4	CH	220/300 (73%)	195 (89%)	25 (11%)	5	20
4	DH	220/300 (73%)	200 (91%)	20 (9%)	9	28
4	EH	220/300 (73%)	189 (86%)	31 (14%)	3	15
4	FH	220/300 (73%)	192 (87%)	28 (13%)	4	17
4	GH	220/300 (73%)	190 (86%)	30 (14%)	3	15
4	HH	220/300 (73%)	193 (88%)	27 (12%)	4	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	IH	220/300 (73%)	192 (87%)	28 (13%)	4	17
4	JH	220/300 (73%)	190 (86%)	30 (14%)	3	15
4	KH	220/300 (73%)	190 (86%)	30 (14%)	3	15
4	LH	220/300 (73%)	190 (86%)	30 (14%)	3	15
4	MH	220/300 (73%)	190 (86%)	30 (14%)	3	15
4	VH	207/300 (69%)	181 (87%)	26 (13%)	4	17
4	WH	207/300 (69%)	184 (89%)	23 (11%)	6	20
4	XH	207/300 (69%)	176 (85%)	31 (15%)	3	13
4	YH	207/300 (69%)	176 (85%)	31 (15%)	3	13
4	ZH	207/300 (69%)	187 (90%)	20 (10%)	8	25
5	AK	129/163 (79%)	108 (84%)	21 (16%)	2	12
5	BK	129/163 (79%)	107 (83%)	22 (17%)	2	11
5	CK	129/163 (79%)	105 (81%)	24 (19%)	1	9
5	DK	129/163 (79%)	108 (84%)	21 (16%)	2	12
5	EK	129/163 (79%)	109 (84%)	20 (16%)	2	13
5	FK	129/163 (79%)	113 (88%)	16 (12%)	4	18
5	GK	129/163 (79%)	112 (87%)	17 (13%)	4	16
5	HK	129/163 (79%)	108 (84%)	21 (16%)	2	12
5	IK	129/163 (79%)	109 (84%)	20 (16%)	2	13
5	JK	129/163 (79%)	110 (85%)	19 (15%)	3	14
5	KK	129/163 (79%)	110 (85%)	19 (15%)	3	14
5	LK	129/163 (79%)	107 (83%)	22 (17%)	2	11
5	MK	129/163 (79%)	111 (86%)	18 (14%)	3	15
6	AL	148/203 (73%)	136 (92%)	12 (8%)	11	31
6	BL	148/203 (73%)	130 (88%)	18 (12%)	5	18
6	CL	148/203 (73%)	122 (82%)	26 (18%)	2	10
6	DL	148/203 (73%)	128 (86%)	20 (14%)	4	15
6	EL	148/203 (73%)	125 (84%)	23 (16%)	2	13
6	FL	148/203 (73%)	138 (93%)	10 (7%)	14	36
6	GL	148/203 (73%)	131 (88%)	17 (12%)	5	19
6	HL	148/203 (73%)	134 (90%)	14 (10%)	8	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	IL	148/203 (73%)	132 (89%)	16 (11%)	6	22
6	JL	148/203 (73%)	135 (91%)	13 (9%)	9	29
6	KL	148/203 (73%)	132 (89%)	16 (11%)	6	22
6	LL	148/203 (73%)	132 (89%)	16 (11%)	6	22
6	ML	148/203 (73%)	129 (87%)	19 (13%)	4	17
7	AM	175/276 (63%)	144 (82%)	31 (18%)	2	10
7	BM	175/276 (63%)	150 (86%)	25 (14%)	3	14
7	CM	175/276 (63%)	148 (85%)	27 (15%)	2	13
7	DM	175/276 (63%)	147 (84%)	28 (16%)	2	12
7	EM	175/276 (63%)	149 (85%)	26 (15%)	3	14
7	FM	175/276 (63%)	150 (86%)	25 (14%)	3	14
7	GM	175/276 (63%)	151 (86%)	24 (14%)	3	15
7	HM	175/276 (63%)	149 (85%)	26 (15%)	3	14
7	IM	175/276 (63%)	151 (86%)	24 (14%)	3	15
7	JM	175/276 (63%)	141 (81%)	34 (19%)	1	8
7	KM	175/276 (63%)	149 (85%)	26 (15%)	3	14
7	LM	175/276 (63%)	151 (86%)	24 (14%)	3	15
7	MM	175/276 (63%)	149 (85%)	26 (15%)	3	14
8	AN	66/107 (62%)	58 (88%)	8 (12%)	5	18
8	BN	66/107 (62%)	59 (89%)	7 (11%)	6	22
8	CN	66/107 (62%)	55 (83%)	11 (17%)	2	11
8	DN	66/107 (62%)	60 (91%)	6 (9%)	9	28
8	EN	66/107 (62%)	58 (88%)	8 (12%)	5	18
8	FN	66/107 (62%)	52 (79%)	14 (21%)	1	6
8	GN	66/107 (62%)	59 (89%)	7 (11%)	6	22
8	HN	66/107 (62%)	56 (85%)	10 (15%)	3	13
8	IN	66/107 (62%)	55 (83%)	11 (17%)	2	11
8	JN	66/107 (62%)	57 (86%)	9 (14%)	3	15
8	KN	66/107 (62%)	53 (80%)	13 (20%)	1	8
8	LN	66/107 (62%)	53 (80%)	13 (20%)	1	8
8	MN	66/107 (62%)	55 (83%)	11 (17%)	2	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	AC	178/257 (69%)	146 (82%)	32 (18%)	2	10
11	BC	178/257 (69%)	149 (84%)	29 (16%)	2	12
11	CC	178/257 (69%)	147 (83%)	31 (17%)	2	11
11	DC	203/257 (79%)	171 (84%)	32 (16%)	2	12
11	EC	178/257 (69%)	150 (84%)	28 (16%)	2	12
11	FC	178/257 (69%)	154 (86%)	24 (14%)	4	15
11	GC	178/257 (69%)	154 (86%)	24 (14%)	4	15
11	HC	203/257 (79%)	169 (83%)	34 (17%)	2	11
11	IC	203/257 (79%)	168 (83%)	35 (17%)	2	11
11	JC	178/257 (69%)	158 (89%)	20 (11%)	6	20
11	KC	178/257 (69%)	158 (89%)	20 (11%)	6	20
11	LC	203/257 (79%)	175 (86%)	28 (14%)	3	15
11	MC	203/257 (79%)	175 (86%)	28 (14%)	3	15
All	All	20484/55449 (37%)	17592 (86%)	2892 (14%)	5	15

All (2892) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AG	865	THR
1	AG	867	ASP
1	AG	869	MET
1	AG	880	ASP
1	AG	885	ILE
1	AG	886	LEU
1	AG	893	LYS
1	AG	900	ILE
1	AG	902	SER
1	AG	910	ASP
1	AG	911	LYS
1	AG	913	VAL
1	AG	930	ILE
1	AG	939	THR
1	AG	944	LEU
1	AG	947	ARG
1	AG	953	LEU
1	AG	962	SER
1	AG	965	LEU

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Mol	Chain	Res	Type
1	AG	972	PHE
1	AG	1010	THR
1	AG	1017	GLN
1	AG	1024	ASN
1	AG	1044	ASP
1	AG	1045	VAL
2	GD	24	LYS
2	GD	30	ILE
2	GD	41	LEU
2	GD	50	ASP
2	GD	52	MET
2	GD	55	MET
2	GD	75	ASN
2	GD	79	LEU
2	GD	84	SER
2	GD	91	ILE
2	GD	98	ILE
2	GD	115	VAL
2	GD	119	ILE
2	GD	124	LYS
2	GD	127	SER
2	GD	135	ILE
2	GD	147	VAL
2	GD	162	TYR
3	GF	213	GLN
3	GF	215	VAL
3	GF	223	ILE
3	GF	232	VAL
1	Gg	791	GLN
1	Gg	793	GLU
1	Gg	808	LEU
1	Gg	817	THR
1	Gg	819	VAL
4	GH	108	ASP
4	GH	138	GLU
4	GH	147	THR
4	GH	176	VAL
4	GH	180	VAL
4	GH	191	ILE
4	GH	212	THR
4	GH	213	LEU
4	GH	218	THR

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Mol	Chain	Res	Type
4	GH	219	LYS
4	GH	220	LEU
4	GH	241	LEU
4	GH	242	ILE
4	GH	245	GLN
4	GH	248	VAL
4	GH	249	ASP
4	GH	250	TYR
4	GH	253	ASP
4	GH	256	VAL
4	GH	287	VAL
4	GH	292	SER
4	GH	296	VAL
4	GH	313	VAL
4	GH	317	LEU
4	GH	320	LEU
4	GH	325	LEU
4	GH	338	GLU
4	GH	344	VAL
4	GH	347	VAL
4	GH	353	VAL
5	GK	45	VAL
5	GK	65	ILE
5	GK	70	VAL
5	GK	83	LEU
5	GK	92	ASN
5	GK	98	LEU
5	GK	99	LEU
5	GK	106	LEU
5	GK	111	LYS
5	GK	126	VAL
5	GK	134	LEU
5	GK	159	LEU
5	GK	162	ASP
5	GK	170	LEU
5	GK	180	VAL
5	GK	182	ILE
5	GK	183	THR
6	GL	57	VAL
6	GL	109	LEU
6	GL	125	LEU
6	GL	129	THR

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Mol	Chain	Res	Type
6	GL	131	LYS
6	GL	134	MET
6	GL	140	LEU
6	GL	155	LEU
6	GL	163	ILE
6	GL	169	THR
6	GL	170	ASP
6	GL	172	VAL
6	GL	174	SER
6	GL	175	ARG
6	GL	193	LEU
6	GL	212	ASN
6	GL	217	ASN
7	GM	114	ASN
7	GM	129	LEU
7	GM	131	THR
7	GM	134	LEU
7	GM	146	LEU
7	GM	150	ILE
7	GM	152	LEU
7	GM	154	LYS
7	GM	173	LEU
7	GM	174	GLN
7	GM	175	ILE
7	GM	176	VAL
7	GM	177	LEU
7	GM	180	ASP
7	GM	182	LYS
7	GM	191	LEU
7	GM	202	LEU
7	GM	204	LEU
7	GM	207	ILE
7	GM	212	LEU
7	GM	257	ASP
7	GM	263	ILE
7	GM	292	MET
7	GM	308	ASP
8	GN	62	ASN
8	GN	77	ASP
8	GN	84	CYS
8	GN	94	GLN
8	GN	101	VAL

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Mol	Chain	Res	Type
8	GN	111	GLU
8	GN	114	LEU
2	Gd	30	ILE
2	Gd	36	ASP
2	Gd	54	GLU
2	Gd	58	VAL
2	Gd	59	GLU
2	Gd	60	LYS
2	Gd	61	VAL
2	Gd	63	THR
2	Gd	82	ARG
2	Gd	92	GLU
2	Gd	97	ARG
2	Gd	126	GLU
2	Gd	128	LEU
2	Gd	142	LYS
2	Gd	145	ILE
2	Gd	147	VAL
2	Gd	150	ASN
3	Gf	212	ILE
3	Gf	215	VAL
3	Gf	216	ILE
3	Gf	243	MET
3	Gf	244	VAL
3	Gf	253	ARG
2	HD	26	LYS
2	HD	38	THR
2	HD	51	SER
2	HD	52	MET
2	HD	55	MET
2	HD	82	ARG
2	HD	85	VAL
2	HD	108	VAL
2	HD	115	VAL
2	HD	117	VAL
2	HD	142	LYS
2	HD	147	VAL
2	HD	156	LEU
2	HD	162	TYR
3	HF	208	ILE
3	HF	215	VAL
3	HF	216	ILE

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Mol	Chain	Res	Type
3	HF	223	ILE
3	HF	230	LEU
3	HF	231	THR
3	HF	232	VAL
3	HF	238	ILE
1	Hg	800	ASP
1	Hg	811	ASP
2	Dd	31	ASN
2	Dd	36	ASP
2	Dd	41	LEU
2	Dd	43	GLU
2	Dd	52	MET
2	Dd	55	MET
2	Dd	60	LYS
2	Dd	61	VAL
2	Dd	85	VAL
2	Dd	91	ILE
2	Dd	92	GLU
2	Dd	108	VAL
2	Dd	115	VAL
2	Dd	123	THR
2	Dd	132	LEU
2	Dd	141	LYS
2	Dd	142	LYS
2	Dd	146	HIS
4	HH	108	ASP
4	HH	122	LEU
4	HH	137	SER
4	HH	147	THR
4	HH	168	VAL
4	HH	180	VAL
4	HH	205	GLN
4	HH	211	ASN
4	HH	226	LEU
4	HH	239	LEU
4	HH	241	LEU
4	HH	248	VAL
4	HH	250	TYR
4	HH	253	ASP
4	HH	278	ASP
4	HH	279	LEU
4	HH	280	LEU

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Mol	Chain	Res	Type
4	HH	284	LEU
4	HH	287	VAL
4	HH	296	VAL
4	HH	297	VAL
4	HH	307	SER
4	HH	320	LEU
4	HH	338	GLU
4	HH	345	LEU
4	HH	356	LEU
4	HH	361	LEU
5	HK	40	LYS
5	HK	45	VAL
5	HK	58	THR
5	HK	63	LYS
5	HK	65	ILE
5	HK	70	VAL
5	HK	72	GLN
5	HK	73	ASN
5	HK	98	LEU
5	HK	101	GLU
5	HK	106	LEU
5	HK	111	LYS
5	HK	116	VAL
5	HK	144	LEU
5	HK	149	VAL
5	HK	153	ILE
5	HK	156	THR
5	HK	159	LEU
5	HK	170	LEU
5	HK	180	VAL
5	HK	183	THR
6	HL	51	GLN
6	HL	57	VAL
6	HL	91	VAL
6	HL	93	LEU
6	HL	109	LEU
6	HL	131	LYS
6	HL	148	LEU
6	HL	155	LEU
6	HL	165	VAL
6	HL	170	ASP
6	HL	172	VAL

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Mol	Chain	Res	Type
6	HL	174	SER
6	HL	203	LEU
6	HL	212	ASN
7	HM	127	ASN
7	HM	129	LEU
7	HM	134	LEU
7	HM	144	THR
7	HM	146	LEU
7	HM	149	ASN
7	HM	152	LEU
7	HM	153	GLN
7	HM	162	VAL
7	HM	175	ILE
7	HM	176	VAL
7	HM	182	LYS
7	HM	183	VAL
7	HM	184	LEU
7	HM	188	PHE
7	HM	204	LEU
7	HM	207	ILE
7	HM	212	LEU
7	HM	222	ILE
7	HM	233	VAL
7	HM	260	VAL
7	HM	290	ASP
7	HM	292	MET
7	HM	299	LEU
7	HM	304	TRP
7	HM	308	ASP
8	HN	44	LYS
8	HN	51	CYS
8	HN	70	CYS
8	HN	81	LEU
8	HN	91	VAL
8	HN	95	LEU
8	HN	101	VAL
8	HN	111	GLU
8	HN	114	LEU
8	HN	115	GLN
2	Hd	26	LYS
2	Hd	27	LYS
2	Hd	36	ASP

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Mol	Chain	Res	Type
2	Hd	41	LEU
2	Hd	53	LEU
2	Hd	54	GLU
2	Hd	58	VAL
2	Hd	61	VAL
2	Hd	63	THR
2	Hd	70	THR
2	Hd	73	ILE
2	Hd	78	ASN
2	Hd	88	SER
2	Hd	94	LEU
2	Hd	98	ILE
2	Hd	115	VAL
2	Hd	150	ASN
2	Hd	153	VAL
3	Hf	212	ILE
3	Hf	215	VAL
3	Hf	216	ILE
3	Hf	219	ARG
3	Hf	223	ILE
3	Hf	233	ARG
3	Hf	244	VAL
3	Hf	247	ILE
3	Hf	250	LEU
3	Hf	262	ILE
1	Bg	796	GLN
1	Bg	800	ASP
1	Bg	808	LEU
1	Bg	809	VAL
1	Bg	815	VAL
1	Bg	819	VAL
1	BG	864	LYS
1	BG	865	THR
1	BG	880	ASP
1	BG	885	ILE
1	BG	900	ILE
1	BG	902	SER
1	BG	910	ASP
1	BG	911	LYS
1	BG	912	MET
1	BG	913	VAL
1	BG	916	PHE

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Mol	Chain	Res	Type
1	BG	930	ILE
1	BG	944	LEU
1	BG	953	LEU
1	BG	962	SER
1	BG	965	LEU
1	BG	972	PHE
1	BG	1010	THR
1	BG	1028	THR
2	ID	51	SER
2	ID	73	ILE
2	ID	78	ASN
2	ID	85	VAL
2	ID	103	HIS
2	ID	108	VAL
2	ID	115	VAL
2	ID	124	LYS
2	ID	126	GLU
2	ID	147	VAL
2	ID	154	VAL
2	ID	160	LYS
2	ID	161	ILE
3	IF	215	VAL
3	IF	223	ILE
3	IF	230	LEU
3	IF	231	THR
3	IF	243	MET
3	IF	256	THR
1	Ig	793	GLU
1	Ig	795	GLN
1	Ig	800	ASP
1	Ig	808	LEU
1	Ig	809	VAL
1	Ig	814	GLN
1	Ig	817	THR
1	Ig	819	VAL
4	IH	108	ASP
4	IH	110	LYS
4	IH	125	GLU
4	IH	147	THR
4	IH	152	THR
4	IH	180	VAL
4	IH	185	THR

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Mol	Chain	Res	Type
4	IH	203	ASN
4	IH	215	ILE
4	IH	218	THR
4	IH	219	LYS
4	IH	228	VAL
4	IH	230	LEU
4	IH	238	MET
4	IH	239	LEU
4	IH	240	THR
4	IH	242	ILE
4	IH	245	GLN
4	IH	248	VAL
4	IH	255	ARG
4	IH	256	VAL
4	IH	257	GLN
4	IH	285	GLU
4	IH	313	VAL
4	IH	332	ASP
4	IH	334	THR
4	IH	353	VAL
4	IH	361	LEU
5	IK	45	VAL
5	IK	46	ASP
5	IK	50	ASP
5	IK	75	LEU
5	IK	83	LEU
5	IK	88	SER
5	IK	98	LEU
5	IK	106	LEU
5	IK	108	GLN
5	IK	111	LYS
5	IK	112	ILE
5	IK	116	VAL
5	IK	126	VAL
5	IK	144	LEU
5	IK	153	ILE
5	IK	159	LEU
5	IK	180	VAL
5	IK	182	ILE
5	IK	183	THR
5	IK	188	VAL
6	IL	57	VAL

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Mol	Chain	Res	Type
6	IL	91	VAL
6	IL	100	ASP
6	IL	109	LEU
6	IL	121	ASP
6	IL	129	THR
6	IL	131	LYS
6	IL	137	SER
6	IL	148	LEU
6	IL	165	VAL
6	IL	172	VAL
6	IL	174	SER
6	IL	190	MET
6	IL	203	LEU
6	IL	212	ASN
6	IL	217	ASN
7	IM	115	ARG
7	IM	116	PHE
7	IM	129	LEU
7	IM	131	THR
7	IM	134	LEU
7	IM	146	LEU
7	IM	149	ASN
7	IM	152	LEU
7	IM	162	VAL
7	IM	176	VAL
7	IM	180	ASP
7	IM	182	LYS
7	IM	184	LEU
7	IM	188	PHE
7	IM	190	ASN
7	IM	194	LEU
7	IM	202	LEU
7	IM	204	LEU
7	IM	205	TYR
7	IM	207	ILE
7	IM	212	LEU
7	IM	221	LYS
7	IM	292	MET
7	IM	303	GLU
8	IN	44	LYS
8	IN	70	CYS
8	IN	71	THR

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Mol	Chain	Res	Type
8	IN	78	LEU
8	IN	81	LEU
8	IN	86	LEU
8	IN	94	GLN
8	IN	95	LEU
8	IN	102	VAL
8	IN	107	TYR
8	IN	112	CYS
2	Id	26	LYS
2	Id	41	LEU
2	Id	61	VAL
2	Id	63	THR
2	Id	70	THR
2	Id	71	LEU
2	Id	79	LEU
2	Id	104	PHE
2	Id	108	VAL
2	Id	115	VAL
2	Id	123	THR
2	Id	128	LEU
2	Id	138	GLN
2	Id	150	ASN
2	Id	153	VAL
3	If	208	ILE
3	If	212	ILE
3	If	216	ILE
3	If	230	LEU
3	If	238	ILE
3	If	244	VAL
3	If	248	ASP
3	If	250	LEU
3	If	255	LEU
3	If	261	VAL
2	JD	24	LYS
2	JD	25	PHE
2	JD	26	LYS
2	JD	30	ILE
2	JD	50	ASP
2	JD	51	SER
2	JD	54	GLU
2	JD	79	LEU
2	JD	85	VAL

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Mol	Chain	Res	Type
2	JD	108	VAL
2	JD	111	LYS
2	JD	115	VAL
2	JD	126	GLU
2	JD	128	LEU
2	JD	154	VAL
2	JD	156	LEU
3	JF	208	ILE
3	JF	215	VAL
3	JF	223	ILE
3	JF	232	VAL
3	JF	256	THR
1	Jg	800	ASP
1	Jg	802	LEU
1	Jg	808	LEU
1	Jg	809	VAL
1	Jg	814	GLN
1	Jg	817	THR
1	Jg	819	VAL
1	Jg	821	THR
4	JH	107	ILE
4	JH	108	ASP
4	JH	119	LEU
4	JH	134	TYR
4	JH	138	GLU
4	JH	147	THR
4	JH	152	THR
4	JH	154	THR
4	JH	158	VAL
4	JH	161	SER
4	JH	169	ILE
4	JH	180	VAL
4	JH	204	ILE
4	JH	219	LYS
4	JH	221	TYR
4	JH	235	THR
4	JH	238	MET
4	JH	248	VAL
4	JH	249	ASP
4	JH	254	LEU
4	JH	269	GLU
4	JH	278	ASP

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Mol	Chain	Res	Type
4	JH	284	LEU
4	JH	313	VAL
4	JH	315	THR
4	JH	320	LEU
4	JH	321	SER
4	JH	344	VAL
4	JH	345	LEU
4	JH	347	VAL
5	JK	40	LYS
5	JK	45	VAL
5	JK	50	ASP
5	JK	57	MET
5	JK	58	THR
5	JK	63	LYS
5	JK	70	VAL
5	JK	76	ILE
5	JK	92	ASN
5	JK	99	LEU
5	JK	125	SER
5	JK	126	VAL
5	JK	129	GLU
5	JK	144	LEU
5	JK	153	ILE
5	JK	156	THR
5	JK	162	ASP
5	JK	170	LEU
5	JK	183	THR
6	JL	47	TYR
6	JL	55	ARG
6	JL	57	VAL
6	JL	130	ASP
6	JL	154	LEU
6	JL	155	LEU
6	JL	165	VAL
6	JL	172	VAL
6	JL	174	SER
6	JL	185	GLN
6	JL	193	LEU
6	JL	204	LYS
6	JL	212	ASN
7	JM	127	ASN
7	JM	129	LEU

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Mol	Chain	Res	Type
7	JM	134	LEU
7	JM	137	TYR
7	JM	146	LEU
7	JM	149	ASN
7	JM	153	GLN
7	JM	160	ASN
7	JM	176	VAL
7	JM	180	ASP
7	JM	183	VAL
7	JM	184	LEU
7	JM	190	ASN
7	JM	191	LEU
7	JM	192	ARG
7	JM	202	LEU
7	JM	203	SER
7	JM	204	LEU
7	JM	210	ASP
7	JM	212	LEU
7	JM	214	ILE
7	JM	221	LYS
7	JM	222	ILE
7	JM	224	LEU
7	JM	245	TYR
7	JM	263	ILE
7	JM	277	SER
7	JM	292	MET
7	JM	298	VAL
7	JM	301	MET
7	JM	303	GLU
7	JM	306	GLN
7	JM	308	ASP
7	JM	310	LYS
8	JN	62	ASN
8	JN	78	LEU
8	JN	82	MET
8	JN	84	CYS
8	JN	91	VAL
8	JN	95	LEU
8	JN	101	VAL
8	JN	114	LEU
8	JN	115	GLN
2	Jd	24	LYS

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Mol	Chain	Res	Type
2	Jd	32	ASN
2	Jd	36	ASP
2	Jd	52	MET
2	Jd	59	GLU
2	Jd	61	VAL
2	Jd	67	LYS
2	Jd	68	ASP
2	Jd	70	THR
2	Jd	73	ILE
2	Jd	79	LEU
2	Jd	97	ARG
2	Jd	108	VAL
2	Jd	115	VAL
2	Jd	119	ILE
2	Jd	123	THR
2	Jd	128	LEU
2	Jd	135	ILE
2	Jd	142	LYS
2	Jd	145	ILE
2	Jd	150	ASN
3	Jf	215	VAL
3	Jf	216	ILE
3	Jf	223	ILE
3	Jf	226	ASN
4	AH	108	ASP
4	AH	147	THR
4	AH	160	LEU
4	AH	180	VAL
4	AH	181	PHE
4	AH	205	GLN
4	AH	211	ASN
4	AH	212	THR
4	AH	225	ASN
4	AH	231	ARG
4	AH	233	LEU
4	AH	242	ILE
4	AH	248	VAL
4	AH	253	ASP
4	AH	257	GLN
4	AH	279	LEU
4	AH	285	GLU
4	AH	297	VAL

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Mol	Chain	Res	Type
4	AH	320	LEU
4	AH	325	LEU
4	AH	345	LEU
2	KD	35	ASP
2	KD	51	SER
2	KD	55	MET
2	KD	77	TYR
2	KD	79	LEU
2	KD	85	VAL
2	KD	114	SER
2	KD	118	LEU
2	KD	127	SER
2	KD	132	LEU
2	KD	135	ILE
2	KD	141	LYS
2	KD	154	VAL
2	KD	160	LYS
1	CG	865	THR
1	CG	869	MET
1	CG	880	ASP
1	CG	886	LEU
1	CG	895	LYS
1	CG	898	LYS
1	CG	900	ILE
1	CG	910	ASP
1	CG	913	VAL
1	CG	916	PHE
1	CG	918	THR
1	CG	925	GLU
1	CG	930	ILE
1	CG	944	LEU
1	CG	962	SER
1	CG	965	LEU
1	CG	972	PHE
1	CG	1010	THR
1	CG	1028	THR
11	CC	90	ASN
11	CC	92	ASP
11	CC	100	LEU
11	CC	101	VAL
11	CC	106	ILE
11	CC	113	GLU

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Mol	Chain	Res	Type
11	CC	118	LEU
11	CC	120	LEU
11	CC	128	ILE
11	CC	147	THR
11	CC	152	LEU
11	CC	166	LEU
11	CC	175	GLU
11	CC	196	LEU
11	CC	205	GLU
11	CC	212	LEU
11	CC	215	LYS
11	CC	216	LEU
11	CC	227	VAL
11	CC	231	ASP
11	CC	234	VAL
11	CC	235	THR
11	CC	241	ILE
11	CC	246	ARG
11	CC	248	LEU
11	CC	249	ARG
11	CC	250	ILE
11	CC	251	THR
11	CC	253	LEU
11	CC	258	VAL
11	CC	259	ASN
3	KF	208	ILE
3	KF	215	VAL
3	KF	216	ILE
3	KF	222	LEU
3	KF	223	ILE
3	KF	231	THR
3	KF	238	ILE
3	KF	250	LEU
3	KF	256	THR
3	KF	262	ILE
1	Kg	794	ILE
1	Kg	795	GLN
1	Kg	802	LEU
1	Kg	808	LEU
1	Kg	809	VAL
1	Kg	814	GLN
1	Kg	819	VAL

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Mol	Chain	Res	Type
4	KH	105	GLU
4	KH	108	ASP
4	KH	135	GLU
4	KH	147	THR
4	KH	180	VAL
4	KH	191	ILE
4	KH	195	ASP
4	KH	208	LYS
4	KH	218	THR
4	KH	226	LEU
4	KH	242	ILE
4	KH	245	GLN
4	KH	248	VAL
4	KH	249	ASP
4	KH	256	VAL
4	KH	278	ASP
4	KH	284	LEU
4	KH	287	VAL
4	KH	293	ARG
4	KH	313	VAL
4	KH	316	ASN
4	KH	317	LEU
4	KH	320	LEU
4	KH	327	SER
4	KH	334	THR
4	KH	344	VAL
4	KH	345	LEU
4	KH	346	LEU
4	KH	347	VAL
4	KH	353	VAL
5	KK	41	LEU
5	KK	50	ASP
5	KK	63	LYS
5	KK	70	VAL
5	KK	75	LEU
5	KK	77	SER
5	KK	83	LEU
5	KK	90	ARG
5	KK	92	ASN
5	KK	106	LEU
5	KK	111	LYS
5	KK	112	ILE

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Mol	Chain	Res	Type
5	KK	126	VAL
5	KK	144	LEU
5	KK	157	GLN
5	KK	162	ASP
5	KK	180	VAL
5	KK	182	ILE
5	KK	183	THR
6	KL	93	LEU
6	KL	112	GLN
6	KL	129	THR
6	KL	130	ASP
6	KL	143	ILE
6	KL	149	ASN
6	KL	155	LEU
6	KL	160	GLN
6	KL	172	VAL
6	KL	174	SER
6	KL	193	LEU
6	KL	203	LEU
6	KL	210	ASP
6	KL	212	ASN
6	KL	216	ASP
6	KL	230	GLU
7	KM	127	ASN
7	KM	129	LEU
7	KM	146	LEU
7	KM	149	ASN
7	KM	150	ILE
7	KM	152	LEU
7	KM	160	ASN
7	KM	176	VAL
7	KM	177	LEU
7	KM	180	ASP
7	KM	183	VAL
7	KM	185	ILE
7	KM	190	ASN
7	KM	192	ARG
7	KM	204	LEU
7	KM	205	TYR
7	KM	207	ILE
7	KM	212	LEU
7	KM	231	LEU

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Mol	Chain	Res	Type
7	KM	235	LEU
7	KM	245	TYR
7	KM	246	LEU
7	KM	257	ASP
7	KM	292	MET
7	KM	299	LEU
7	KM	303	GLU
8	KN	62	ASN
8	KN	67	THR
8	KN	69	TYR
8	KN	71	THR
8	KN	80	PHE
8	KN	84	CYS
8	KN	94	GLN
8	KN	105	ASP
8	KN	108	VAL
8	KN	111	GLU
8	KN	112	CYS
8	KN	115	GLN
8	KN	116	LYS
1	Ag	801	MET
1	Ag	808	LEU
1	Ag	814	GLN
1	Ag	817	THR
1	Ag	822	GLU
2	Kd	30	ILE
2	Kd	35	ASP
2	Kd	39	ILE
2	Kd	41	LEU
2	Kd	59	GLU
2	Kd	60	LYS
2	Kd	61	VAL
2	Kd	63	THR
2	Kd	91	ILE
2	Kd	93	GLU
2	Kd	94	LEU
2	Kd	115	VAL
2	Kd	118	LEU
2	Kd	119	ILE
2	Kd	132	LEU
2	Kd	142	LYS
2	Kd	150	ASN

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Mol	Chain	Res	Type
3	Kf	215	VAL
3	Kf	230	LEU
3	Kf	232	VAL
3	Kf	236	SER
3	Kf	238	ILE
3	Kf	244	VAL
3	Kf	247	ILE
3	Kf	260	GLN
2	LD	32	ASN
2	LD	35	ASP
2	LD	50	ASP
2	LD	51	SER
2	LD	53	LEU
2	LD	54	GLU
2	LD	62	ILE
2	LD	71	LEU
2	LD	85	VAL
2	LD	93	GLU
2	LD	100	LYS
2	LD	115	VAL
2	LD	123	THR
2	LD	127	SER
2	LD	134	ASP
2	LD	135	ILE
2	LD	156	LEU
3	LF	215	VAL
3	LF	222	LEU
3	LF	223	ILE
3	LF	231	THR
3	LF	238	ILE
3	LF	253	ARG
3	LF	256	THR
1	Lg	793	GLU
1	Lg	795	GLN
1	Lg	808	LEU
1	Lg	809	VAL
1	Lg	814	GLN
1	Lg	815	VAL
1	Lg	819	VAL
1	Lg	821	THR
4	LH	107	ILE
4	LH	108	ASP

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Mol	Chain	Res	Type
4	LH	109	LYS
4	LH	114	ASP
4	LH	115	MET
4	LH	119	LEU
4	LH	138	GLU
4	LH	147	THR
4	LH	180	VAL
4	LH	191	ILE
4	LH	216	GLN
4	LH	226	LEU
4	LH	231	ARG
4	LH	234	ASN
4	LH	242	ILE
4	LH	248	VAL
4	LH	250	TYR
4	LH	253	ASP
4	LH	254	LEU
4	LH	256	VAL
4	LH	284	LEU
4	LH	287	VAL
4	LH	293	ARG
4	LH	297	VAL
4	LH	313	VAL
4	LH	320	LEU
4	LH	342	SER
4	LH	344	VAL
4	LH	347	VAL
4	LH	356	LEU
5	LK	45	VAL
5	LK	46	ASP
5	LK	50	ASP
5	LK	67	VAL
5	LK	70	VAL
5	LK	75	LEU
5	LK	91	LEU
5	LK	98	LEU
5	LK	111	LYS
5	LK	112	ILE
5	LK	116	VAL
5	LK	117	THR
5	LK	125	SER
5	LK	126	VAL

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Mol	Chain	Res	Type
5	LK	129	GLU
5	LK	144	LEU
5	LK	149	VAL
5	LK	150	ASP
5	LK	153	ILE
5	LK	156	THR
5	LK	180	VAL
5	LK	183	THR
6	LL	57	VAL
6	LL	93	LEU
6	LL	113	ASP
6	LL	125	LEU
6	LL	127	ILE
6	LL	130	ASP
6	LL	143	ILE
6	LL	149	ASN
6	LL	155	LEU
6	LL	162	THR
6	LL	170	ASP
6	LL	172	VAL
6	LL	174	SER
6	LL	193	LEU
6	LL	204	LYS
6	LL	216	ASP
7	LM	131	THR
7	LM	134	LEU
7	LM	136	LEU
7	LM	138	LEU
7	LM	146	LEU
7	LM	152	LEU
7	LM	173	LEU
7	LM	175	ILE
7	LM	176	VAL
7	LM	177	LEU
7	LM	178	LYS
7	LM	191	LEU
7	LM	199	LYS
7	LM	208	LYS
7	LM	212	LEU
7	LM	221	LYS
7	LM	233	VAL
7	LM	245	TYR

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Mol	Chain	Res	Type
7	LM	263	ILE
7	LM	284	LEU
7	LM	292	MET
7	LM	299	LEU
7	LM	303	GLU
7	LM	308	ASP
8	LN	45	MET
8	LN	52	ASP
8	LN	72	ARG
8	LN	78	LEU
8	LN	81	LEU
8	LN	95	LEU
8	LN	100	LEU
8	LN	101	VAL
8	LN	102	VAL
8	LN	104	ASN
8	LN	108	VAL
8	LN	112	CYS
8	LN	115	GLN
2	CD	26	LYS
2	CD	30	ILE
2	CD	38	THR
2	CD	41	LEU
2	CD	43	GLU
2	CD	51	SER
2	CD	52	MET
2	CD	55	MET
2	CD	67	LYS
2	CD	70	THR
2	CD	78	ASN
2	CD	85	VAL
2	CD	86	ASP
2	CD	91	ILE
2	CD	118	LEU
2	CD	119	ILE
2	CD	127	SER
2	CD	156	LEU
2	CD	161	ILE
2	Ld	36	ASP
2	Ld	52	MET
2	Ld	54	GLU
2	Ld	60	LYS

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Mol	Chain	Res	Type
2	Ld	61	VAL
2	Ld	63	THR
2	Ld	69	ASN
2	Ld	72	THR
2	Ld	111	LYS
2	Ld	118	LEU
2	Ld	119	ILE
2	Ld	128	LEU
2	Ld	130	GLU
2	Ld	135	ILE
2	Ld	141	LYS
2	Ld	142	LYS
2	Ld	150	ASN
2	Ld	154	VAL
3	Lf	215	VAL
3	Lf	216	ILE
3	Lf	238	ILE
3	Lf	244	VAL
3	Lf	245	LYS
3	Lf	260	GLN
3	Lf	261	VAL
3	Lf	262	ILE
1	DG	865	THR
1	DG	873	LEU
1	DG	885	ILE
1	DG	898	LYS
1	DG	900	ILE
1	DG	902	SER
1	DG	911	LYS
1	DG	913	VAL
1	DG	916	PHE
1	DG	930	ILE
1	DG	939	THR
1	DG	944	LEU
1	DG	950	HIS
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	1024	ASN

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Mol	Chain	Res	Type
1	DG	1044	ASP
5	AK	45	VAL
5	AK	67	VAL
5	AK	70	VAL
5	AK	76	ILE
5	AK	91	LEU
5	AK	92	ASN
5	AK	98	LEU
5	AK	112	ILE
5	AK	114	ILE
5	AK	116	VAL
5	AK	120	SER
5	AK	126	VAL
5	AK	127	LYS
5	AK	129	GLU
5	AK	144	LEU
5	AK	147	GLN
5	AK	159	LEU
5	AK	162	ASP
5	AK	180	VAL
5	AK	182	ILE
5	AK	183	THR
2	MD	30	ILE
2	MD	32	ASN
2	MD	41	LEU
2	MD	55	MET
2	MD	61	VAL
2	MD	71	LEU
2	MD	73	ILE
2	MD	86	ASP
2	MD	109	LEU
2	MD	115	VAL
2	MD	123	THR
2	MD	124	LYS
2	MD	127	SER
2	MD	131	ILE
2	MD	136	ASP
2	MD	145	ILE
2	MD	147	VAL
2	MD	154	VAL
2	MD	160	LYS
3	MF	215	VAL

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Mol	Chain	Res	Type
3	MF	216	ILE
3	MF	231	THR
3	MF	253	ARG
1	Cg	793	GLU
1	Cg	810	GLN
1	Cg	812	TRP
1	Cg	815	VAL
1	Mg	793	GLU
1	Mg	794	ILE
1	Mg	795	GLN
1	Mg	808	LEU
1	Mg	812	TRP
1	Mg	814	GLN
1	Mg	817	THR
4	MH	107	ILE
4	MH	109	LYS
4	MH	134	TYR
4	MH	135	GLU
4	MH	147	THR
4	MH	158	VAL
4	MH	180	VAL
4	MH	211	ASN
4	MH	213	LEU
4	MH	218	THR
4	MH	231	ARG
4	MH	235	THR
4	MH	240	THR
4	MH	245	GLN
4	MH	248	VAL
4	MH	249	ASP
4	MH	250	TYR
4	MH	253	ASP
4	MH	264	LYS
4	MH	280	LEU
4	MH	287	VAL
4	MH	313	VAL
4	MH	316	ASN
4	MH	320	LEU
4	MH	321	SER
4	MH	327	SER
4	MH	334	THR
4	MH	344	VAL

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Mol	Chain	Res	Type
4	MH	355	GLN
4	MH	359	GLU
5	MK	50	ASP
5	MK	67	VAL
5	MK	72	GLN
5	MK	75	LEU
5	MK	76	ILE
5	MK	86	ASP
5	MK	88	SER
5	MK	92	ASN
5	MK	101	GLU
5	MK	111	LYS
5	MK	118	SER
5	MK	126	VAL
5	MK	127	LYS
5	MK	144	LEU
5	MK	153	ILE
5	MK	159	LEU
5	MK	162	ASP
5	MK	182	ILE
3	Df	215	VAL
3	Df	222	LEU
3	Df	232	VAL
3	Df	250	LEU
3	Df	262	ILE
6	ML	57	VAL
6	ML	90	THR
6	ML	93	LEU
6	ML	104	LYS
6	ML	109	LEU
6	ML	113	ASP
6	ML	125	LEU
6	ML	142	GLU
6	ML	143	ILE
6	ML	162	THR
6	ML	163	ILE
6	ML	172	VAL
6	ML	177	HIS
6	ML	181	LEU
6	ML	182	SER
6	ML	193	LEU
6	ML	212	ASN

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Mol	Chain	Res	Type
6	ML	220	ILE
6	ML	230	GLU
7	MM	127	ASN
7	MM	129	LEU
7	MM	131	THR
7	MM	134	LEU
7	MM	146	LEU
7	MM	149	ASN
7	MM	150	ILE
7	MM	152	LEU
7	MM	160	ASN
7	MM	176	VAL
7	MM	178	LYS
7	MM	183	VAL
7	MM	184	LEU
7	MM	196	MET
7	MM	205	TYR
7	MM	212	LEU
7	MM	224	LEU
7	MM	242	LYS
7	MM	259	SER
7	MM	263	ILE
7	MM	264	SER
7	MM	279	ILE
7	MM	298	VAL
7	MM	299	LEU
7	MM	308	ASP
7	MM	314	ARG
8	MN	39	ASP
8	MN	48	ILE
8	MN	49	ASN
8	MN	57	ARG
8	MN	95	LEU
8	MN	100	LEU
8	MN	101	VAL
8	MN	104	ASN
8	MN	105	ASP
8	MN	108	VAL
8	MN	112	CYS
2	Md	25	PHE
2	Md	41	LEU
2	Md	61	VAL

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Mol	Chain	Res	Type
2	Md	62	ILE
2	Md	63	THR
2	Md	69	ASN
2	Md	107	ARG
2	Md	108	VAL
2	Md	123	THR
2	Md	142	LYS
2	Md	147	VAL
2	Md	150	ASN
3	Mf	216	ILE
3	Mf	245	LYS
3	Mf	255	LEU
3	Mf	261	VAL
3	Mf	262	ILE
3	VF	207	ARG
3	VF	208	ILE
3	VF	215	VAL
3	VF	219	ARG
3	VF	230	LEU
3	VF	232	VAL
3	VF	238	ILE
3	VF	253	ARG
3	VF	254	ILE
3	VF	256	THR
1	VG	793	GLU
1	VG	813	LYS
1	VG	818	GLN
1	VG	819	VAL
4	VH	107	ILE
4	VH	108	ASP
4	VH	122	LEU
4	VH	147	THR
4	VH	152	THR
4	VH	170	ARG
4	VH	180	VAL
4	VH	196	LEU
4	VH	198	ASP
4	VH	203	ASN
4	VH	204	ILE
4	VH	226	LEU
4	VH	240	THR
4	VH	241	LEU

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Mol	Chain	Res	Type
4	VH	242	ILE
4	VH	248	VAL
4	VH	253	ASP
4	VH	256	VAL
4	VH	287	VAL
4	VH	296	VAL
4	VH	297	VAL
4	VH	313	VAL
4	VH	316	ASN
4	VH	328	MET
4	VH	329	THR
4	VH	358	VAL
3	WF	215	VAL
3	WF	231	THR
3	WF	263	LYS
1	WG	793	GLU
1	WG	794	ILE
1	WG	800	ASP
1	WG	801	MET
1	WG	802	LEU
4	WH	105	GLU
4	WH	108	ASP
4	WH	117	ARG
4	WH	122	LEU
4	WH	132	GLN
4	WH	147	THR
4	WH	154	THR
4	WH	180	VAL
4	WH	204	ILE
4	WH	207	ASP
4	WH	208	LYS
4	WH	215	ILE
4	WH	218	THR
4	WH	238	MET
4	WH	248	VAL
4	WH	249	ASP
4	WH	253	ASP
4	WH	278	ASP
4	WH	279	LEU
4	WH	313	VAL
4	WH	315	THR
4	WH	354	MET

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Mol	Chain	Res	Type
4	WH	356	LEU
3	XF	208	ILE
3	XF	215	VAL
3	XF	216	ILE
3	XF	230	LEU
3	XF	246	LEU
1	XG	792	GLN
1	XG	793	GLU
1	XG	795	GLN
1	XG	802	LEU
1	XG	808	LEU
1	XG	810	GLN
1	XG	814	GLN
3	CF	215	VAL
3	CF	223	ILE
3	CF	229	THR
3	CF	232	VAL
3	CF	233	ARG
1	EG	869	MET
1	EG	875	THR
1	EG	880	ASP
1	EG	886	LEU
1	EG	890	VAL
1	EG	900	ILE
1	EG	913	VAL
1	EG	930	ILE
1	EG	944	LEU
1	EG	953	LEU
1	EG	955	ARG
1	EG	962	SER
1	EG	965	LEU
1	EG	966	GLN
1	EG	972	PHE
1	EG	1010	THR
1	EG	1017	GLN
1	EG	1044	ASP
1	EG	1045	VAL
4	XH	107	ILE
4	XH	109	LYS
4	XH	113	LYS
4	XH	114	ASP
4	XH	115	MET

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Mol	Chain	Res	Type
4	XH	130	LEU
4	XH	138	GLU
4	XH	147	THR
4	XH	168	VAL
4	XH	180	VAL
4	XH	203	ASN
4	XH	207	ASP
4	XH	219	LYS
4	XH	233	LEU
4	XH	238	MET
4	XH	239	LEU
4	XH	240	THR
4	XH	242	ILE
4	XH	248	VAL
4	XH	250	TYR
4	XH	253	ASP
4	XH	256	VAL
4	XH	297	VAL
4	XH	303	ARG
4	XH	308	ASN
4	XH	313	VAL
4	XH	319	ILE
4	XH	321	SER
4	XH	325	LEU
4	XH	339	MET
4	XH	358	VAL
3	YF	211	TYR
3	YF	212	ILE
3	YF	215	VAL
3	YF	223	ILE
3	YF	226	ASN
3	YF	251	GLN
3	YF	256	THR
6	AL	93	LEU
6	AL	100	ASP
6	AL	113	ASP
6	AL	129	THR
6	AL	130	ASP
6	AL	155	LEU
6	AL	172	VAL
6	AL	181	LEU
6	AL	189	MET

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Mol	Chain	Res	Type
6	AL	193	LEU
6	AL	212	ASN
6	AL	219	ILE
1	YG	793	GLU
1	YG	795	GLN
1	YG	802	LEU
1	YG	810	GLN
1	YG	816	GLU
1	YG	822	GLU
4	YH	109	LYS
4	YH	122	LEU
4	YH	125	GLU
4	YH	147	THR
4	YH	152	THR
4	YH	155	SER
4	YH	160	LEU
4	YH	168	VAL
4	YH	171	LEU
4	YH	176	VAL
4	YH	180	VAL
4	YH	208	LYS
4	YH	209	THR
4	YH	215	ILE
4	YH	218	THR
4	YH	222	ASN
4	YH	234	ASN
4	YH	235	THR
4	YH	242	ILE
4	YH	248	VAL
4	YH	253	ASP
4	YH	262	ASN
4	YH	295	LEU
4	YH	296	VAL
4	YH	306	LEU
4	YH	320	LEU
4	YH	321	SER
4	YH	332	ASP
4	YH	344	VAL
4	YH	347	VAL
4	YH	358	VAL
3	ZF	212	ILE
3	ZF	215	VAL

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Mol	Chain	Res	Type
3	ZF	216	ILE
3	ZF	230	LEU
3	ZF	231	THR
3	ZF	233	ARG
2	AD	24	LYS
2	AD	32	ASN
2	AD	35	ASP
2	AD	50	ASP
2	AD	51	SER
2	AD	55	MET
2	AD	67	LYS
2	AD	68	ASP
2	AD	73	ILE
2	AD	79	LEU
2	AD	85	VAL
2	AD	91	ILE
2	AD	115	VAL
2	AD	117	VAL
2	AD	118	LEU
2	AD	123	THR
2	AD	127	SER
2	AD	131	ILE
2	AD	145	ILE
2	AD	154	VAL
2	AD	160	LYS
1	ZG	792	GLN
1	ZG	793	GLU
1	ZG	796	GLN
1	ZG	814	GLN
1	ZG	816	GLU
1	ZG	818	GLN
1	ZG	822	GLU
4	ZH	108	ASP
4	ZH	158	VAL
4	ZH	180	VAL
4	ZH	202	PHE
4	ZH	203	ASN
4	ZH	216	GLN
4	ZH	218	THR
4	ZH	225	ASN
4	ZH	235	THR
4	ZH	242	ILE

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Mol	Chain	Res	Type
4	ZH	248	VAL
4	ZH	253	ASP
4	ZH	256	VAL
4	ZH	259	TYR
4	ZH	262	ASN
4	ZH	280	LEU
4	ZH	297	VAL
4	ZH	306	LEU
4	ZH	317	LEU
4	ZH	357	LYS
7	AM	115	ARG
7	AM	129	LEU
7	AM	131	THR
7	AM	134	LEU
7	AM	140	ASN
7	AM	146	LEU
7	AM	149	ASN
7	AM	152	LEU
7	AM	173	LEU
7	AM	176	VAL
7	AM	177	LEU
7	AM	180	ASP
7	AM	182	LYS
7	AM	184	LEU
7	AM	185	ILE
7	AM	188	PHE
7	AM	189	VAL
7	AM	190	ASN
7	AM	202	LEU
7	AM	204	LEU
7	AM	205	TYR
7	AM	212	LEU
7	AM	215	ARG
7	AM	222	ILE
7	AM	269	GLN
7	AM	271	SER
7	AM	277	SER
7	AM	287	THR
7	AM	292	MET
7	AM	308	ASP
7	AM	315	TYR
8	AN	48	ILE

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Mol	Chain	Res	Type
8	AN	62	ASN
8	AN	75	VAL
8	AN	77	ASP
8	AN	78	LEU
8	AN	84	CYS
8	AN	108	VAL
8	AN	116	LYS
2	Ad	27	LYS
2	Ad	41	LEU
2	Ad	52	MET
2	Ad	53	LEU
2	Ad	61	VAL
2	Ad	63	THR
2	Ad	68	ASP
2	Ad	85	VAL
2	Ad	93	GLU
2	Ad	94	LEU
2	Ad	98	ILE
2	Ad	108	VAL
2	Ad	115	VAL
2	Ad	124	LYS
2	Ad	132	LEU
2	Ad	141	LYS
2	Ad	150	ASN
2	Ad	154	VAL
2	Ad	156	LEU
3	Af	215	VAL
3	Af	216	ILE
3	Af	238	ILE
3	Af	247	ILE
3	Af	250	LEU
3	Af	261	VAL
2	BD	25	PHE
2	BD	32	ASN
2	BD	41	LEU
2	BD	46	VAL
2	BD	50	ASP
2	BD	51	SER
2	BD	55	MET
2	BD	71	LEU
2	BD	73	ILE
2	BD	78	ASN

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Mol	Chain	Res	Type
2	BD	85	VAL
2	BD	108	VAL
2	BD	115	VAL
2	BD	123	THR
2	BD	131	ILE
2	BD	161	ILE
3	BF	208	ILE
3	BF	215	VAL
3	BF	216	ILE
3	BF	222	LEU
3	BF	223	ILE
3	BF	232	VAL
3	BF	233	ARG
4	BH	105	GLU
4	BH	107	ILE
4	BH	147	THR
4	BH	154	THR
4	BH	171	LEU
4	BH	179	LEU
4	BH	180	VAL
4	BH	204	ILE
4	BH	208	LYS
4	BH	233	LEU
4	BH	238	MET
4	BH	242	ILE
4	BH	245	GLN
4	BH	248	VAL
4	BH	253	ASP
4	BH	256	VAL
4	BH	278	ASP
4	BH	287	VAL
4	BH	313	VAL
4	BH	315	THR
4	BH	316	ASN
4	BH	317	LEU
4	BH	319	ILE
4	BH	344	VAL
4	BH	345	LEU
4	BH	357	LYS
5	BK	41	LEU
5	BK	50	ASP
5	BK	55	LYS

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Mol	Chain	Res	Type
5	BK	63	LYS
5	BK	67	VAL
5	BK	70	VAL
5	BK	75	LEU
5	BK	83	LEU
5	BK	92	ASN
5	BK	102	ILE
5	BK	111	LYS
5	BK	112	ILE
5	BK	122	LYS
5	BK	125	SER
5	BK	126	VAL
5	BK	152	ARG
5	BK	156	THR
5	BK	162	ASP
5	BK	170	LEU
5	BK	180	VAL
5	BK	182	ILE
5	BK	183	THR
6	BL	91	VAL
6	BL	93	LEU
6	BL	109	LEU
6	BL	112	GLN
6	BL	125	LEU
6	BL	129	THR
6	BL	133	PHE
6	BL	155	LEU
6	BL	165	VAL
6	BL	172	VAL
6	BL	181	LEU
6	BL	182	SER
6	BL	189	MET
6	BL	193	LEU
6	BL	212	ASN
6	BL	225	GLN
6	BL	227	ARG
6	BL	228	ARG
7	BM	129	LEU
7	BM	130	ARG
7	BM	136	LEU
7	BM	146	LEU
7	BM	152	LEU

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Mol	Chain	Res	Type
7	BM	171	ARG
7	BM	173	LEU
7	BM	176	VAL
7	BM	177	LEU
7	BM	184	LEU
7	BM	190	ASN
7	BM	191	LEU
7	BM	204	LEU
7	BM	205	TYR
7	BM	212	LEU
7	BM	222	ILE
7	BM	231	LEU
7	BM	256	HIS
7	BM	264	SER
7	BM	277	SER
7	BM	292	MET
7	BM	299	LEU
7	BM	304	TRP
7	BM	314	ARG
7	BM	316	ASN
8	BN	65	TYR
8	BN	68	CYS
8	BN	78	LEU
8	BN	94	GLN
8	BN	114	LEU
8	BN	115	GLN
8	BN	116	LYS
1	FG	869	MET
1	FG	880	ASP
1	FG	886	LEU
1	FG	893	LYS
1	FG	895	LYS
1	FG	898	LYS
1	FG	899	LEU
1	FG	913	VAL
1	FG	930	ILE
1	FG	938	ASN
1	FG	941	ARG
1	FG	944	LEU
1	FG	953	LEU
1	FG	962	SER
1	FG	963	SER

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Mol	Chain	Res	Type
1	FG	965	LEU
1	FG	972	PHE
1	FG	1010	THR
1	FG	1017	GLN
1	FG	1044	ASP
1	FG	1045	VAL
2	Bd	30	ILE
2	Bd	41	LEU
2	Bd	59	GLU
2	Bd	61	VAL
2	Bd	63	THR
2	Bd	97	ARG
2	Bd	115	VAL
2	Bd	117	VAL
2	Bd	123	THR
2	Bd	141	LYS
2	Bd	142	LYS
2	Bd	145	ILE
3	Bf	208	ILE
3	Bf	216	ILE
3	Bf	222	LEU
3	Bf	232	VAL
3	Bf	233	ARG
3	Bf	236	SER
3	Bf	250	LEU
3	Bf	255	LEU
3	Bf	260	GLN
3	Bf	261	VAL
1	Dg	793	GLU
1	Dg	798	THR
1	Dg	800	ASP
1	Dg	802	LEU
1	Dg	803	THR
1	Dg	808	LEU
1	Dg	809	VAL
1	Dg	810	GLN
1	Dg	819	VAL
1	Dg	821	THR
11	EC	61	GLU
11	EC	79	ILE
11	EC	97	ASN
11	EC	99	LEU

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Mol	Chain	Res	Type
11	EC	105	ILE
11	EC	110	LEU
11	EC	116	THR
11	EC	117	LEU
11	EC	118	ASN
11	EC	119	LEU
11	EC	127	ILE
11	EC	140	PHE
11	EC	143	THR
11	EC	146	THR
11	EC	148	ARG
11	EC	151	LEU
11	EC	153	MET
11	EC	156	VAL
11	EC	166	LEU
11	EC	170	LYS
11	EC	180	THR
11	EC	184	TRP
11	EC	204	GLU
11	EC	211	LEU
11	EC	221	VAL
11	EC	229	THR
11	EC	249	ILE
11	EC	266	VAL
11	FC	83	LEU
11	FC	97	ASN
11	FC	99	LEU
11	FC	105	ILE
11	FC	112	GLU
11	FC	116	THR
11	FC	119	LEU
11	FC	127	ILE
11	FC	146	THR
11	FC	148	ARG
11	FC	149	GLN
11	FC	151	LEU
11	FC	163	VAL
11	FC	166	LEU
11	FC	184	TRP
11	FC	195	LEU
11	FC	205	ASP
11	FC	214	LYS

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Mol	Chain	Res	Type
11	FC	226	VAL
11	FC	233	VAL
11	FC	255	LEU
11	FC	257	VAL
11	FC	258	ASN
11	FC	266	VAL
11	DC	30	SER
11	DC	31	LEU
11	DC	34	LEU
11	DC	37	MET
11	DC	47	LYS
11	DC	54	ILE
11	DC	56	GLU
11	DC	83	LEU
11	DC	84	ASN
11	DC	91	ASP
11	DC	99	LEU
11	DC	115	ASN
11	DC	123	GLN
11	DC	127	ILE
11	DC	128	SER
11	DC	141	ILE
11	DC	146	THR
11	DC	148	ARG
11	DC	151	LEU
11	DC	154	ASP
11	DC	155	TYR
11	DC	156	VAL
11	DC	169	THR
11	DC	172	GLU
11	DC	174	GLU
11	DC	203	LYS
11	DC	214	LYS
11	DC	218	MET
11	DC	231	LEU
11	DC	239	GLU
11	DC	255	LEU
11	DC	258	ASN
11	GC	62	GLU
11	GC	84	LEU
11	GC	85	ASN
11	GC	86	LYS

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Mol	Chain	Res	Type
11	GC	92	ASP
11	GC	100	LEU
11	GC	126	ILE
11	GC	147	THR
11	GC	152	LEU
11	GC	157	VAL
11	GC	170	THR
11	GC	173	GLU
11	GC	175	GLU
11	GC	181	THR
11	GC	182	GLU
11	GC	191	GLN
11	GC	196	LEU
11	GC	197	GLU
11	GC	205	GLU
11	GC	214	ARG
11	GC	222	VAL
11	GC	240	GLU
11	GC	242	HIS
11	GC	259	ASN
2	ED	23	MET
2	ED	31	ASN
2	ED	35	ASP
2	ED	41	LEU
2	ED	63	THR
2	ED	70	THR
2	ED	73	ILE
2	ED	94	LEU
2	ED	95	THR
2	ED	105	ARG
2	ED	108	VAL
2	ED	115	VAL
2	ED	130	GLU
2	ED	131	ILE
2	ED	137	TYR
2	ED	154	VAL
11	HC	27	ASP
11	HC	30	SER
11	HC	31	LEU
11	HC	34	LEU
11	HC	37	MET
11	HC	47	LYS

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Mol	Chain	Res	Type
11	HC	49	GLN
11	HC	83	LEU
11	HC	84	ASN
11	HC	85	LYS
11	HC	89	ASN
11	HC	91	ASP
11	HC	99	LEU
11	HC	112	GLU
11	HC	141	ILE
11	HC	146	THR
11	HC	151	LEU
11	HC	154	ASP
11	HC	156	VAL
11	HC	157	LYS
11	HC	169	THR
11	HC	172	GLU
11	HC	180	THR
11	HC	195	LEU
11	HC	201	ARG
11	HC	203	LYS
11	HC	233	VAL
11	HC	239	GLU
11	HC	240	ILE
11	HC	241	HIS
11	HC	242	ILE
11	HC	255	LEU
11	HC	256	ASN
11	HC	258	ASN
11	MC	30	SER
11	MC	31	LEU
11	MC	34	LEU
11	MC	46	GLN
11	MC	57	MET
11	MC	84	ASN
11	MC	85	LYS
11	MC	91	ASP
11	MC	99	LEU
11	MC	103	HIS
11	MC	112	GLU
11	MC	117	LEU
11	MC	146	THR
11	MC	151	LEU

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Mol	Chain	Res	Type
11	MC	156	VAL
11	MC	165	LEU
11	MC	169	THR
11	MC	174	GLU
11	MC	195	LEU
11	MC	196	GLU
11	MC	203	LYS
11	MC	204	GLU
11	MC	230	ASP
11	MC	233	VAL
11	MC	239	GLU
11	MC	241	HIS
11	MC	244	ASP
11	MC	255	LEU
11	JC	64	LEU
11	JC	96	PHE
11	JC	99	LEU
11	JC	105	ILE
11	JC	109	VAL
11	JC	111	LEU
11	JC	112	GLU
11	JC	116	THR
11	JC	127	ILE
11	JC	143	THR
11	JC	151	LEU
11	JC	157	LYS
11	JC	159	GLU
11	JC	163	VAL
11	JC	166	LEU
11	JC	168	LYS
11	JC	170	LYS
11	JC	184	TRP
11	JC	233	VAL
11	JC	258	ASN
11	KC	62	GLU
11	KC	66	SER
11	KC	100	LEU
11	KC	106	ILE
11	KC	112	LEU
11	KC	118	LEU
11	KC	147	THR
11	KC	152	LEU

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Mol	Chain	Res	Type
11	KC	166	LEU
11	KC	167	LEU
11	KC	169	LYS
11	KC	170	THR
11	KC	175	GLU
11	KC	196	LEU
11	KC	211	ILE
11	KC	222	VAL
11	KC	227	VAL
11	KC	250	ILE
11	KC	257	ASN
11	KC	267	VAL
11	LC	28	THR
11	LC	35	GLN
11	LC	39	ASP
11	LC	46	GLN
11	LC	49	GLN
11	LC	81	GLU
11	LC	89	ASN
11	LC	105	ILE
11	LC	116	THR
11	LC	117	LEU
11	LC	118	ASN
11	LC	119	LEU
11	LC	123	GLN
11	LC	125	ILE
11	LC	146	THR
11	LC	151	LEU
11	LC	154	ASP
11	LC	157	LYS
11	LC	169	THR
11	LC	203	LYS
11	LC	204	GLU
11	LC	215	LEU
11	LC	220	MET
11	LC	226	VAL
11	LC	233	VAL
11	LC	242	ILE
11	LC	247	LEU
11	LC	255	LEU
4	CH	107	ILE
4	CH	109	LYS

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Mol	Chain	Res	Type
4	CH	132	GLN
4	CH	154	THR
4	CH	180	VAL
4	CH	182	LEU
4	CH	183	ASP
4	CH	204	ILE
4	CH	205	GLN
4	CH	207	ASP
4	CH	212	THR
4	CH	213	LEU
4	CH	233	LEU
4	CH	248	VAL
4	CH	249	ASP
4	CH	268	THR
4	CH	270	GLU
4	CH	287	VAL
4	CH	296	VAL
4	CH	306	LEU
4	CH	313	VAL
4	CH	321	SER
4	CH	344	VAL
4	CH	353	VAL
4	CH	361	LEU
5	CK	45	VAL
5	CK	50	ASP
5	CK	63	LYS
5	CK	65	ILE
5	CK	66	LYS
5	CK	67	VAL
5	CK	70	VAL
5	CK	72	GLN
5	CK	76	ILE
5	CK	78	ILE
5	CK	83	LEU
5	CK	86	ASP
5	CK	92	ASN
5	CK	98	LEU
5	CK	102	ILE
5	CK	111	LYS
5	CK	124	VAL
5	CK	126	VAL
5	CK	132	LEU

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Mol	Chain	Res	Type
5	CK	144	LEU
5	CK	156	THR
5	CK	162	ASP
5	CK	180	VAL
5	CK	183	THR
6	CL	49	ASN
6	CL	57	VAL
6	CL	91	VAL
6	CL	93	LEU
6	CL	104	LYS
6	CL	109	LEU
6	CL	113	ASP
6	CL	121	ASP
6	CL	125	LEU
6	CL	127	ILE
6	CL	129	THR
6	CL	130	ASP
6	CL	131	LYS
6	CL	140	LEU
6	CL	155	LEU
6	CL	163	ILE
6	CL	172	VAL
6	CL	181	LEU
6	CL	193	LEU
6	CL	203	LEU
6	CL	210	ASP
6	CL	211	LYS
6	CL	212	ASN
6	CL	219	ILE
6	CL	227	ARG
6	CL	232	GLN
7	CM	115	ARG
7	CM	129	LEU
7	CM	134	LEU
7	CM	146	LEU
7	CM	149	ASN
7	CM	152	LEU
7	CM	155	LEU
7	CM	162	VAL
7	CM	175	ILE
7	CM	176	VAL
7	CM	178	LYS

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Mol	Chain	Res	Type
7	CM	182	LYS
7	CM	184	LEU
7	CM	190	ASN
7	CM	194	LEU
7	CM	202	LEU
7	CM	207	ILE
7	CM	212	LEU
7	CM	231	LEU
7	CM	235	LEU
7	CM	263	ILE
7	CM	266	VAL
7	CM	292	MET
7	CM	301	MET
7	CM	303	GLU
7	CM	308	ASP
7	CM	315	TYR
8	CN	48	ILE
8	CN	59	VAL
8	CN	64	PHE
8	CN	65	TYR
8	CN	78	LEU
8	CN	85	CYS
8	CN	94	GLN
8	CN	95	LEU
8	CN	100	LEU
8	CN	108	VAL
8	CN	114	LEU
2	Cd	25	PHE
2	Cd	26	LYS
2	Cd	30	ILE
2	Cd	41	LEU
2	Cd	59	GLU
2	Cd	61	VAL
2	Cd	91	ILE
2	Cd	115	VAL
2	Cd	119	ILE
2	Cd	123	THR
2	Cd	142	LYS
2	Cd	145	ILE
2	Cd	147	VAL
2	Cd	153	VAL
3	Cf	215	VAL

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Mol	Chain	Res	Type
3	Cf	216	ILE
3	Cf	223	ILE
3	Cf	232	VAL
3	Cf	233	ARG
3	Cf	250	LEU
3	Cf	251	GLN
3	Cf	260	GLN
3	Cf	261	VAL
2	DD	31	ASN
2	DD	41	LEU
2	DD	47	SER
2	DD	50	ASP
2	DD	53	LEU
2	DD	55	MET
2	DD	73	ILE
2	DD	79	LEU
2	DD	85	VAL
2	DD	93	GLU
2	DD	115	VAL
2	DD	118	LEU
2	DD	126	GLU
2	DD	127	SER
2	DD	135	ILE
2	DD	154	VAL
3	DF	215	VAL
3	DF	216	ILE
3	DF	231	THR
3	DF	237	LYS
3	DF	238	ILE
3	DF	256	THR
4	DH	105	GLU
4	DH	115	MET
4	DH	130	LEU
4	DH	139	TYR
4	DH	147	THR
4	DH	180	VAL
4	DH	205	GLN
4	DH	212	THR
4	DH	241	LEU
4	DH	248	VAL
4	DH	253	ASP
4	DH	254	LEU

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Mol	Chain	Res	Type
4	DH	256	VAL
4	DH	262	ASN
4	DH	280	LEU
4	DH	284	LEU
4	DH	287	VAL
4	DH	321	SER
4	DH	332	ASP
4	DH	345	LEU
1	GG	865	THR
1	GG	869	MET
1	GG	880	ASP
1	GG	881	GLU
1	GG	886	LEU
1	GG	895	LYS
1	GG	898	LYS
1	GG	910	ASP
1	GG	911	LYS
1	GG	913	VAL
1	GG	916	PHE
1	GG	930	ILE
1	GG	942	THR
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	1033	SER
1	GG	1045	VAL
5	DK	45	VAL
5	DK	50	ASP
5	DK	63	LYS
5	DK	65	ILE
5	DK	72	GLN
5	DK	73	ASN
5	DK	92	ASN
5	DK	95	SER
5	DK	100	ASN
5	DK	111	LYS

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Mol	Chain	Res	Type
5	DK	115	THR
5	DK	134	LEU
5	DK	149	VAL
5	DK	156	THR
5	DK	159	LEU
5	DK	162	ASP
5	DK	163	LYS
5	DK	166	THR
5	DK	170	LEU
5	DK	180	VAL
5	DK	183	THR
6	DL	47	TYR
6	DL	57	VAL
6	DL	101	SER
6	DL	109	LEU
6	DL	115	GLN
6	DL	129	THR
6	DL	142	GLU
6	DL	155	LEU
6	DL	162	THR
6	DL	165	VAL
6	DL	172	VAL
6	DL	174	SER
6	DL	181	LEU
6	DL	193	LEU
6	DL	194	TRP
6	DL	203	LEU
6	DL	212	ASN
6	DL	216	ASP
6	DL	217	ASN
6	DL	225	GLN
7	DM	129	LEU
7	DM	134	LEU
7	DM	140	ASN
7	DM	144	THR
7	DM	149	ASN
7	DM	152	LEU
7	DM	176	VAL
7	DM	177	LEU
7	DM	178	LYS
7	DM	180	ASP
7	DM	184	LEU

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Mol	Chain	Res	Type
7	DM	185	ILE
7	DM	189	VAL
7	DM	192	ARG
7	DM	199	LYS
7	DM	207	ILE
7	DM	212	LEU
7	DM	222	ILE
7	DM	228	VAL
7	DM	253	VAL
7	DM	255	THR
7	DM	257	ASP
7	DM	262	GLU
7	DM	263	ILE
7	DM	271	SER
7	DM	277	SER
7	DM	292	MET
7	DM	312	PHE
8	DN	70	CYS
8	DN	81	LEU
8	DN	86	LEU
8	DN	95	LEU
8	DN	102	VAL
8	DN	114	LEU
3	EF	208	ILE
3	EF	215	VAL
3	EF	229	THR
3	EF	231	THR
3	EF	238	ILE
1	Eg	795	GLN
1	Eg	797	ARG
1	Eg	808	LEU
1	Eg	809	VAL
4	EH	107	ILE
4	EH	108	ASP
4	EH	117	ARG
4	EH	122	LEU
4	EH	134	TYR
4	EH	147	THR
4	EH	156	GLN
4	EH	160	LEU
4	EH	180	VAL
4	EH	196	LEU

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Mol	Chain	Res	Type
4	EH	207	ASP
4	EH	221	TYR
4	EH	245	GLN
4	EH	248	VAL
4	EH	249	ASP
4	EH	253	ASP
4	EH	256	VAL
4	EH	257	GLN
4	EH	278	ASP
4	EH	285	GLU
4	EH	306	LEU
4	EH	313	VAL
4	EH	317	LEU
4	EH	319	ILE
4	EH	320	LEU
4	EH	321	SER
4	EH	325	LEU
4	EH	346	LEU
4	EH	353	VAL
4	EH	356	LEU
4	EH	361	LEU
5	EK	45	VAL
5	EK	50	ASP
5	EK	65	ILE
5	EK	66	LYS
5	EK	70	VAL
5	EK	72	GLN
5	EK	73	ASN
5	EK	75	LEU
5	EK	78	ILE
5	EK	102	ILE
5	EK	108	GLN
5	EK	114	ILE
5	EK	125	SER
5	EK	126	VAL
5	EK	144	LEU
5	EK	149	VAL
5	EK	156	THR
5	EK	166	THR
5	EK	180	VAL
5	EK	182	ILE
6	EL	49	ASN

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Mol	Chain	Res	Type
6	EL	57	VAL
6	EL	93	LEU
6	EL	99	ARG
6	EL	104	LYS
6	EL	109	LEU
6	EL	125	LEU
6	EL	129	THR
6	EL	139	ARG
6	EL	140	LEU
6	EL	143	ILE
6	EL	165	VAL
6	EL	169	THR
6	EL	172	VAL
6	EL	174	SER
6	EL	181	LEU
6	EL	190	MET
6	EL	193	LEU
6	EL	203	LEU
6	EL	212	ASN
6	EL	219	ILE
6	EL	221	HIS
6	EL	228	ARG
7	EM	117	ARG
7	EM	124	VAL
7	EM	129	LEU
7	EM	131	THR
7	EM	134	LEU
7	EM	146	LEU
7	EM	149	ASN
7	EM	152	LEU
7	EM	173	LEU
7	EM	175	ILE
7	EM	176	VAL
7	EM	180	ASP
7	EM	183	VAL
7	EM	185	ILE
7	EM	212	LEU
7	EM	224	LEU
7	EM	245	TYR
7	EM	255	THR
7	EM	257	ASP
7	EM	271	SER

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Mol	Chain	Res	Type
7	EM	274	THR
7	EM	277	SER
7	EM	290	ASP
7	EM	292	MET
7	EM	301	MET
7	EM	316	ASN
8	EN	66	SER
8	EN	69	TYR
8	EN	71	THR
8	EN	78	LEU
8	EN	86	LEU
8	EN	101	VAL
8	EN	113	SER
8	EN	114	LEU
2	Ed	25	PHE
2	Ed	26	LYS
2	Ed	27	LYS
2	Ed	30	ILE
2	Ed	36	ASP
2	Ed	41	LEU
2	Ed	52	MET
2	Ed	63	THR
2	Ed	70	THR
2	Ed	91	ILE
2	Ed	115	VAL
2	Ed	117	VAL
2	Ed	123	THR
2	Ed	128	LEU
2	Ed	141	LYS
3	Ef	208	ILE
3	Ef	212	ILE
3	Ef	215	VAL
3	Ef	216	ILE
3	Ef	223	ILE
3	Ef	232	VAL
3	Ef	233	ARG
3	Ef	238	ILE
3	Ef	244	VAL
3	Ef	246	LEU
3	Ef	254	ILE
2	FD	35	ASP
2	FD	46	VAL

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Mol	Chain	Res	Type
2	FD	50	ASP
2	FD	51	SER
2	FD	52	MET
2	FD	70	THR
2	FD	82	ARG
2	FD	85	VAL
2	FD	91	ILE
2	FD	108	VAL
2	FD	115	VAL
2	FD	119	ILE
2	FD	124	LYS
2	FD	127	SER
2	FD	154	VAL
2	FD	156	LEU
2	FD	160	LYS
3	FF	213	GLN
3	FF	215	VAL
3	FF	230	LEU
3	FF	231	THR
3	FF	233	ARG
3	FF	238	ILE
3	FF	250	LEU
3	FF	255	LEU
1	Fg	794	ILE
1	Fg	813	LYS
1	Fg	814	GLN
1	Fg	821	THR
4	FH	105	GLU
4	FH	139	TYR
4	FH	147	THR
4	FH	152	THR
4	FH	154	THR
4	FH	156	GLN
4	FH	171	LEU
4	FH	180	VAL
4	FH	218	THR
4	FH	238	MET
4	FH	242	ILE
4	FH	248	VAL
4	FH	249	ASP
4	FH	265	SER
4	FH	272	ILE

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Mol	Chain	Res	Type
4	FH	279	LEU
4	FH	287	VAL
4	FH	296	VAL
4	FH	297	VAL
4	FH	313	VAL
4	FH	316	ASN
4	FH	317	LEU
4	FH	321	SER
4	FH	339	MET
4	FH	341	LYS
4	FH	342	SER
4	FH	347	VAL
4	FH	361	LEU
5	FK	45	VAL
5	FK	70	VAL
5	FK	92	ASN
5	FK	95	SER
5	FK	106	LEU
5	FK	111	LYS
5	FK	117	THR
5	FK	126	VAL
5	FK	129	GLU
5	FK	144	LEU
5	FK	149	VAL
5	FK	159	LEU
5	FK	177	ASN
5	FK	180	VAL
5	FK	182	ILE
5	FK	183	THR
6	FL	93	LEU
6	FL	102	LYS
6	FL	114	ILE
6	FL	155	LEU
6	FL	156	ASN
6	FL	165	VAL
6	FL	172	VAL
6	FL	193	LEU
6	FL	212	ASN
6	FL	225	GLN
1	HG	869	MET
1	HG	874	ASP
1	HG	880	ASP

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Mol	Chain	Res	Type
1	HG	886	LEU
1	HG	898	LYS
1	HG	899	LEU
1	HG	900	ILE
1	HG	905	LEU
1	HG	916	PHE
1	HG	919	MET
1	HG	925	GLU
1	HG	930	ILE
1	HG	944	LEU
1	HG	953	LEU
1	HG	962	SER
1	HG	963	SER
1	HG	965	LEU
1	HG	966	GLN
1	HG	972	PHE
1	HG	1002	GLU
1	HG	1021	GLN
1	HG	1024	ASN
1	HG	1033	SER
1	HG	1044	ASP
1	IG	868	ILE
1	IG	869	MET
1	IG	880	ASP
1	IG	885	ILE
1	IG	886	LEU
1	IG	898	LYS
1	IG	904	ASN
1	IG	911	LYS
1	IG	919	MET
1	IG	930	ILE
1	IG	939	THR
1	IG	941	ARG
1	IG	942	THR
1	IG	944	LEU
1	IG	953	LEU
1	IG	956	TYR
1	IG	962	SER
1	IG	965	LEU
1	IG	972	PHE
1	IG	1010	THR
1	IG	1017	GLN

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Mol	Chain	Res	Type
1	IG	1044	ASP
1	IG	1045	VAL
1	JG	880	ASP
1	JG	886	LEU
1	JG	890	VAL
1	JG	900	ILE
1	JG	913	VAL
1	JG	918	THR
1	JG	919	MET
1	JG	930	ILE
1	JG	939	THR
1	JG	941	ARG
1	JG	944	LEU
1	JG	953	LEU
1	JG	955	ARG
1	JG	956	TYR
1	JG	962	SER
1	JG	963	SER
1	JG	965	LEU
1	JG	966	GLN
1	JG	972	PHE
1	JG	1042	THR
1	JG	1043	GLN
1	JG	1044	ASP
1	KG	869	MET
1	KG	873	LEU
1	KG	885	ILE
1	KG	886	LEU
1	KG	893	LYS
1	KG	898	LYS
1	KG	900	ILE
1	KG	913	VAL
1	KG	930	ILE
1	KG	938	ASN
1	KG	942	THR
1	KG	944	LEU
1	KG	953	LEU
1	KG	956	TYR
1	KG	962	SER
1	KG	963	SER
1	KG	965	LEU
1	KG	972	PHE

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Mol	Chain	Res	Type
1	KG	1040	LEU
1	KG	1044	ASP
1	LG	869	MET
1	LG	873	LEU
1	LG	875	THR
1	LG	881	GLU
1	LG	886	LEU
1	LG	894	LEU
1	LG	895	LYS
1	LG	899	LEU
1	LG	902	SER
1	LG	913	VAL
1	LG	916	PHE
1	LG	925	GLU
1	LG	944	LEU
1	LG	956	TYR
1	LG	962	SER
1	LG	963	SER
1	LG	965	LEU
1	LG	966	GLN
1	LG	972	PHE
1	LG	1010	THR
1	LG	1028	THR
1	MG	873	LEU
1	MG	885	ILE
1	MG	900	ILE
1	MG	910	ASP
1	MG	916	PHE
1	MG	930	ILE
1	MG	933	TYR
1	MG	944	LEU
1	MG	953	LEU
1	MG	962	SER
1	MG	963	SER
1	MG	965	LEU
1	MG	972	PHE
1	MG	1010	THR
1	MG	1011	VAL
1	MG	1017	GLN
1	MG	1044	ASP
1	NG	869	MET
1	NG	870	PHE

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Mol	Chain	Res	Type
1	NG	886	LEU
1	NG	895	LYS
1	NG	898	LYS
1	NG	900	ILE
1	NG	911	LYS
1	NG	912	MET
1	NG	913	VAL
1	NG	916	PHE
1	NG	918	THR
1	NG	919	MET
1	NG	930	ILE
1	NG	944	LEU
1	NG	953	LEU
1	NG	962	SER
1	NG	963	SER
1	NG	965	LEU
1	NG	966	GLN
1	NG	1010	THR
1	NG	1017	GLN
1	NG	1024	ASN
1	OG	868	ILE
1	OG	869	MET
1	OG	880	ASP
1	OG	881	GLU
1	OG	886	LEU
1	OG	898	LYS
1	OG	900	ILE
1	OG	912	MET
1	OG	918	THR
1	OG	930	ILE
1	OG	938	ASN
1	OG	939	THR
1	OG	944	LEU
1	OG	953	LEU
1	OG	956	TYR
1	OG	962	SER
1	OG	963	SER
1	OG	965	LEU
1	OG	966	GLN
1	OG	972	PHE
1	OG	1010	THR
1	OG	1017	GLN

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Mol	Chain	Res	Type
1	OG	1028	THR
1	OG	1044	ASP
1	PG	869	MET
1	PG	885	ILE
1	PG	886	LEU
1	PG	890	VAL
1	PG	895	LYS
1	PG	898	LYS
1	PG	900	ILE
1	PG	911	LYS
1	PG	913	VAL
1	PG	930	ILE
1	PG	944	LEU
1	PG	950	HIS
1	PG	962	SER
1	PG	965	LEU
1	PG	966	GLN
1	PG	972	PHE
1	PG	1010	THR
1	PG	1031	VAL
1	PG	1037	LEU
11	AC	64	LEU
11	AC	89	ASN
11	AC	91	ASP
11	AC	99	LEU
11	AC	103	HIS
11	AC	105	ILE
11	AC	110	LEU
11	AC	112	GLU
11	AC	116	THR
11	AC	143	THR
11	AC	146	THR
11	AC	148	ARG
11	AC	151	LEU
11	AC	153	MET
11	AC	163	VAL
11	AC	165	LEU
11	AC	169	THR
11	AC	176	TRP
11	AC	185	LYS
11	AC	190	GLN
11	AC	193	THR

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Mol	Chain	Res	Type
11	AC	199	ILE
11	AC	203	LYS
11	AC	209	MET
11	AC	214	LYS
11	AC	221	VAL
11	AC	233	VAL
11	AC	240	ILE
11	AC	248	ARG
11	AC	255	LEU
11	AC	258	ASN
11	AC	266	VAL
7	FM	129	LEU
7	FM	134	LEU
7	FM	136	LEU
7	FM	143	THR
7	FM	146	LEU
7	FM	149	ASN
7	FM	152	LEU
7	FM	160	ASN
7	FM	162	VAL
7	FM	176	VAL
7	FM	184	LEU
7	FM	185	ILE
7	FM	191	LEU
7	FM	199	LYS
7	FM	204	LEU
7	FM	207	ILE
7	FM	212	LEU
7	FM	259	SER
7	FM	263	ILE
7	FM	277	SER
7	FM	284	LEU
7	FM	292	MET
7	FM	298	VAL
7	FM	308	ASP
7	FM	313	ASP
8	FN	48	ILE
8	FN	57	ARG
8	FN	59	VAL
8	FN	62	ASN
8	FN	69	TYR
8	FN	70	CYS

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Mol	Chain	Res	Type
8	FN	76	MET
8	FN	81	LEU
8	FN	86	LEU
8	FN	91	VAL
8	FN	94	GLN
8	FN	101	VAL
8	FN	102	VAL
8	FN	115	GLN
2	Fd	27	LYS
2	Fd	30	ILE
2	Fd	41	LEU
2	Fd	53	LEU
2	Fd	54	GLU
2	Fd	60	LYS
2	Fd	61	VAL
2	Fd	63	THR
2	Fd	82	ARG
2	Fd	86	ASP
2	Fd	92	GLU
2	Fd	93	GLU
2	Fd	108	VAL
2	Fd	115	VAL
2	Fd	117	VAL
2	Fd	123	THR
2	Fd	142	LYS
2	Fd	150	ASN
2	Fd	153	VAL
3	Ff	208	ILE
3	Ff	216	ILE
3	Ff	236	SER
3	Ff	238	ILE
3	Ff	244	VAL
11	BC	70	GLN
11	BC	87	GLN
11	BC	90	ASN
11	BC	100	LEU
11	BC	106	ILE
11	BC	117	THR
11	BC	118	LEU
11	BC	128	ILE
11	BC	142	ILE
11	BC	143	THR

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Mol	Chain	Res	Type
11	BC	147	THR
11	BC	149	ARG
11	BC	152	LEU
11	BC	164	VAL
11	BC	166	LEU
11	BC	167	LEU
11	BC	169	LYS
11	BC	170	THR
11	BC	181	THR
11	BC	191	GLN
11	BC	196	LEU
11	BC	202	ARG
11	BC	216	LEU
11	BC	219	MET
11	BC	222	VAL
11	BC	227	VAL
11	BC	245	ASP
11	BC	259	ASN
11	BC	264	ARG
11	IC	28	THR
11	IC	31	LEU
11	IC	47	LYS
11	IC	50	LYS
11	IC	54	ILE
11	IC	59	LEU
11	IC	61	GLU
11	IC	69	GLN
11	IC	80	ASP
11	IC	89	ASN
11	IC	99	LEU
11	IC	105	ILE
11	IC	110	LEU
11	IC	112	GLU
11	IC	125	ILE
11	IC	127	ILE
11	IC	142	THR
11	IC	146	THR
11	IC	151	LEU
11	IC	163	VAL
11	IC	164	THR
11	IC	165	LEU
11	IC	166	LEU

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Mol	Chain	Res	Type
11	IC	168	LYS
11	IC	190	GLN
11	IC	195	LEU
11	IC	204	GLU
11	IC	210	ILE
11	IC	218	MET
11	IC	226	VAL
11	IC	231	LEU
11	IC	240	ILE
11	IC	244	ASP
11	IC	248	ARG
11	IC	254	GLU
3	AF	208	ILE
3	AF	215	VAL
3	AF	219	ARG
3	AF	243	MET
3	AF	256	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (258) such sidechains are listed below:

Mol	Chain	Res	Type
1	AG	951	HIS
2	GD	80	GLN
3	GF	260	GLN
4	GH	234	ASN
4	GH	245	GLN
6	GL	49	ASN
6	GL	112	GLN
7	GM	160	ASN
7	GM	166	ASN
7	GM	267	ASN
8	GN	79	GLN
3	Gf	266	GLN
2	HD	75	ASN
2	HD	78	ASN
1	Hg	791	GLN
1	Hg	807	GLN
2	Dd	80	GLN
2	Dd	152	GLN
4	HH	205	GLN
5	HK	147	GLN
6	HL	110	GLN

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Mol	Chain	Res	Type
6	HL	112	GLN
6	HL	226	ASN
7	HM	160	ASN
7	HM	164	GLN
8	HN	115	GLN
2	Hd	32	ASN
2	Hd	152	GLN
1	BG	966	GLN
1	BG	1017	GLN
2	ID	152	GLN
3	IF	266	GLN
1	Ig	810	GLN
4	IH	245	GLN
4	IH	355	GLN
6	IL	112	GLN
6	IL	185	GLN
6	IL	196	ASN
7	IM	318	GLN
8	IN	79	GLN
8	IN	96	ASN
2	Id	32	ASN
2	Id	138	GLN
2	Id	152	GLN
2	JD	138	GLN
1	Jg	807	GLN
1	Jg	810	GLN
1	Jg	814	GLN
1	Jg	818	GLN
4	JH	203	ASN
4	JH	205	GLN
6	JL	112	GLN
6	JL	221	HIS
6	JL	225	GLN
7	JM	190	ASN
7	JM	295	ASN
8	JN	115	GLN
2	Jd	75	ASN
2	Jd	103	HIS
4	AH	156	GLN
4	AH	159	ASN
4	AH	203	ASN
4	AH	216	GLN

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Mol	Chain	Res	Type
4	AH	257	GLN
2	KD	32	ASN
2	KD	80	GLN
2	KD	138	GLN
1	CG	1017	GLN
11	CC	70	GLN
11	CC	124	GLN
11	CC	193	ASN
1	Kg	810	GLN
1	Kg	818	GLN
4	KH	159	ASN
4	KH	205	GLN
4	KH	257	GLN
4	KH	282	HIS
4	KH	308	ASN
5	KK	100	ASN
7	KM	267	ASN
8	KN	49	ASN
8	KN	61	ASN
1	Ag	791	GLN
2	Kd	32	ASN
2	Kd	75	ASN
4	LH	216	GLN
4	LH	277	ASN
6	LL	196	ASN
6	LL	217	ASN
7	LM	160	ASN
8	LN	49	ASN
8	LN	79	GLN
2	CD	80	GLN
2	CD	152	GLN
1	DG	950	HIS
1	DG	1017	GLN
5	AK	72	GLN
5	AK	147	GLN
5	AK	157	GLN
2	MD	31	ASN
1	Cg	791	GLN
1	Cg	807	GLN
1	Cg	818	GLN
5	MK	147	GLN
3	Df	251	GLN

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Mol	Chain	Res	Type
6	ML	112	GLN
6	ML	141	ASN
7	MM	267	ASN
7	MM	269	GLN
8	MN	88	HIS
3	Mf	266	GLN
3	VF	213	GLN
3	VF	260	GLN
4	VH	234	ASN
4	VH	257	GLN
4	VH	355	GLN
3	WF	213	GLN
3	WF	266	GLN
4	WH	222	ASN
4	WH	257	GLN
4	WH	262	ASN
1	XG	807	GLN
1	EG	966	GLN
4	XH	257	GLN
4	XH	262	ASN
4	XH	316	ASN
4	XH	350	HIS
4	YH	118	ASN
4	YH	132	GLN
4	YH	205	GLN
3	ZF	260	GLN
2	AD	78	ASN
4	ZH	118	ASN
4	ZH	245	GLN
4	ZH	257	GLN
7	AM	267	ASN
7	AM	316	ASN
8	AN	61	ASN
2	Ad	32	ASN
2	Ad	80	GLN
3	Af	266	GLN
2	BD	152	GLN
3	BF	226	ASN
4	BH	156	GLN
4	BH	308	ASN
6	BL	110	GLN
6	BL	149	ASN

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Mol	Chain	Res	Type
6	BL	196	ASN
6	BL	217	ASN
7	BM	128	ASN
7	BM	153	GLN
7	BM	174	GLN
7	BM	249	GLN
7	BM	267	ASN
7	BM	295	ASN
8	BN	49	ASN
8	BN	61	ASN
8	BN	79	GLN
8	BN	94	GLN
2	Bd	69	ASN
1	Dg	807	GLN
1	Dg	810	GLN
11	EC	115	ASN
11	DC	49	GLN
11	DC	82	GLN
11	DC	115	ASN
11	DC	162	ASN
11	GC	105	ASN
11	GC	116	ASN
11	GC	124	GLN
11	GC	163	ASN
11	GC	193	ASN
2	ED	78	ASN
11	HC	35	GLN
11	HC	123	GLN
11	MC	69	GLN
11	MC	190	GLN
11	KC	163	ASN
11	LC	86	GLN
11	LC	118	ASN
4	CH	118	ASN
4	CH	132	GLN
4	CH	156	GLN
4	CH	245	GLN
4	CH	257	GLN
4	CH	340	GLN
6	CL	217	ASN
6	CL	226	ASN
6	CL	232	GLN

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Mol	Chain	Res	Type
7	CM	164	GLN
7	CM	174	GLN
7	CM	229	ASN
7	CM	249	GLN
7	CM	306	GLN
8	CN	96	ASN
2	Cd	32	ASN
2	Cd	146	HIS
3	Cf	251	GLN
2	DD	78	ASN
2	DD	80	GLN
3	DF	266	GLN
4	DH	173	GLN
4	DH	203	ASN
4	DH	205	GLN
4	DH	216	GLN
5	DK	72	GLN
5	DK	100	ASN
6	DL	49	ASN
6	DL	232	GLN
7	DM	166	ASN
7	DM	190	ASN
7	DM	318	GLN
8	DN	115	GLN
3	EF	260	GLN
1	Eg	814	GLN
1	Eg	818	GLN
4	EH	118	ASN
4	EH	173	GLN
4	EH	225	ASN
4	EH	308	ASN
5	EK	61	ASN
5	EK	87	GLN
6	EL	156	ASN
6	EL	183	GLN
6	EL	196	ASN
7	EM	160	ASN
7	EM	190	ASN
7	EM	229	ASN
2	Ed	152	GLN
3	Ef	266	GLN
2	FD	78	ASN

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Mol	Chain	Res	Type
2	FD	80	GLN
1	Fg	814	GLN
4	FH	118	ASN
6	FL	110	GLN
1	HG	938	ASN
1	HG	966	GLN
1	JG	966	GLN
1	JG	1017	GLN
1	JG	1020	GLN
1	LG	970	ASN
1	LG	1018	GLN
1	LG	1020	GLN
1	MG	1003	ASN
1	MG	1020	GLN
1	NG	966	GLN
1	OG	1020	GLN
11	AC	86	GLN
11	AC	162	ASN
7	FM	295	ASN
8	FN	115	GLN
2	Fd	75	ASN
3	Ff	266	GLN
11	BC	191	GLN
11	IC	104	ASN
11	IC	118	ASN
11	IC	190	GLN
11	IC	198	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no 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	IX	1
10	GX	1
10	AX	1
10	ZX	1
10	CX	1
10	WX	1
10	YX	1
10	EX	1
10	MX	1
10	HX	1
10	LX	1
10	VX	1
10	BX	1
10	KX	1
10	JX	1
10	FX	1
10	DX	1
10	XX	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	IX	38:UNK	C	70:UNK	N	26.35
1	GX	38:UNK	C	70:UNK	N	25.37
1	AX	38:UNK	C	70:UNK	N	25.35
1	ZX	38:UNK	C	70:UNK	N	24.93
1	CX	38:UNK	C	70:UNK	N	24.93
1	WX	38:UNK	C	70:UNK	N	24.81
1	YX	38:UNK	C	70:UNK	N	24.75
1	EX	38:UNK	C	70:UNK	N	24.39

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	MX	38:UNK	C	70:UNK	N	24.13
1	HX	38:UNK	C	70:UNK	N	24.03
1	LX	38:UNK	C	70:UNK	N	23.91
1	VX	38:UNK	C	70:UNK	N	23.13
1	BX	38:UNK	C	70:UNK	N	23.09
1	KX	38:UNK	C	70:UNK	N	22.88
1	JX	38:UNK	C	70:UNK	N	22.83
1	FX	38:UNK	C	70:UNK	N	22.82
1	DX	38:UNK	C	70:UNK	N	22.14
1	XX	38:UNK	C	70:UNK	N	21.04

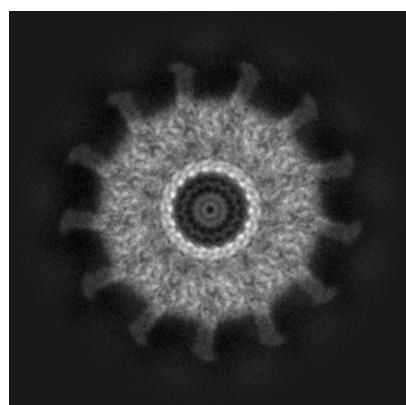
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24020. These allow visual inspection of the internal detail of the map and identification of artifacts.

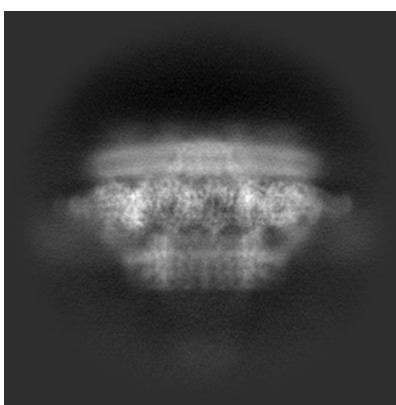
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

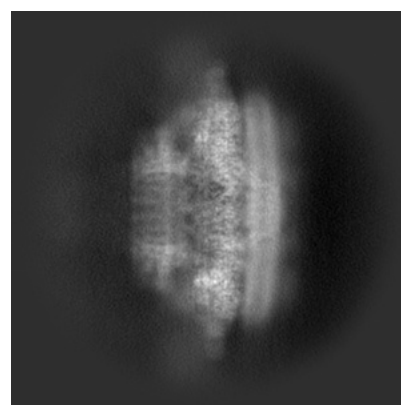
6.1.1 Primary map



X



Y

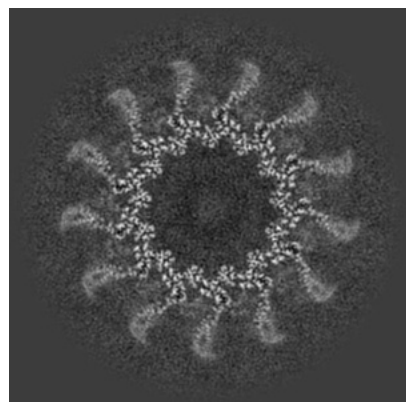


Z

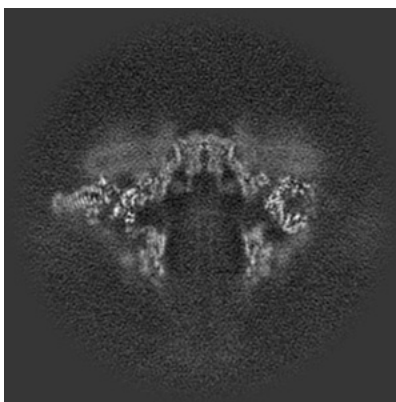
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

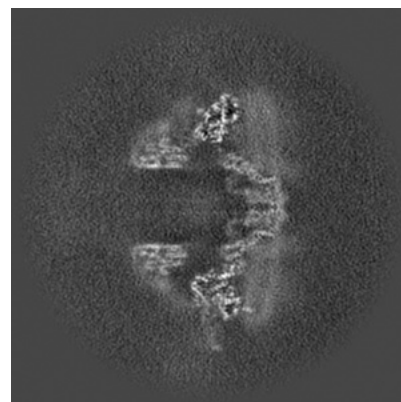
6.2.1 Primary map



X Index: 125



Y Index: 125

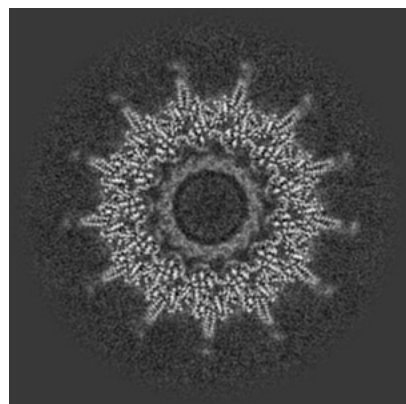


Z Index: 125

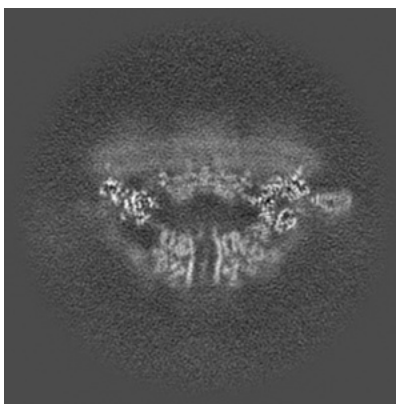
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

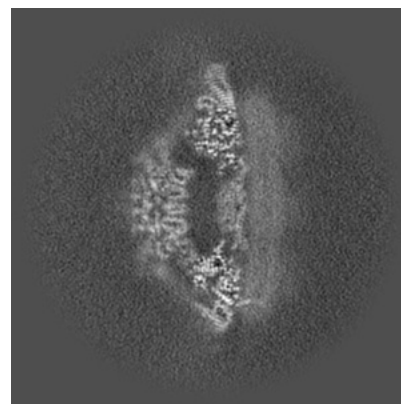
6.3.1 Primary map



X Index: 134



Y Index: 149

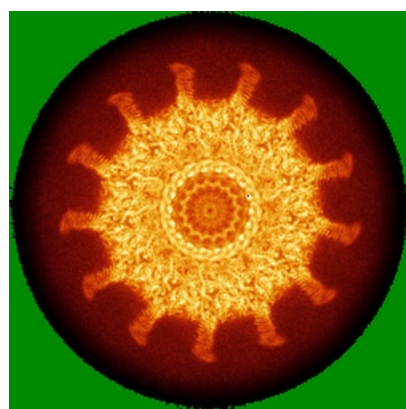


Z Index: 152

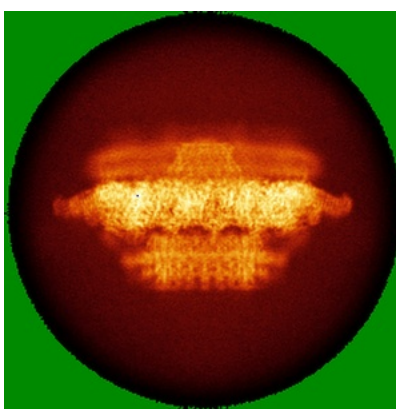
The images above show the largest variance slices of the map in three orthogonal directions.

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

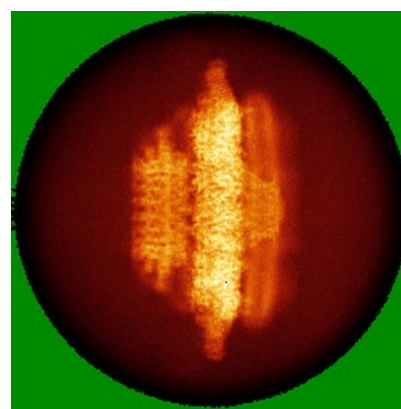
6.4.1 Primary map



X



Y

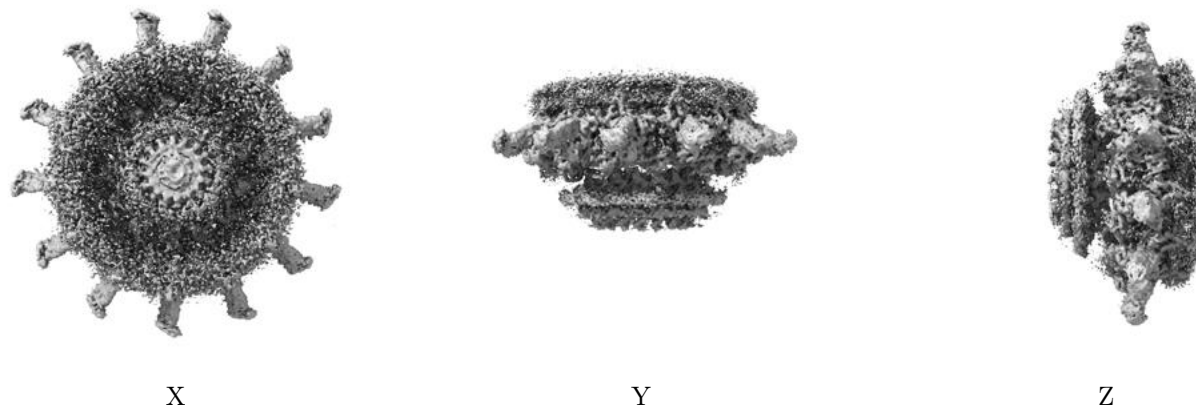


Z

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 [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

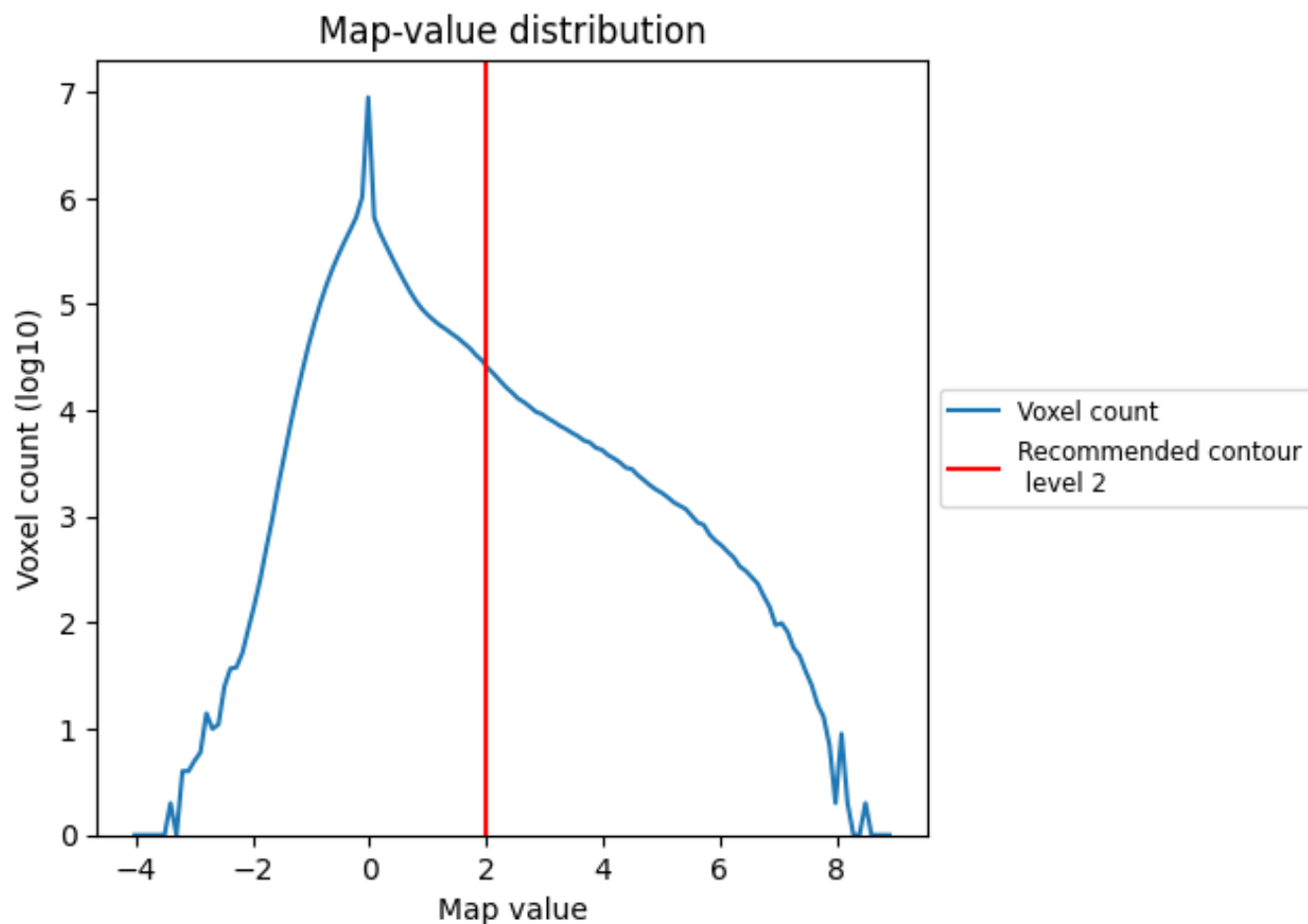
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

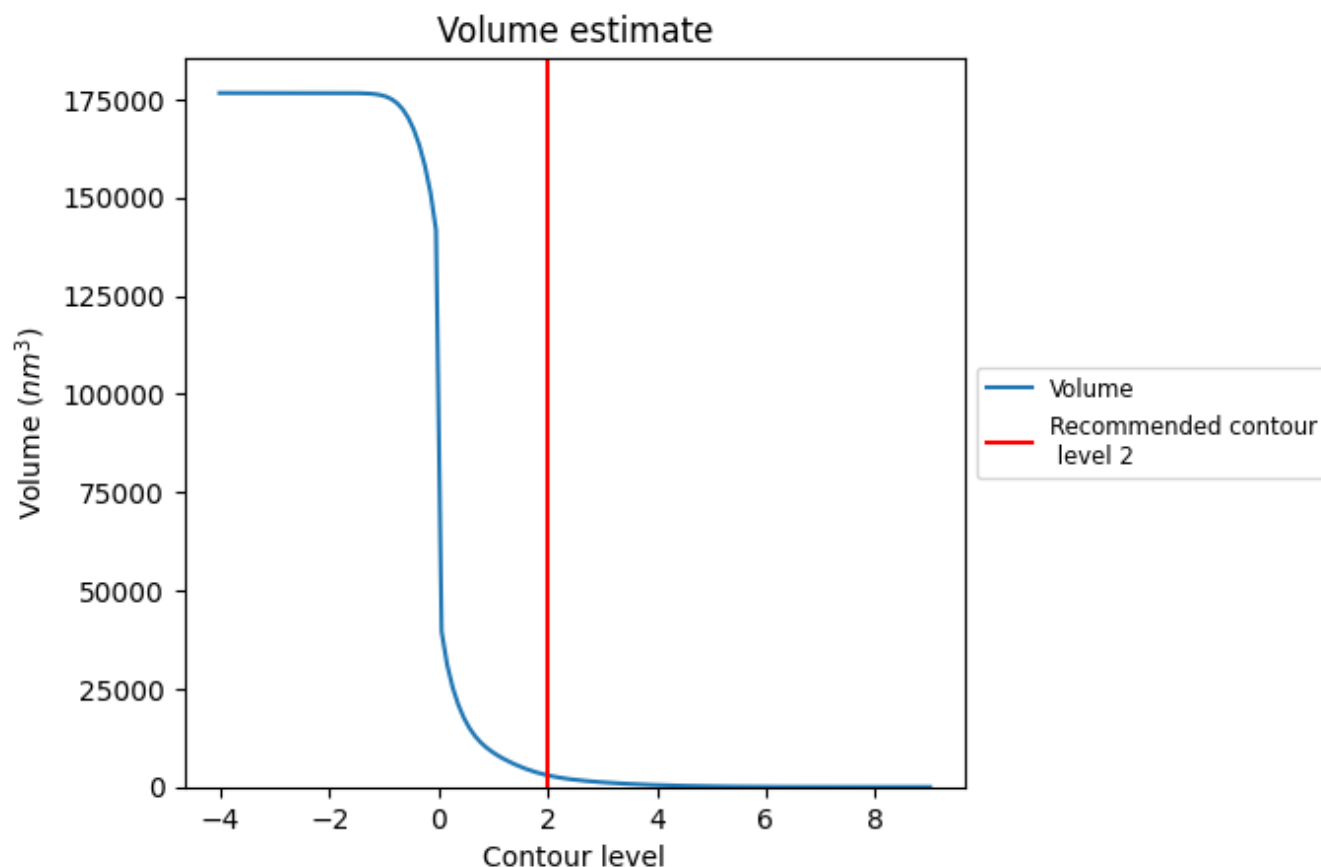
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

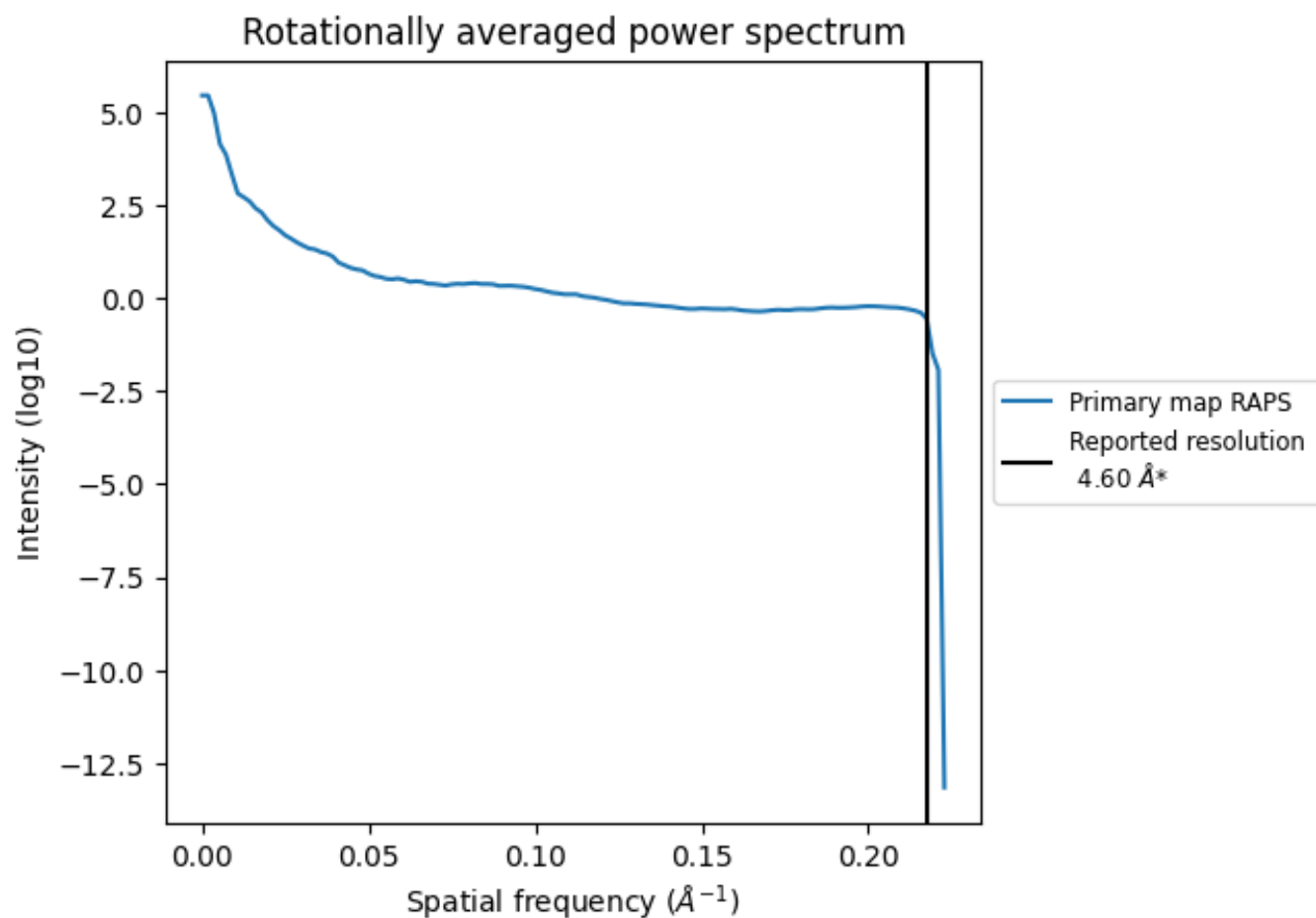
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2956 nm^3 ; this corresponds to an approximate mass of 2670 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

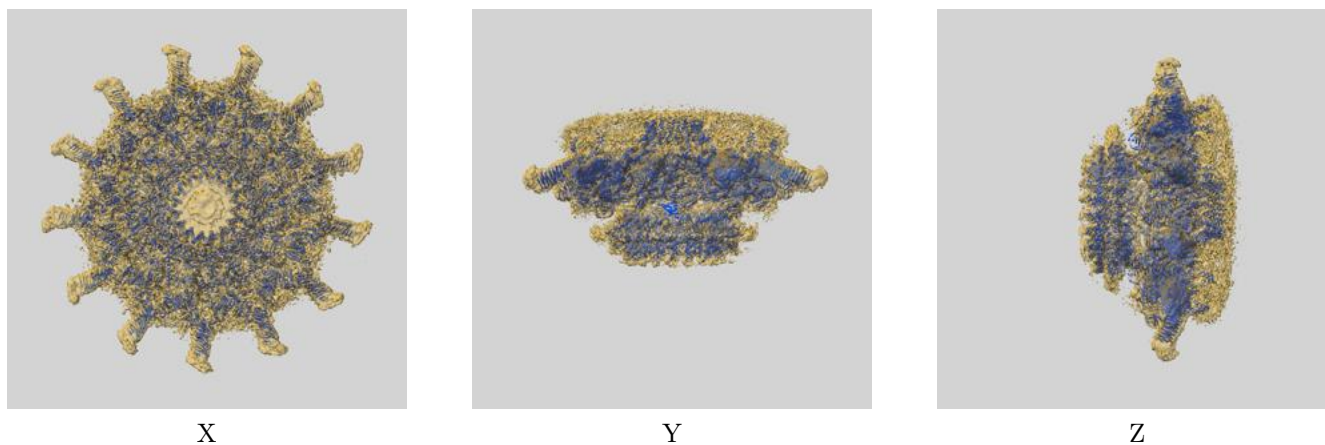
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

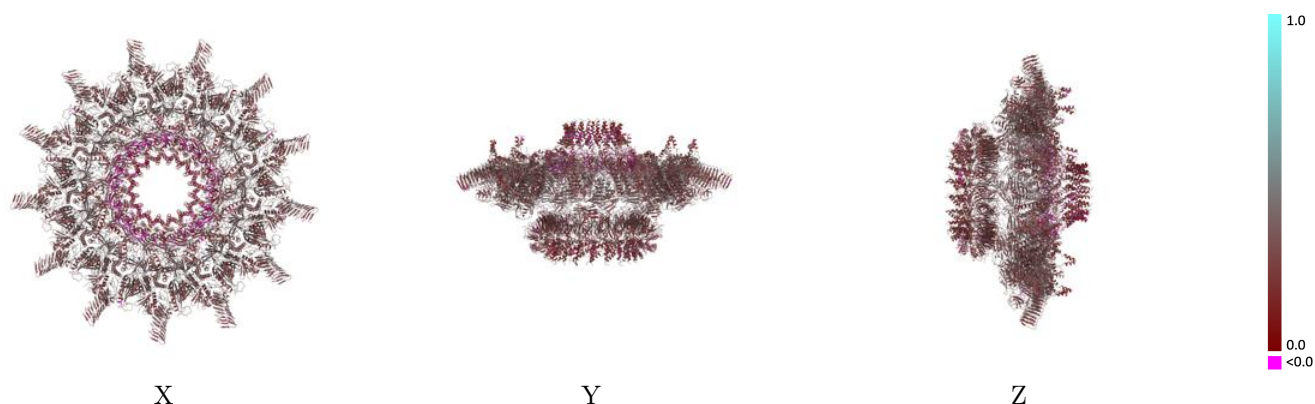
This section contains information regarding the fit between EMDB map EMD-24020 and PDB model 7MUS. Per-residue inclusion information can be found in section [3](#) on page [23](#).

9.1 Map-model overlay [i](#)



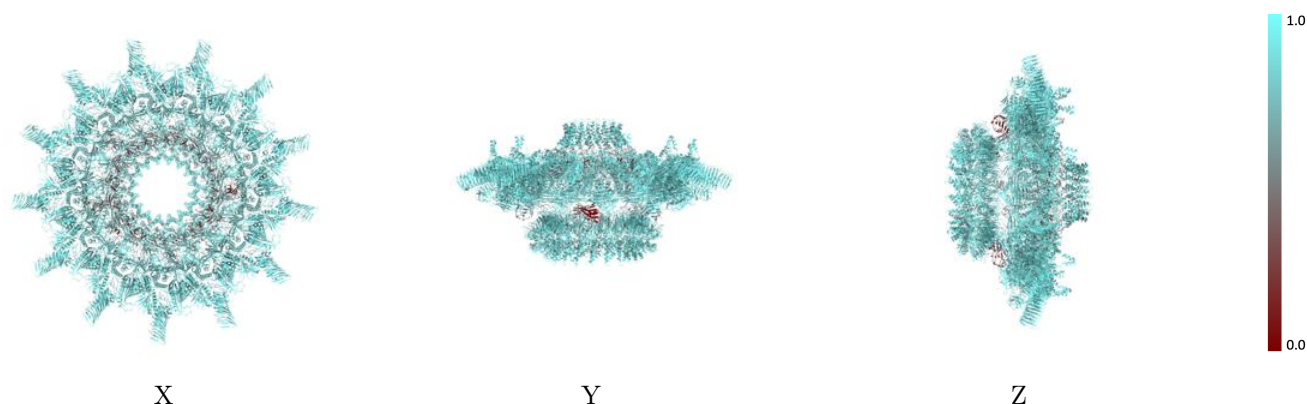
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



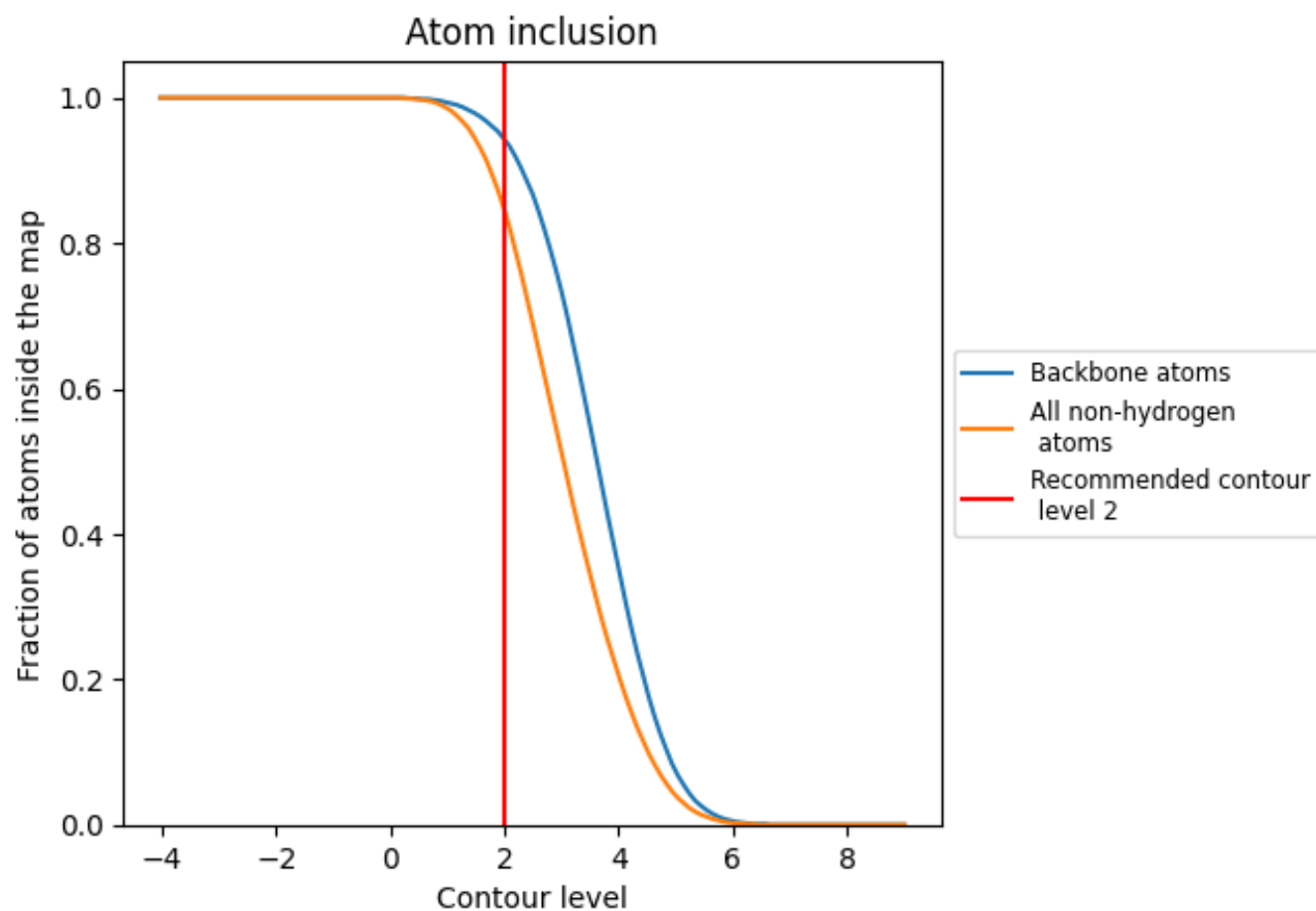
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 85% 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) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8460	 0.3050
AC	 0.8870	 0.3340
AD	 0.8840	 0.3450
AF	 0.8850	 0.2740
AG	 0.6670	 0.1580
AH	 0.8730	 0.3080
AK	 0.8900	 0.3440
AL	 0.8920	 0.3310
AM	 0.8960	 0.3180
AN	 0.8780	 0.3560
AU	 1.0000	 0.4820
AX	 0.7460	 0.2770
Ad	 0.8810	 0.3330
Af	 0.9160	 0.3180
Ag	 0.9040	 0.2670
BC	 0.8770	 0.3380
BD	 0.8730	 0.3400
BF	 0.8510	 0.2650
BG	 0.6670	 0.1480
BH	 0.8690	 0.3090
BK	 0.8840	 0.3480
BL	 0.8960	 0.3300
BM	 0.8780	 0.3330
BN	 0.8930	 0.3620
BU	 1.0000	 0.5020
BX	 0.7710	 0.2630
Bd	 0.8880	 0.3350
Bf	 0.8470	 0.3060
Bg	 0.9120	 0.2750
CC	 0.8740	 0.3420
CD	 0.8930	 0.3380
CF	 0.8580	 0.2620
CG	 0.6580	 0.1580
CH	 0.8700	 0.3140
CK	 0.8930	 0.3450



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Chain	Atom inclusion	Q-score
CL	 0.8930	 0.3230
CM	 0.8840	 0.3280
CN	 0.8740	 0.3690
CU	 1.0000	 0.4640
CX	 0.9080	 0.3150
Cd	 0.8890	 0.3380
Cf	 0.9090	 0.3330
Cg	 0.9010	 0.2640
DC	 0.8530	 0.3270
DD	 0.8760	 0.3520
DF	 0.9090	 0.2730
DG	 0.6480	 0.1630
DH	 0.8690	 0.3050
DK	 0.8980	 0.3500
DL	 0.8920	 0.3280
DM	 0.9060	 0.3290
DN	 0.8650	 0.3550
DU	 1.0000	 0.4930
DX	 0.8210	 0.2710
Dd	 0.8850	 0.3290
Df	 0.8970	 0.3220
Dg	 0.9340	 0.2730
EC	 0.8680	 0.3290
ED	 0.8730	 0.3480
EF	 0.8900	 0.2630
EG	 0.6130	 0.1540
EH	 0.8680	 0.3130
EK	 0.8680	 0.3470
EL	 0.8980	 0.3210
EM	 0.8900	 0.3270
EN	 0.8220	 0.3610
EU	 1.0000	 0.4890
EX	 0.7750	 0.2630
Ed	 0.8740	 0.3280
Ef	 0.8880	 0.3140
Eg	 0.9080	 0.2710
FC	 0.8770	 0.3360
FD	 0.8850	 0.3540
FF	 0.8730	 0.2570
FG	 0.6140	 0.1400
FH	 0.8510	 0.3120
FK	 0.8840	 0.3530

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Chain	Atom inclusion	Q-score
FL	 0.8980	 0.3280
FM	 0.8860	 0.3250
FN	 0.8990	 0.3660
FU	 0.9780	 0.4360
FX	 0.7130	 0.3110
Fd	 0.8930	 0.3350
Ff	 0.8680	 0.3000
Fg	 0.9150	 0.2540
GC	 0.8760	 0.3370
GD	 0.8920	 0.3570
GF	 0.8730	 0.2720
GG	 0.6430	 0.1470
GH	 0.8590	 0.3090
GK	 0.8930	 0.3460
GL	 0.9010	 0.3270
GM	 0.9040	 0.3290
GN	 0.8720	 0.3520
GU	 1.0000	 0.4720
GX	 0.7250	 0.2490
Gd	 0.8740	 0.3380
Gf	 0.8680	 0.3190
Gg	 0.9010	 0.2890
HC	 0.8510	 0.3210
HD	 0.8780	 0.3500
HF	 0.8640	 0.2590
HG	 0.6130	 0.1320
HH	 0.8980	 0.3230
HK	 0.8900	 0.3510
HL	 0.9120	 0.3350
HM	 0.8800	 0.3240
HN	 0.8640	 0.3590
HU	 1.0000	 0.4480
HX	 0.8290	 0.2900
Hd	 0.8860	 0.3380
Hf	 0.8750	 0.3050
Hg	 0.9010	 0.2850
IC	 0.8450	 0.3220
ID	 0.8810	 0.3400
IF	 0.8790	 0.2550
IG	 0.5900	 0.1260
IH	 0.8680	 0.3160
IK	 0.8880	 0.3510

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Chain	Atom inclusion	Q-score
IL	 0.9000	 0.3280
IM	 0.8810	 0.3330
IN	 0.8200	 0.3590
IU	 1.0000	 0.4820
IX	 0.8500	 0.2470
Id	 0.8980	 0.3360
If	 0.8860	 0.2960
Ig	 0.9150	 0.2920
JC	 0.8800	 0.3360
JD	 0.8700	 0.3430
JF	 0.9000	 0.2540
JG	 0.5910	 0.1270
JH	 0.8630	 0.3200
JK	 0.8870	 0.3490
JL	 0.9040	 0.3290
JM	 0.8910	 0.3290
JN	 0.8790	 0.3670
JU	 1.0000	 0.4660
JX	 0.8120	 0.2640
Jd	 0.8730	 0.3350
Jf	 0.8700	 0.3140
Jg	 0.8900	 0.2910
KC	 0.8900	 0.3370
KD	 0.8640	 0.3500
KF	 0.8850	 0.2420
KG	 0.6190	 0.1290
KH	 0.8600	 0.3080
KK	 0.8910	 0.3510
KL	 0.9130	 0.3310
KM	 0.8880	 0.3320
KN	 0.8930	 0.3620
KU	 1.0000	 0.4740
KX	 0.7920	 0.2790
Kd	 0.8720	 0.3340
Kf	 0.8720	 0.3060
Kg	 0.9230	 0.2820
LC	 0.8540	 0.3280
LD	 0.8880	 0.3540
LF	 0.8830	 0.2480
LG	 0.6440	 0.1470
LH	 0.8510	 0.2990
LK	 0.8860	 0.3420

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Chain	Atom inclusion	Q-score
LL	 0.8940	 0.3250
LM	 0.8680	 0.3300
LN	 0.8710	 0.3570
LU	 0.9780	 0.4540
LX	 0.8710	 0.2500
Ld	 0.8890	 0.3440
Lf	 0.8520	 0.3100
Lg	 0.9300	 0.2840
MC	 0.8430	 0.3130
MD	 0.8730	 0.3530
MF	 0.8770	 0.2620
MG	 0.6900	 0.1860
MH	 0.8750	 0.3080
MK	 0.9000	 0.3540
ML	 0.9180	 0.3380
MM	 0.8960	 0.3260
MN	 0.8460	 0.3680
MU	 0.9780	 0.4600
MX	 0.8210	 0.2570
Md	 0.9020	 0.3410
Mf	 0.9000	 0.3340
Mg	 0.8970	 0.2710
NG	 0.7170	 0.1890
OG	 0.6450	 0.1520
PG	 0.6360	 0.1390
VF	 0.8850	 0.2410
VG	 0.8860	 0.2540
VH	 0.7930	 0.2830
VX	 0.8170	 0.2590
WF	 0.8980	 0.2750
WG	 0.8970	 0.2680
WH	 0.5890	 0.2720
WX	 0.8000	 0.2850
XF	 0.8390	 0.2520
XG	 0.9010	 0.2810
XH	 0.7970	 0.2930
XX	 0.8380	 0.2630
YF	 0.8490	 0.2570
YG	 0.8600	 0.2550
YH	 0.7090	 0.2860
YX	 0.7830	 0.2410
ZF	 0.8640	 0.2570

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Chain	Atom inclusion	Q-score
ZG	 0.8930	 0.2640
ZH	 0.6570	 0.2640
ZX	 0.8500	 0.2450