



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 08:22 AM UTC

PDB ID : 7MUQ / pdb_00007muq
EMDB ID : EMD-24018
Title : Reconstruction of the Legionella pneumophila Dot/Icm T4SS 3DVA Map 1
Authors : Sheedlo, M.J.; Durie, C.L.; Swanson, M.; Lacy, D.B.; Ohi, M.D.
Deposited on : 2021-05-14
Resolution : 4.60 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

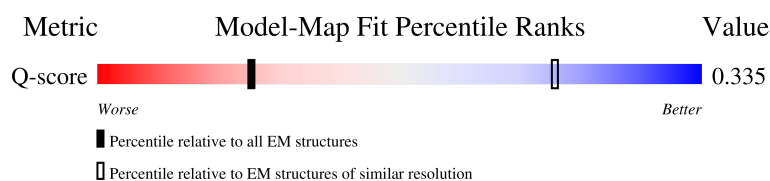
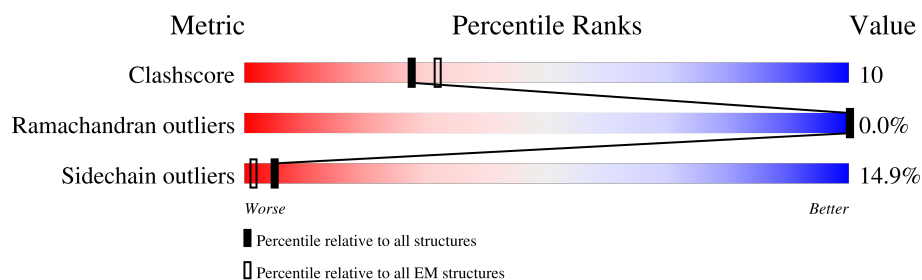
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.60 Å.

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



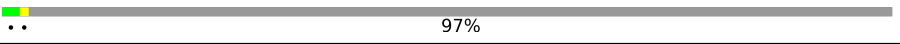
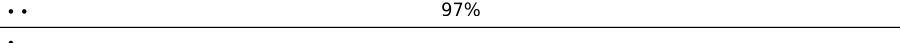
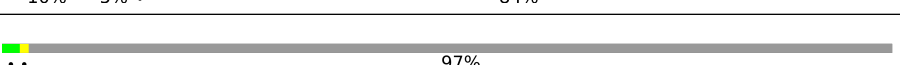
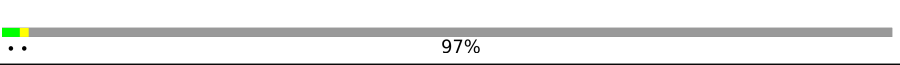
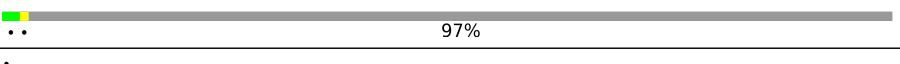
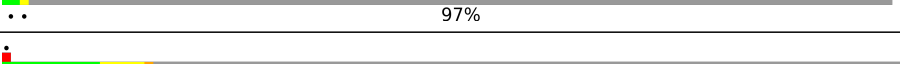
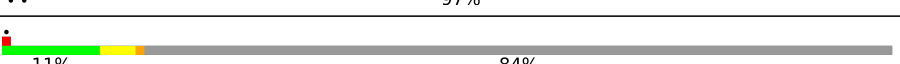
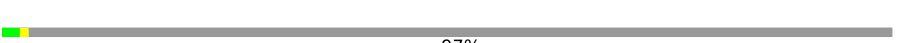
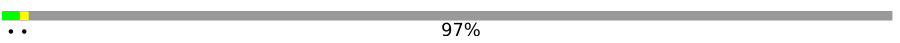
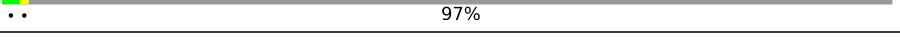
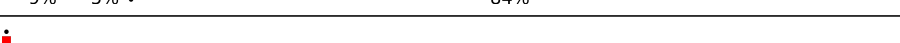
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2407 (4.10 - 5.10)

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

Mol	Chain	Length	Quality of chain
1	AG	1048	 10% 5% 84%
1	Ag	1048	 97%
1	BG	1048	 10% 5% 84%
1	Bg	1048	 97%

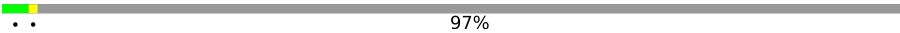
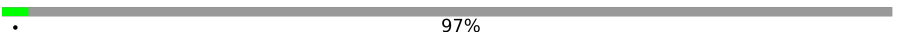
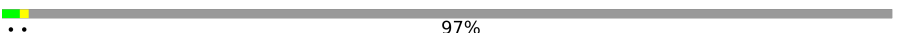
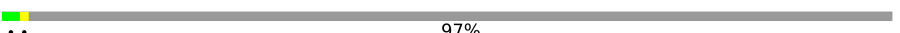
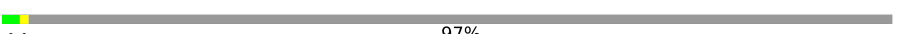
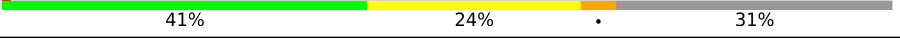
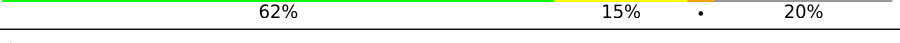
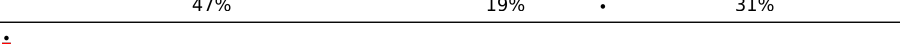
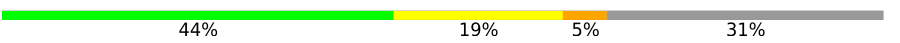
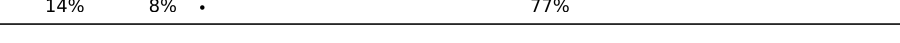
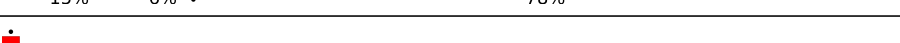
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Mol	Chain	Length	Quality of chain
1	CG	1048	 9% 5% 84%
1	Cg	1048	 97%
1	DG	1048	 9% 6% 84%
1	Dg	1048	 97%
1	EG	1048	 11% 5% 84%
1	Eg	1048	 97%
1	FG	1048	 10% 5% 84%
1	Fg	1048	 97%
1	GG	1048	 10% 5% 84%
1	Gg	1048	 97%
1	HG	1048	 11% 5% 84%
1	Hg	1048	 97%
1	IG	1048	 11% 5% 84%
1	Ig	1048	 97%
1	JG	1048	 11% 5% 84%
1	Jg	1048	 97%
1	KG	1048	 11% 5% 84%
1	Kg	1048	 97%
1	LG	1048	 11% 5% 84%
1	Lg	1048	 97%
1	MG	1048	 10% 5% 84%
1	Mg	1048	 97%
1	NG	1048	 9% 5% 84%
1	OG	1048	 9% 5% 84%
1	PG	1048	 9% 5% 84%

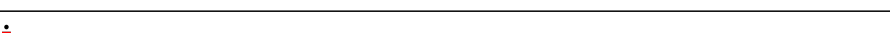
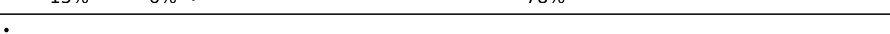
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Mol	Chain	Length	Quality of chain
1	VG	1048	 97%
1	WG	1048	 97%
1	XG	1048	 97%
1	YG	1048	 97%
1	ZG	1048	 97%
2	AC	303	 48% 17% 5% 31%
2	BC	303	 49% 16% 5% 31%
2	CC	303	 41% 24% 5% 31%
2	DC	303	 62% 15% 5% 20%
2	EC	303	 47% 19% 5% 31%
2	FC	303	 44% 22% 5% 31%
2	GC	303	 46% 20% 5% 31%
2	HC	303	 59% 20% 5% 20%
2	IC	303	 58% 19% 5% 20%
2	JC	303	 46% 19% 5% 31%
2	KC	303	 44% 19% 5% 31%
2	LC	303	 60% 18% 5% 20%
2	MC	303	 57% 21% 5% 20%
3	AF	269	 14% 8% 5% 77%
3	Af	269	 15% 6% 5% 78%
3	BF	269	 16% 6% 5% 77%
3	Bf	269	 16% 6% 5% 78%
3	CF	269	 14% 8% 5% 77%
3	Cf	269	 13% 7% 5% 78%
3	DF	269	 14% 8% 5% 77%

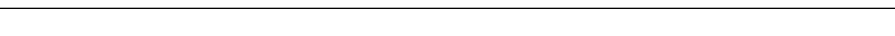
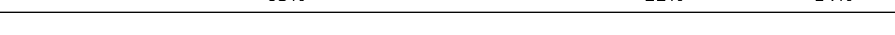
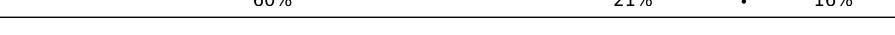
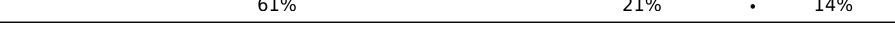
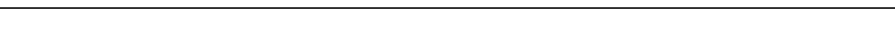
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Mol	Chain	Length	Quality of chain
3	Df	269	
3	EF	269	
3	Ef	269	
3	FF	269	
3	Ff	269	
3	GF	269	
3	Gf	269	
3	HF	269	
3	Hf	269	
3	IF	269	
3	If	269	
3	JF	269	
3	Jf	269	
3	KF	269	
3	Kf	269	
3	LF	269	
3	Lf	269	
3	MF	269	
3	Mf	269	
3	VF	269	
3	WF	269	
3	XF	269	
3	YF	269	
3	ZF	269	
4	AD	163	

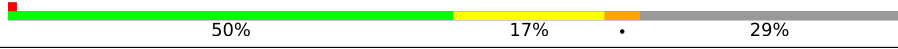
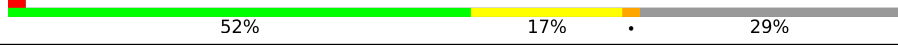
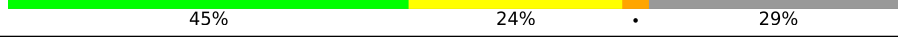
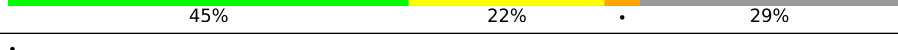
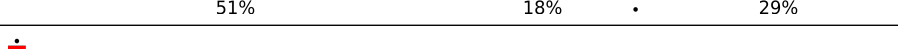
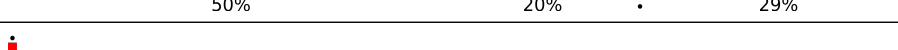
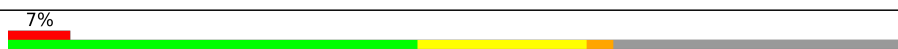
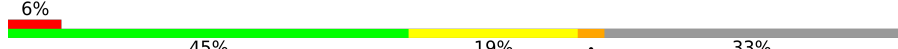
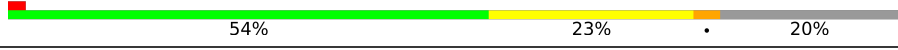
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Mol	Chain	Length	Quality of chain
4	Ad	163	
4	BD	163	
4	Bd	163	
4	CD	163	
4	Cd	163	
4	DD	163	
4	Dd	163	
4	ED	163	
4	Ed	163	
4	FD	163	
4	Fd	163	
4	GD	163	
4	Gd	163	
4	HD	163	
4	Hd	163	
4	ID	163	
4	Id	163	
4	JD	163	
4	Jd	163	
4	KD	163	
4	Kd	163	
4	LD	163	
4	Ld	163	
4	MD	163	
4	Md	163	

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Mol	Chain	Length	Quality of chain
5	AH	361	
5	BH	361	
5	CH	361	
5	DH	361	
5	EH	361	
5	FH	361	
5	GH	361	
5	HH	361	
5	IH	361	
5	JH	361	
5	KH	361	
5	LH	361	
5	MH	361	
5	VH	361	
5	WH	361	
5	XH	361	
5	YH	361	
5	ZH	361	
6	AK	189	
6	BK	189	
6	CK	189	
6	DK	189	
6	EK	189	
6	FK	189	
6	GK	189	

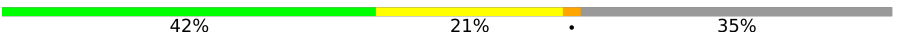
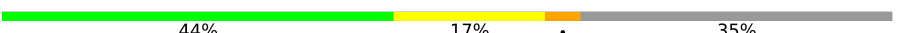
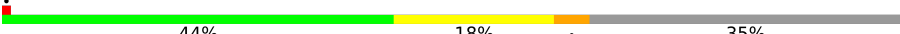
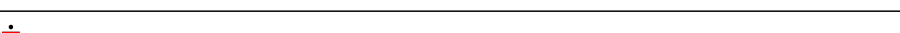
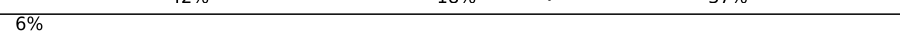
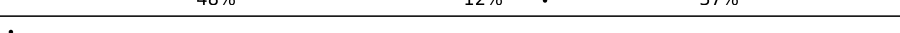
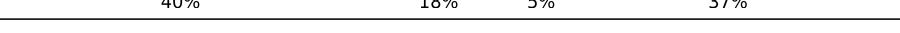
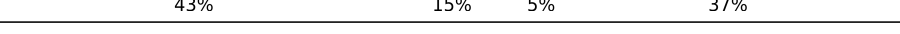
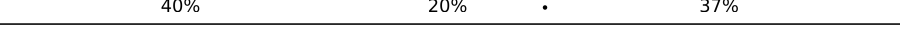
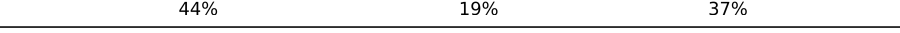
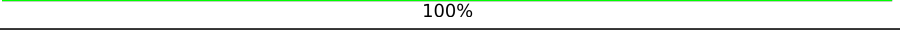
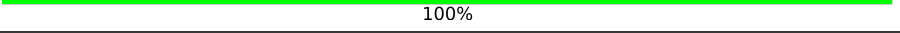
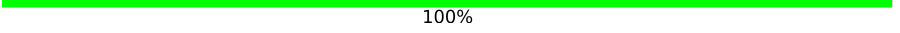
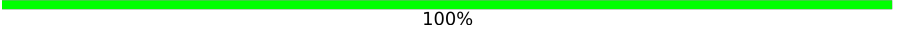
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Mol	Chain	Length	Quality of chain
6	HK	189	
6	IK	189	
6	JK	189	
6	KK	189	
6	LK	189	
6	MK	189	
7	AL	249	
7	BL	249	
7	CL	249	
7	DL	249	
7	EL	249	
7	FL	249	
7	GL	249	
7	HL	249	
7	IL	249	
7	JL	249	
7	KL	249	
7	LL	249	
7	ML	249	
8	AM	320	
8	BM	320	
8	CM	320	
8	DM	320	
8	EM	320	
8	FM	320	

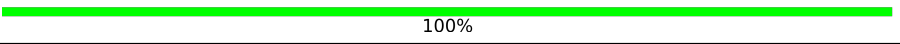
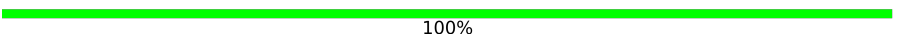
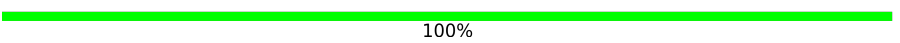
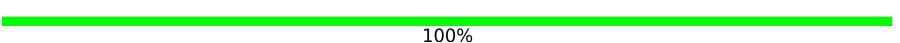
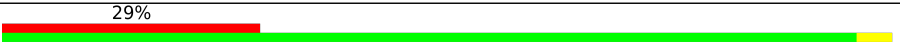
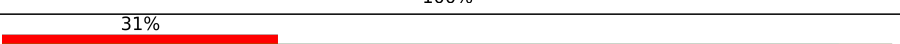
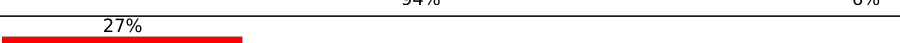
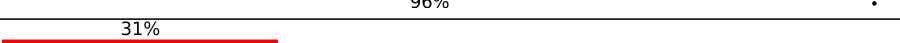
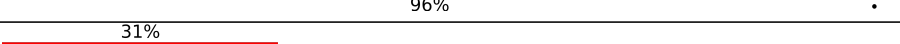
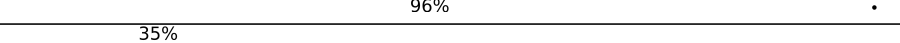
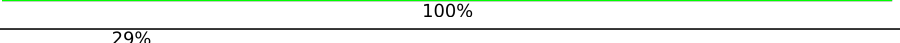
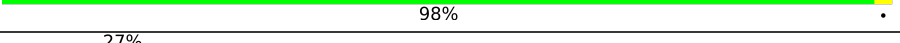
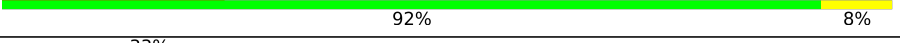
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Mol	Chain	Length	Quality of chain
8	GM	320	
8	HM	320	
8	IM	320	
8	JM	320	
8	KM	320	
8	LM	320	
8	MM	320	
9	AN	124	
9	BN	124	
9	CN	124	
9	DN	124	
9	EN	124	
9	FN	124	
9	GN	124	
9	HN	124	
9	IN	124	
9	JN	124	
9	KN	124	
9	LN	124	
9	MN	124	
10	AU	9	
10	BU	9	
10	CU	9	
10	DU	9	
10	EU	9	

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Mol	Chain	Length	Quality of chain
10	FU	9	
10	GU	9	
10	HU	9	
10	IU	9	
10	JU	9	
10	KU	9	
10	LU	9	
10	MU	9	
11	AX	48	
11	BX	48	
11	CX	48	
11	DX	48	
11	EX	48	
11	FX	48	
11	GX	48	
11	HX	48	
11	IX	48	
11	JX	48	
11	KX	48	
11	LX	48	
11	MX	48	
11	VX	48	
11	WX	48	
11	XX	48	
11	YX	48	

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Mol	Chain	Length	Quality of chain
11	ZX	48	17% 94% 6%

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 192370 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called IcmE protein.

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

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	XG	34	Total	C	N	O	S	0	0
			276	168	47	60	1		
1	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 DotC.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	BC	209	Total	C	N	O	S	0	0
			1667	1061	292	309	5		
2	EC	209	Total	C	N	O	S	0	0
			1667	1061	292	309	5		

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

- Molecule 3 is a protein called DotF.

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

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

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Mol	Chain	Residues	Atoms					AltConf	Trace
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		

- Molecule 4 is a protein called DotD.

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

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	BD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
4	Bd	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
4	AD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
4	Cd	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
4	DD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
4	ED	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
4	Ed	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		
4	FD	140	Total	C	N	O	S	0	0
			1086	692	185	206	3		
4	Fd	137	Total	C	N	O	S	0	0
			1058	672	182	202	2		

- Molecule 5 is a protein called Type IV secretion protein IcmK.

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

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	XH	243	Total	C	N	O	S	0	0
			1875	1201	319	348	7		
5	YH	243	Total	C	N	O	S	0	0
			1875	1201	319	348	7		
5	ZH	243	Total	C	N	O	S	0	0
			1875	1201	319	348	7		
5	BH	258	Total	C	N	O	S	0	0
			1983	1268	336	371	8		
5	CH	258	Total	C	N	O	S	0	0
			1983	1268	336	371	8		
5	DH	258	Total	C	N	O	S	0	0
			1983	1268	336	371	8		
5	EH	258	Total	C	N	O	S	0	0
			1983	1268	336	371	8		
5	FH	258	Total	C	N	O	S	0	0
			1983	1268	336	371	8		

- Molecule 6 is a protein called Inner membrane lipoprotein YiaD.

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

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

- Molecule 7 is a protein called Outer membrane protein, OmpA family protein.

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

- Molecule 8 is a protein called DUF2807 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	GM	208	Total	C	N	O	S	0	0
			1650	1046	293	308	3		
8	HM	208	Total	C	N	O	S	0	0
			1650	1046	293	308	3		

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

- Molecule 9 is a protein called Neurogenic locus notch.

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

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

- Molecule 10 is a protein called Unknown protein fragment.

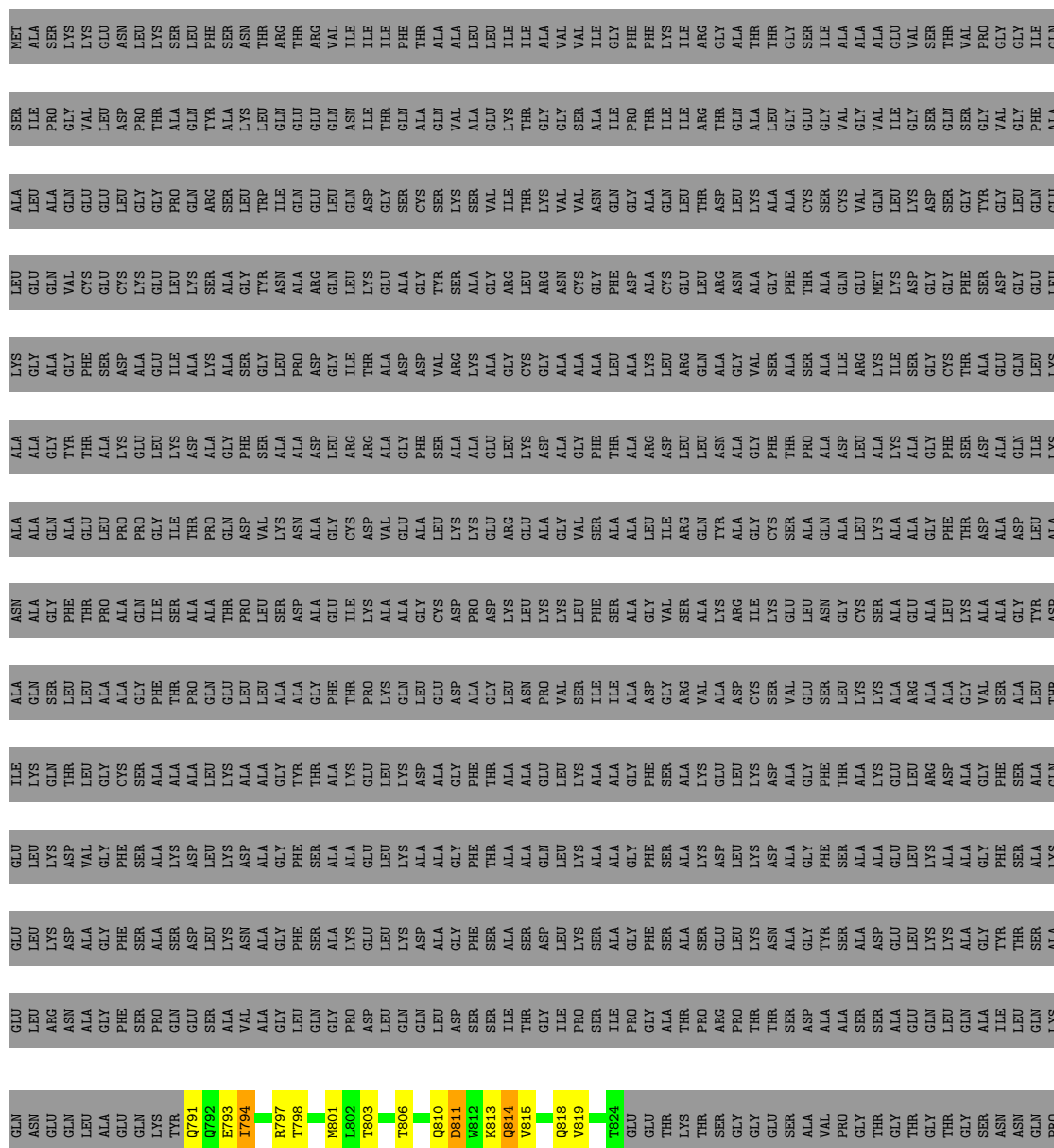
Mol	Chain	Residues	Atoms				AltConf	Trace
10	GU	9	Total	C	N	O	0	0
			45	27	9	9		
10	HU	9	Total	C	N	O	0	0
			45	27	9	9		
10	IU	9	Total	C	N	O	0	0
			45	27	9	9		
10	JU	9	Total	C	N	O	0	0
			45	27	9	9		
10	KU	9	Total	C	N	O	0	0
			45	27	9	9		
10	LU	9	Total	C	N	O	0	0
			45	27	9	9		
10	MU	9	Total	C	N	O	0	0
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

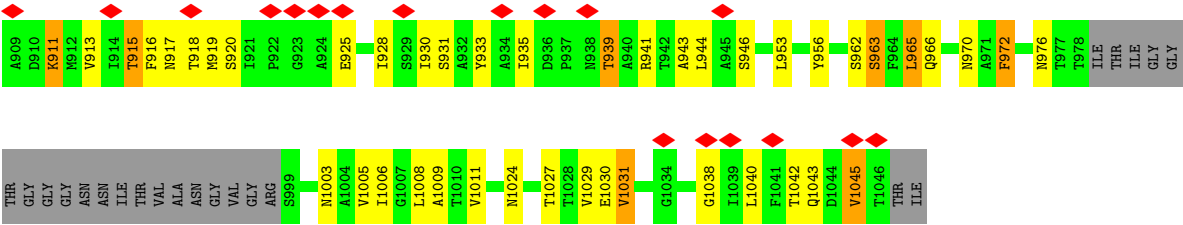
- Molecule 11 is a protein called Unknown protein fragment.

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

- Molecule 1: IcmE protein

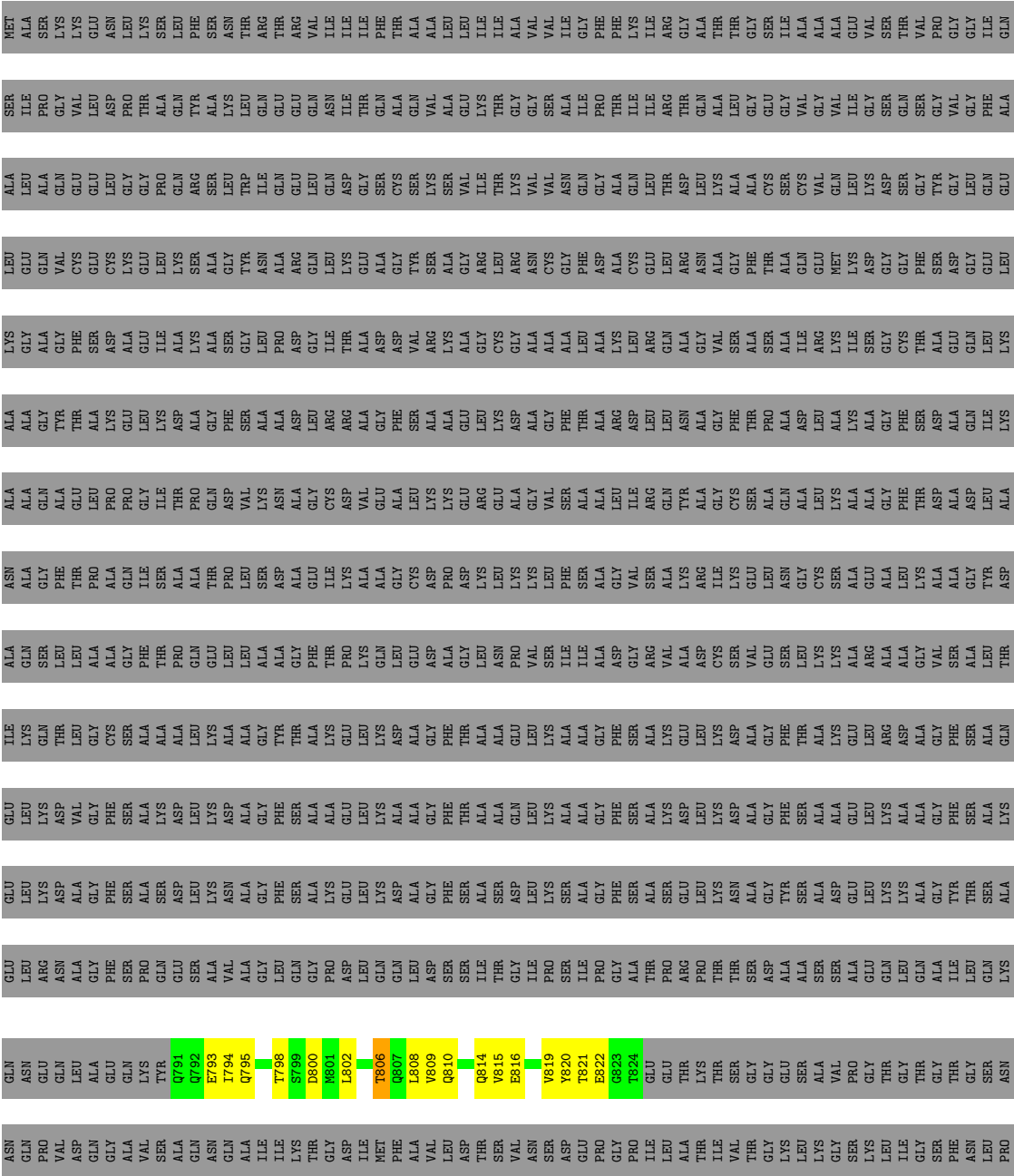
Chain Gg: .. 97%





● Molecule 1: IcmE protein

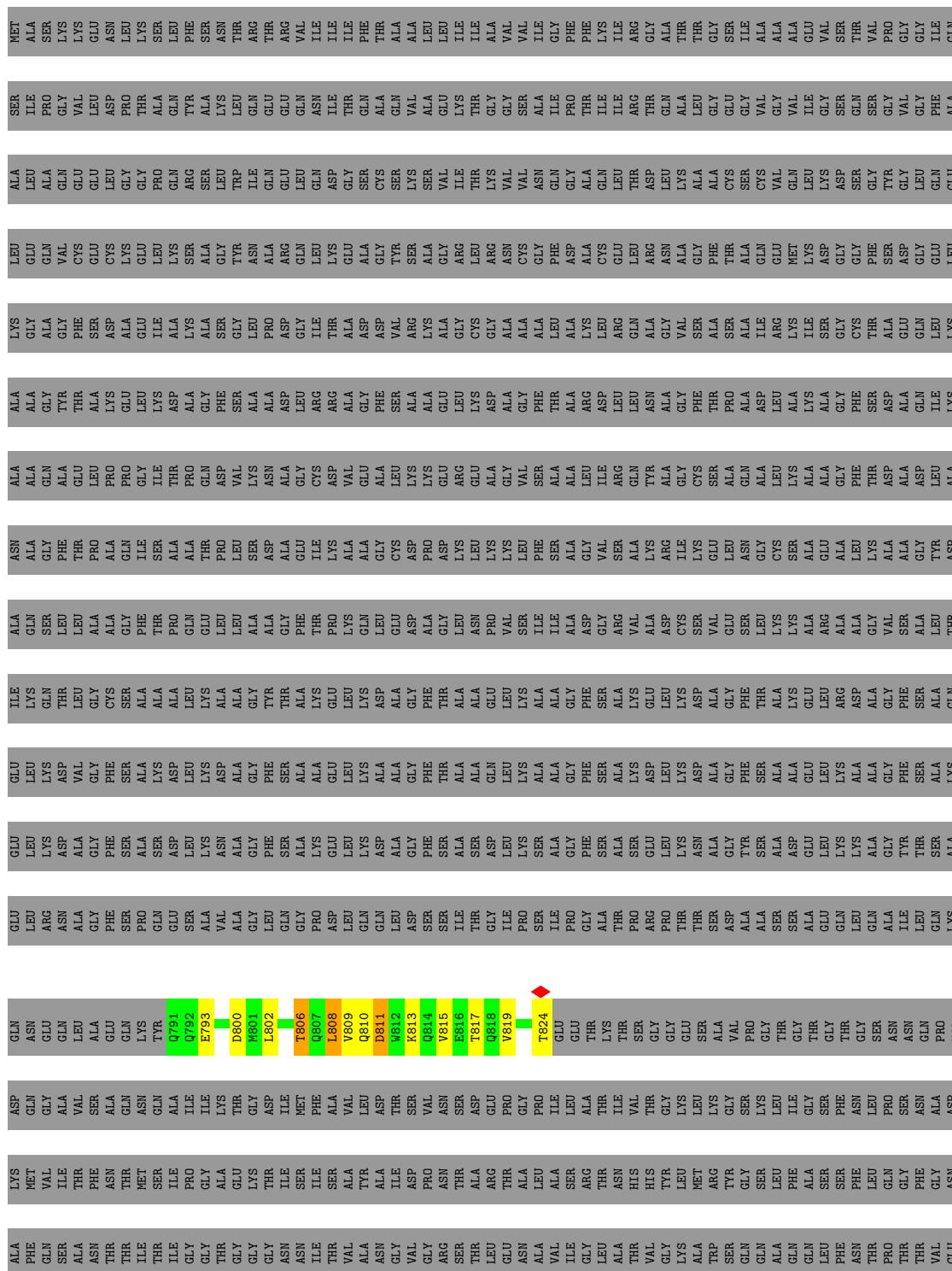
Chain Bg: .. 97%





- Molecule 1: IcmE protein

Chain Kg: 97%



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

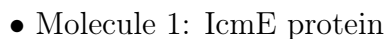
● Molecule 1: IcmE protein

Chain Lg: .. 97%

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



Chain Cg: .. 97%



97%

- Molecule 1: IcmE protein

97%



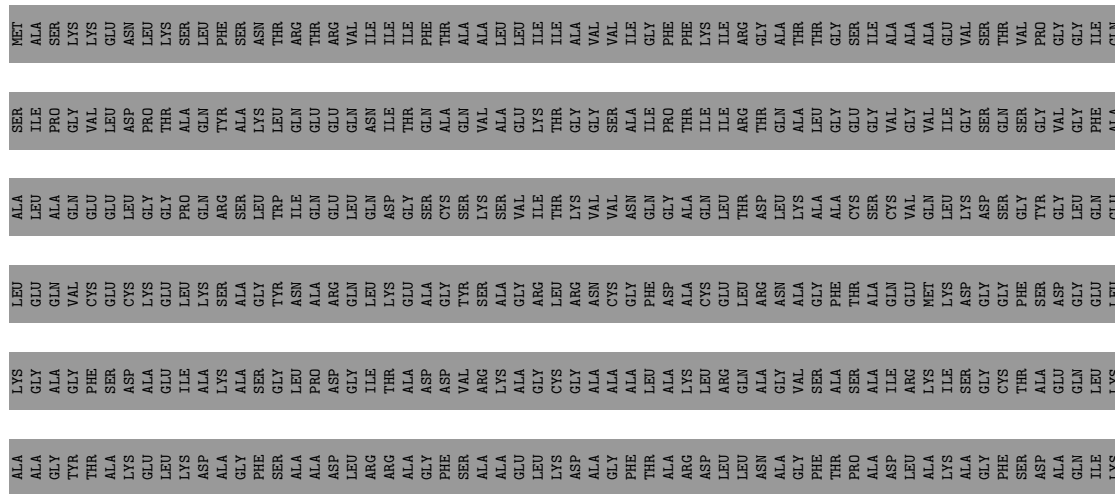


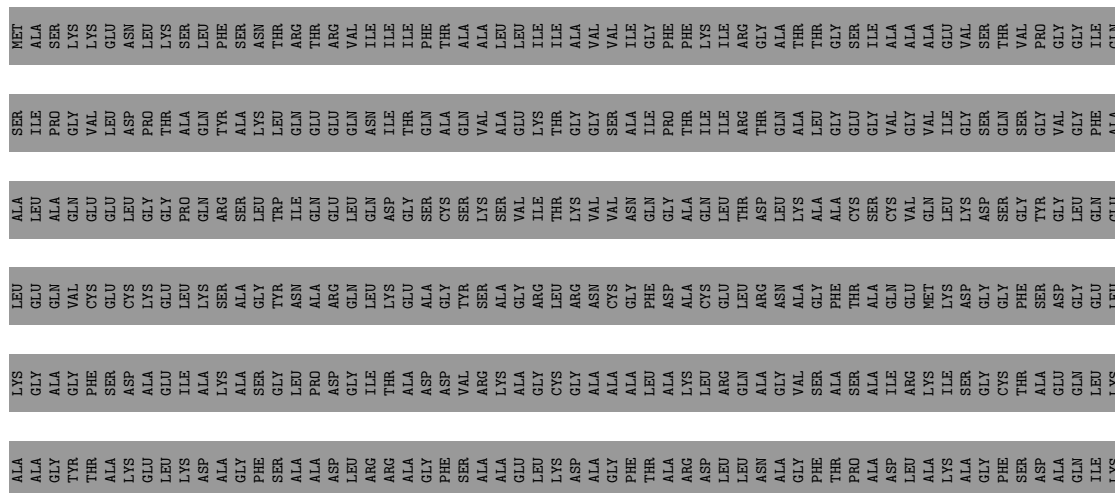
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Chain YG: 97%





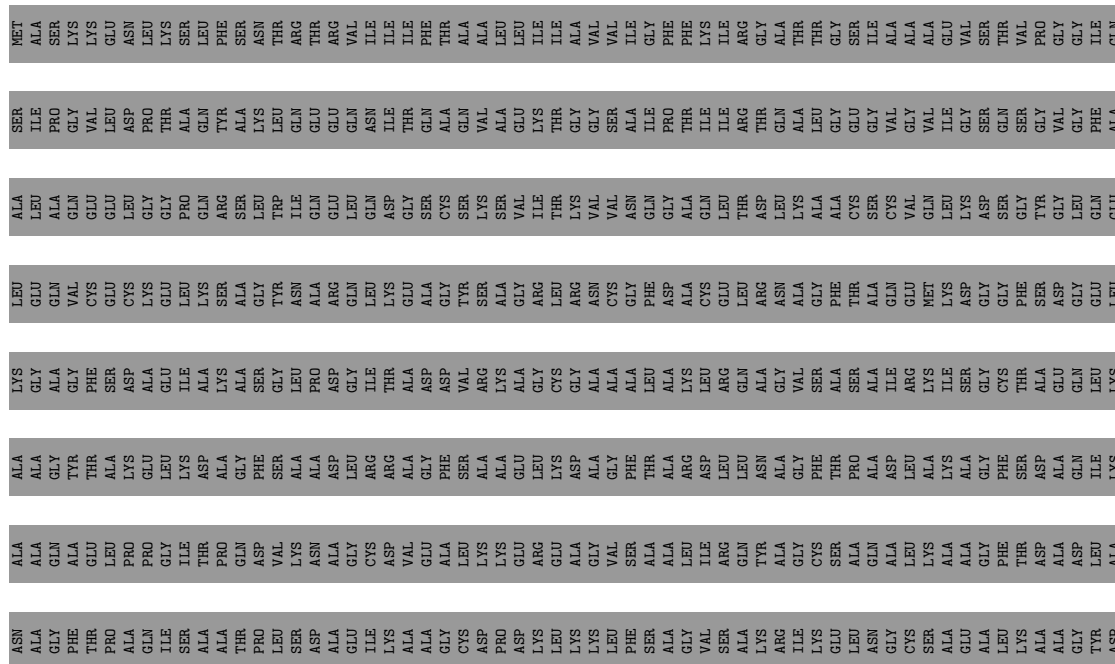




- Molecule 1: IcmE protein

[illegible]



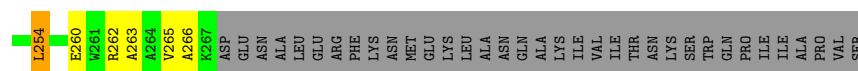




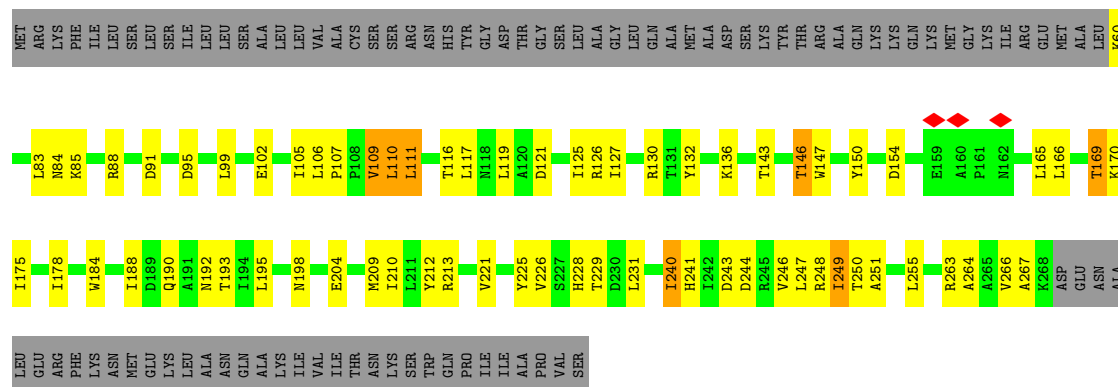
- Molecule 1: IcmE protein

[illegible]

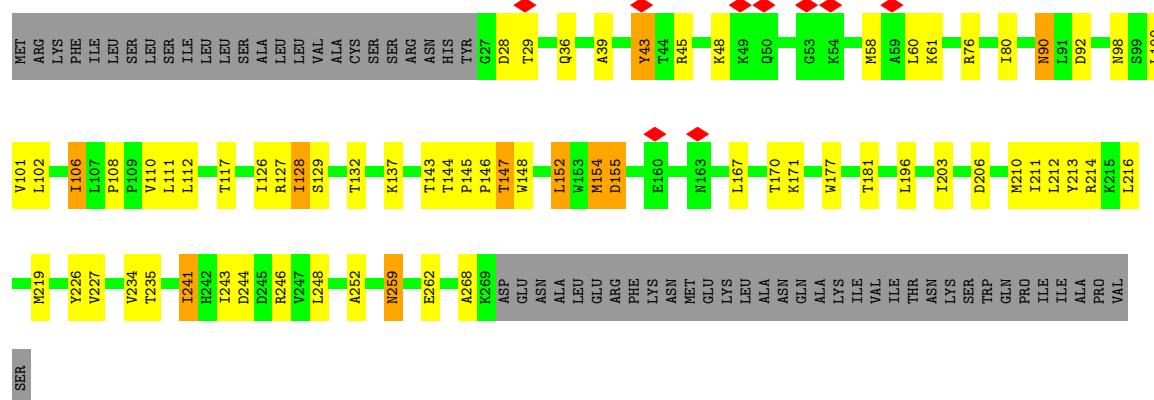




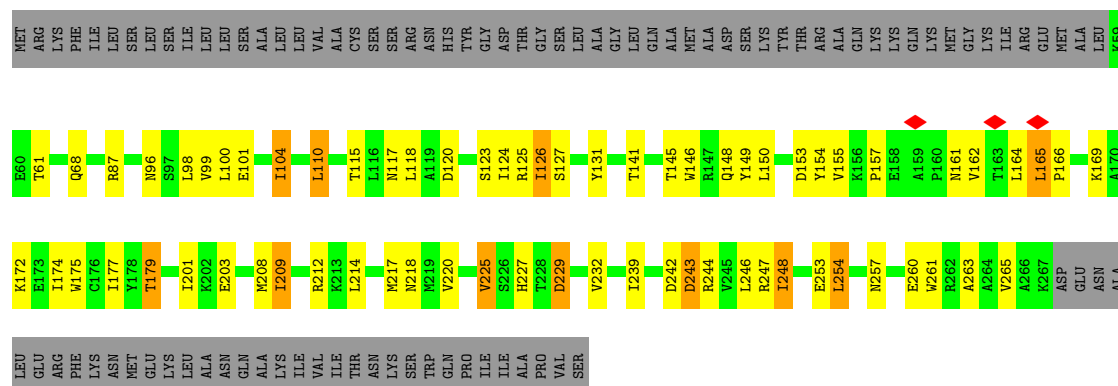
• Molecule 2: DotC



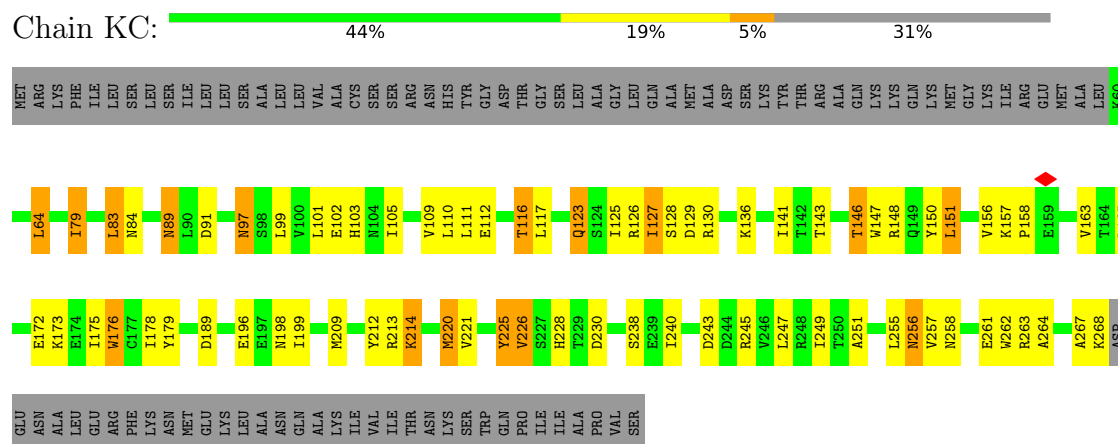
• Molecule 2: DotC



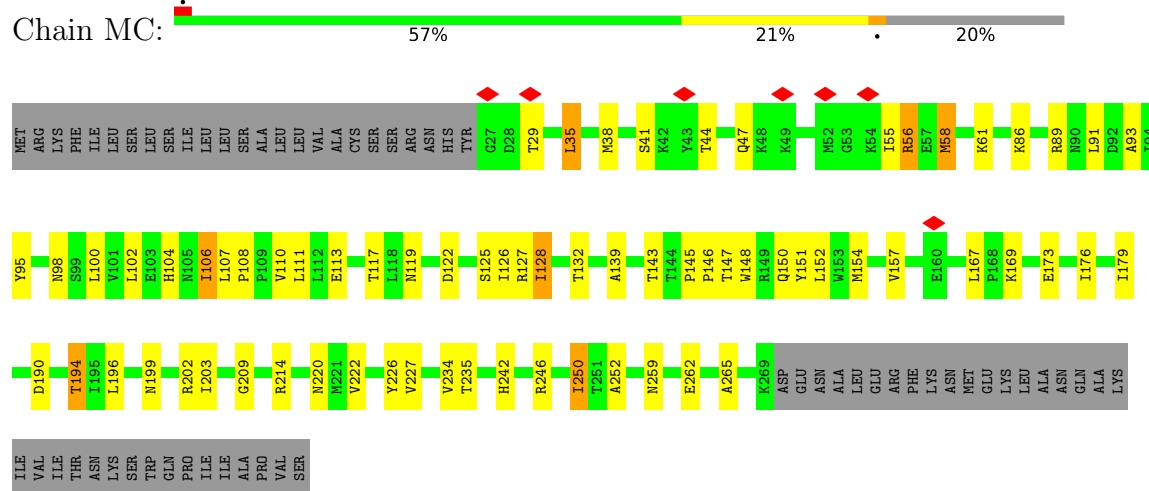
• Molecule 2: DotC



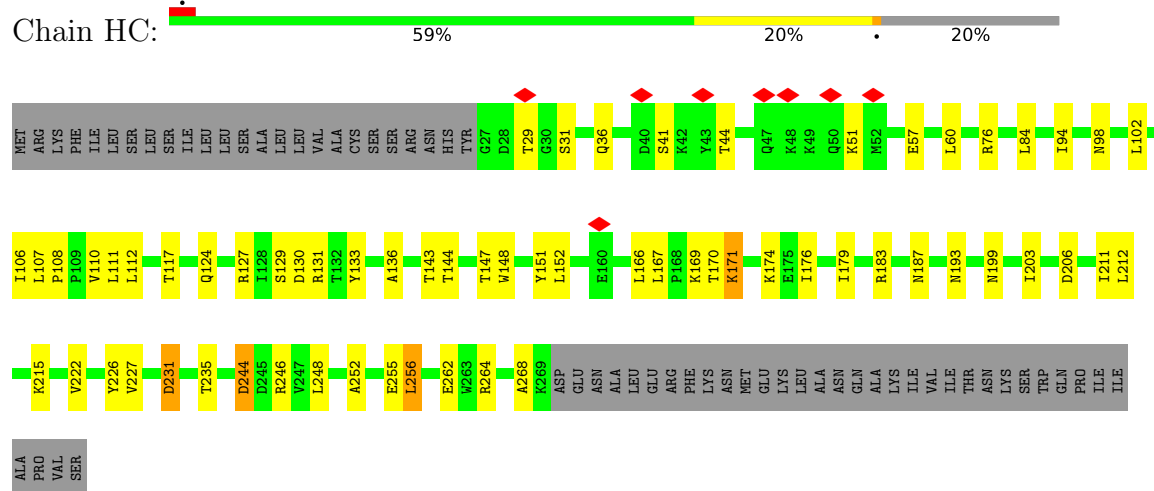
- Molecule 2: DotC



- Molecule 2: DotC

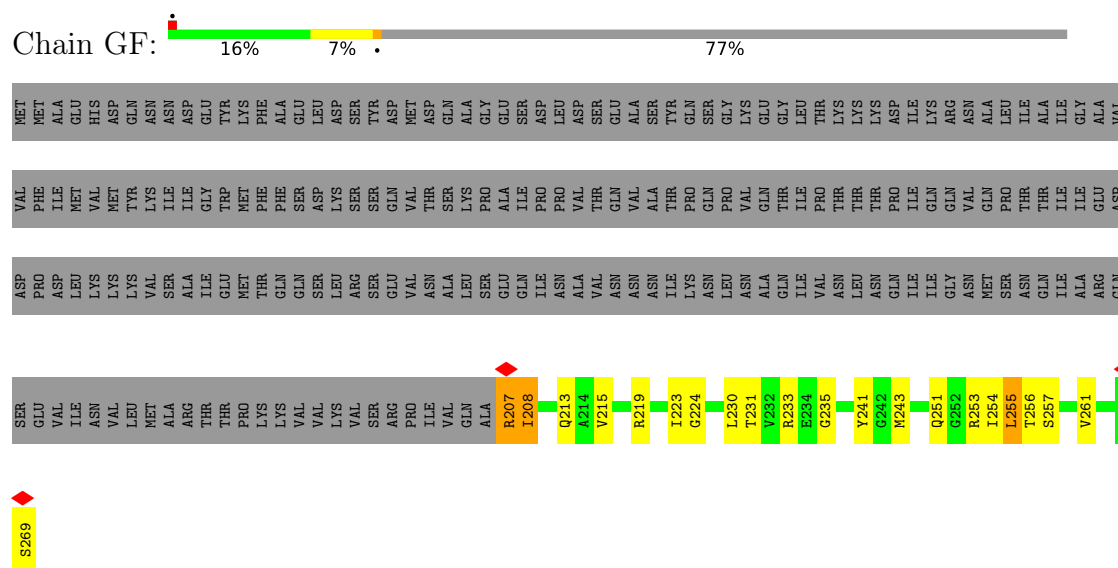


- Molecule 2: DotC

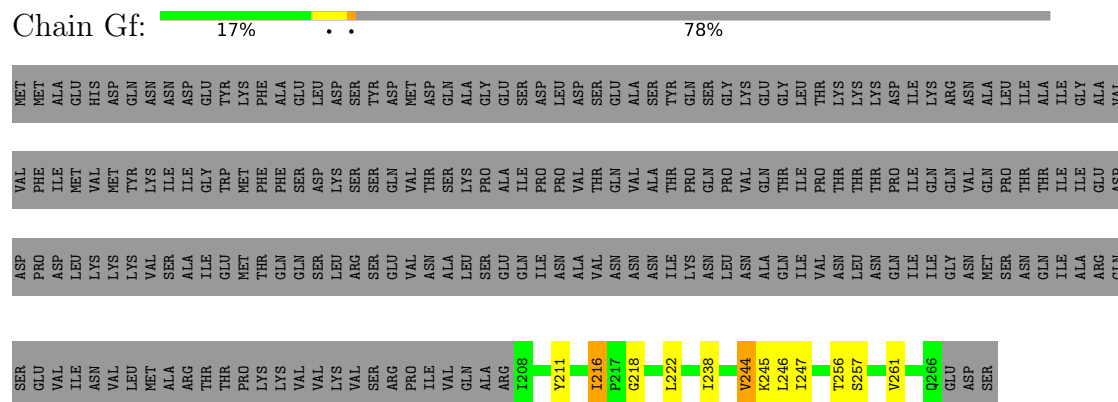


- Molecule 2: DotC

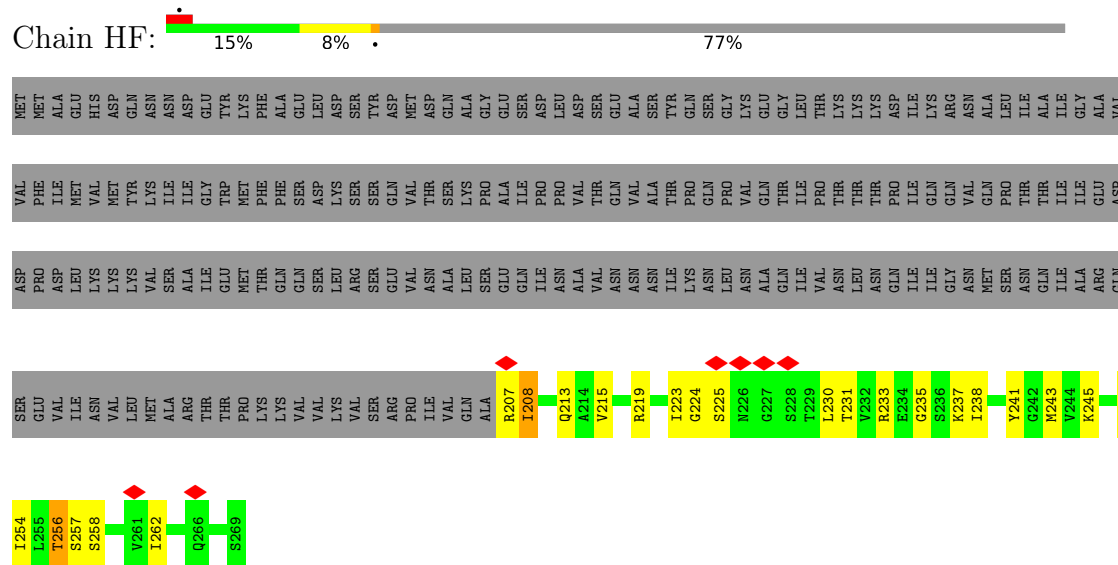




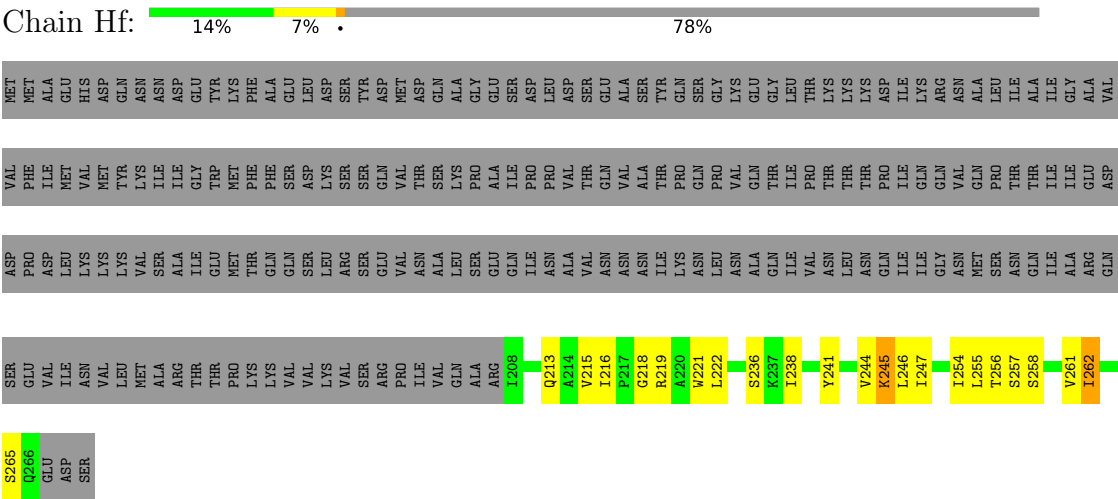
- Molecule 3: DotF



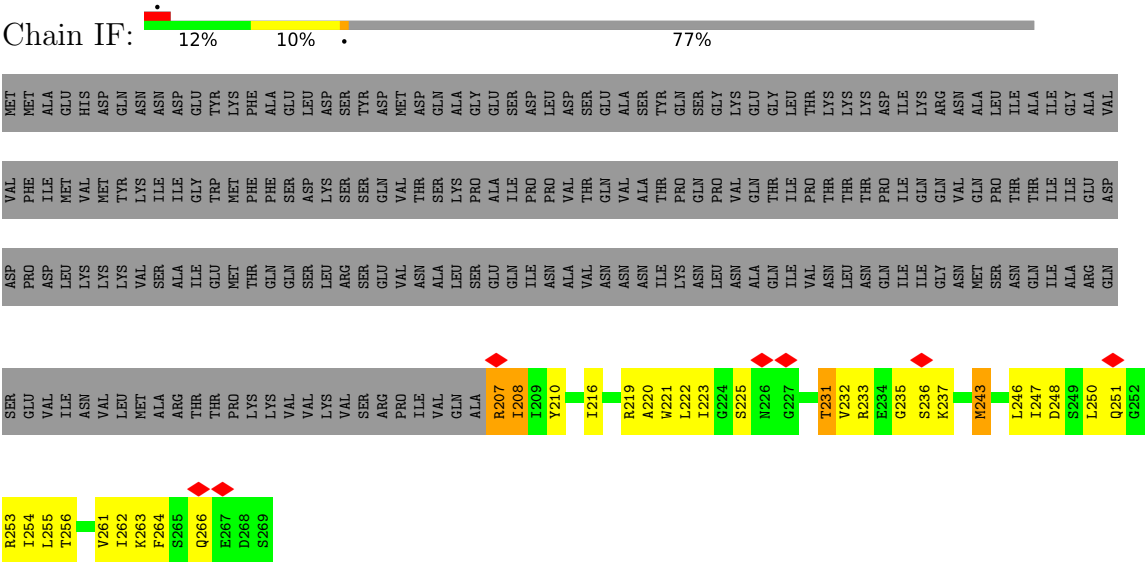
- Molecule 3: DotF



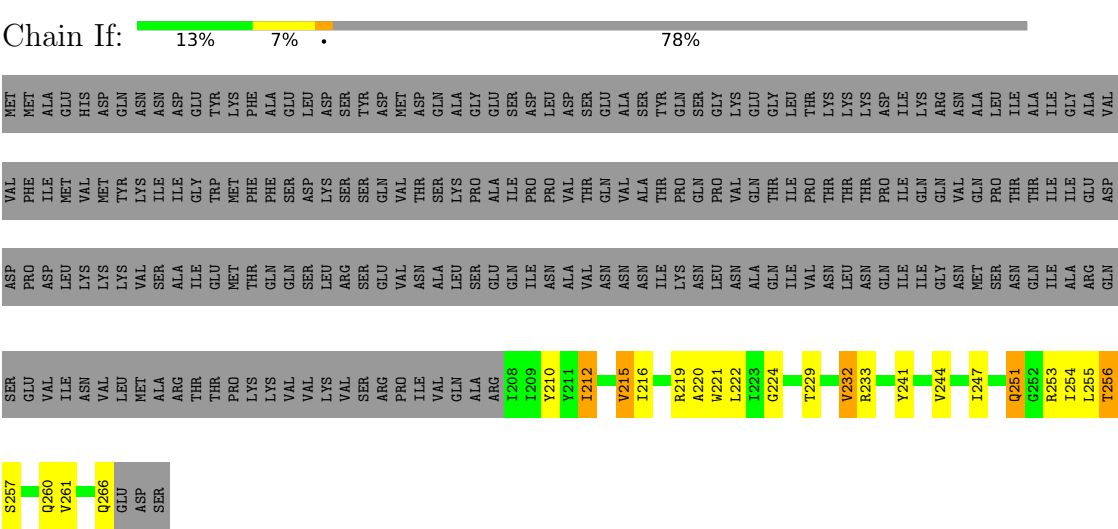
- Molecule 3: DotF



• Molecule 3: DotF

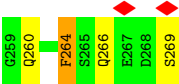
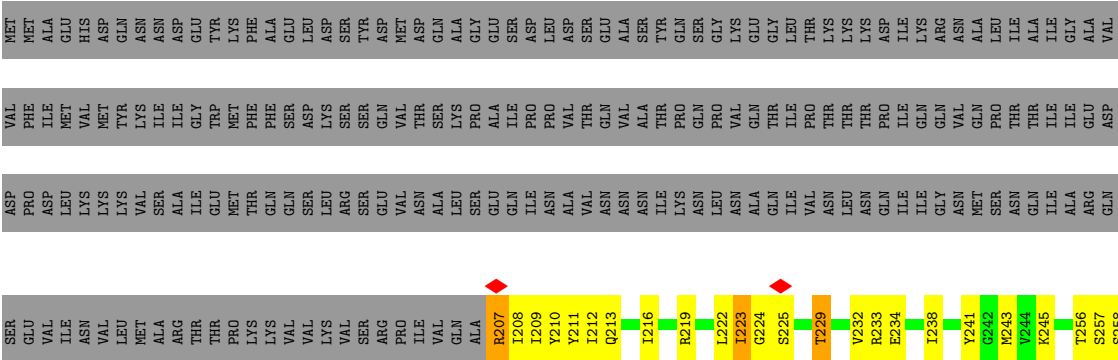


• Molecule 3: DotF

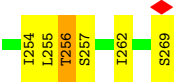
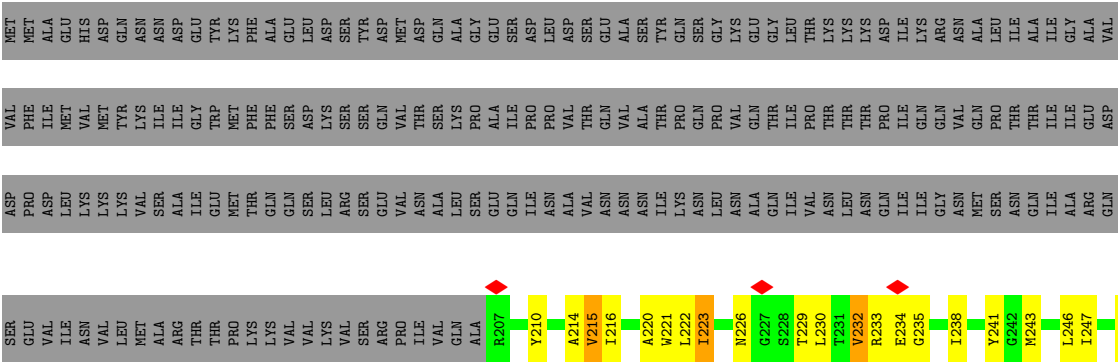




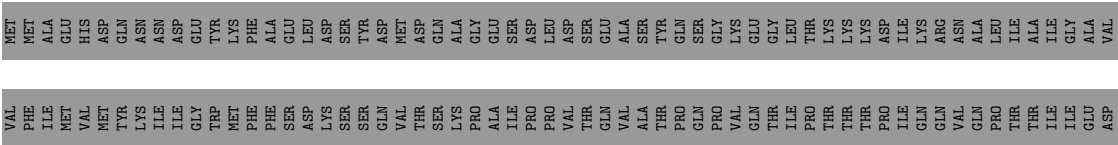
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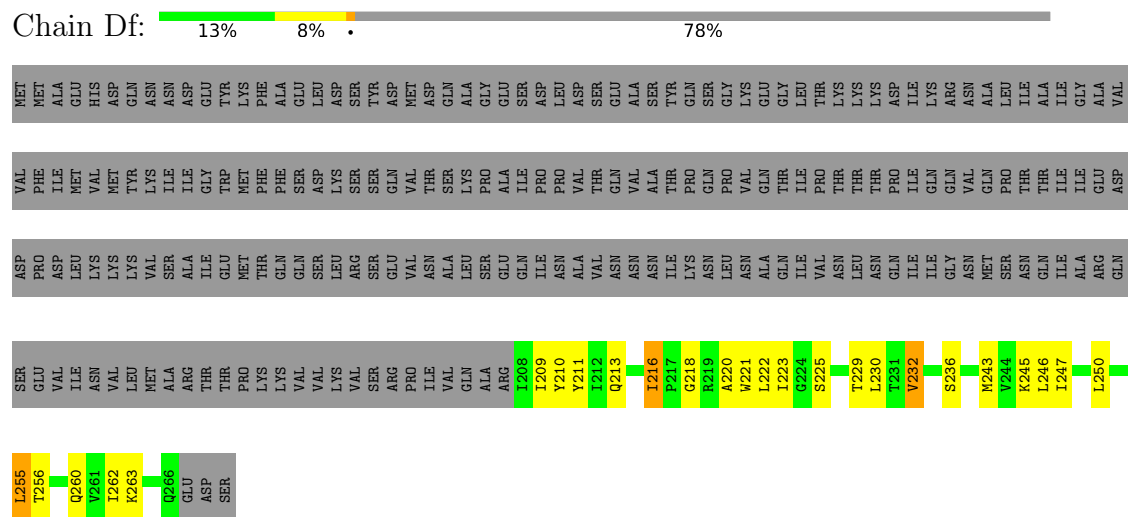
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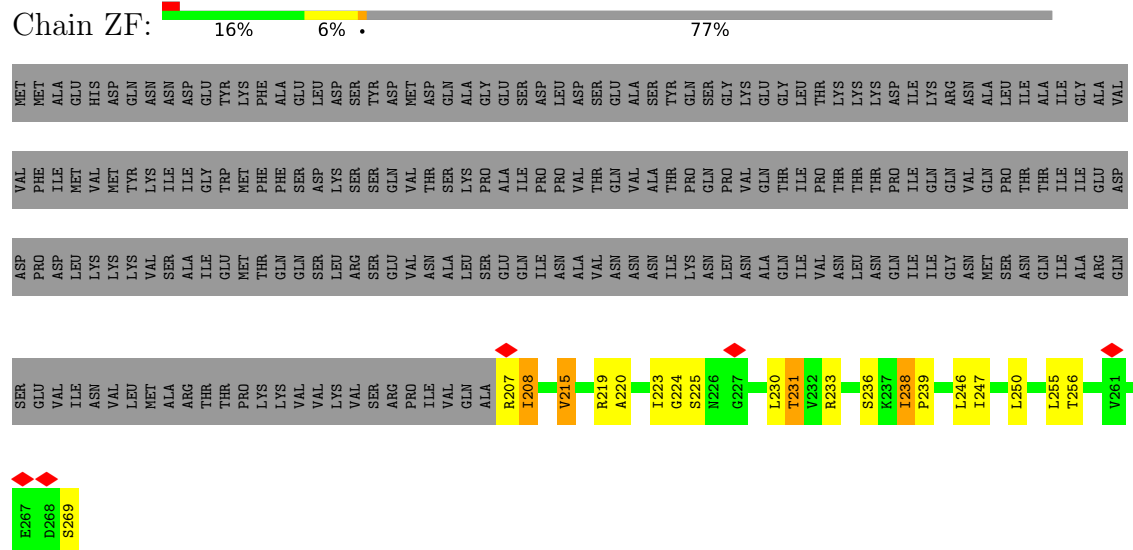
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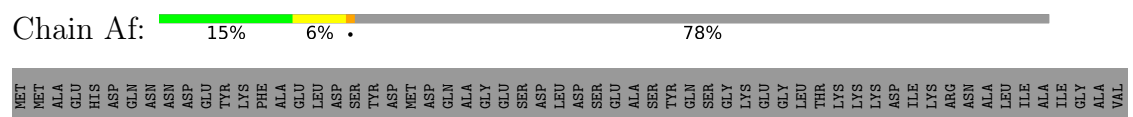
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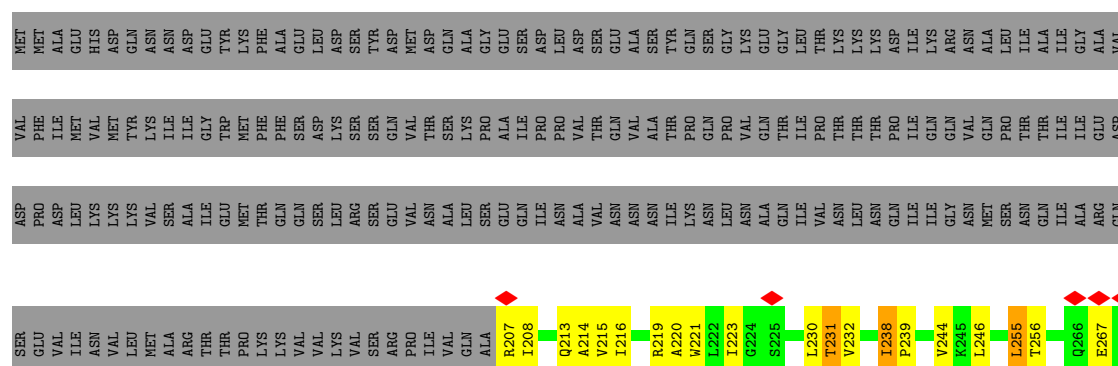
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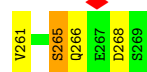
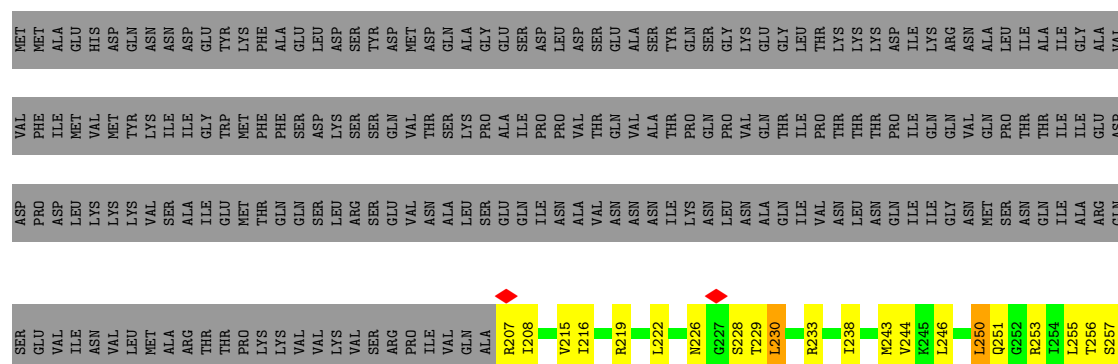
- Molecule 3: DotF



- Molecule 3: DotF

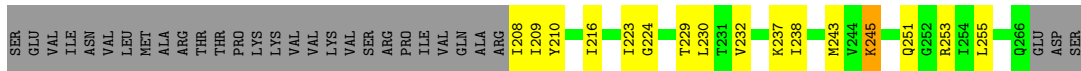


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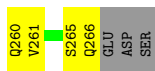
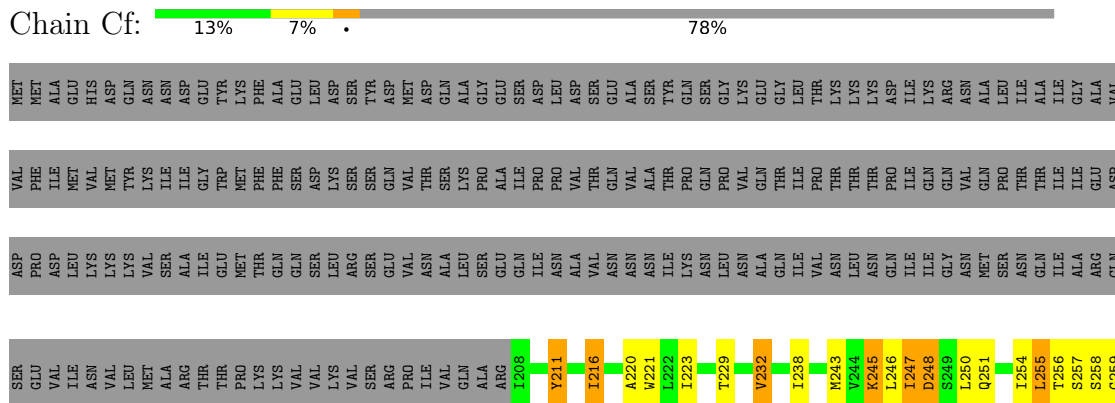


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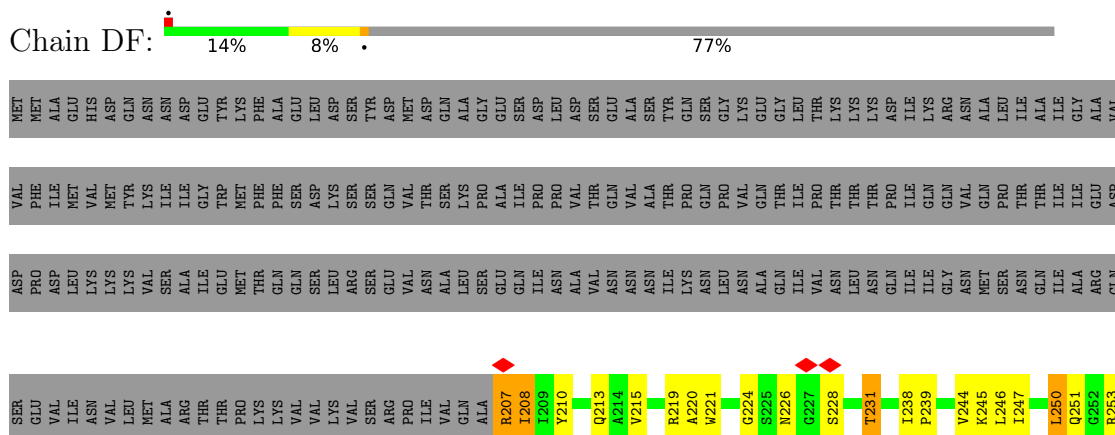




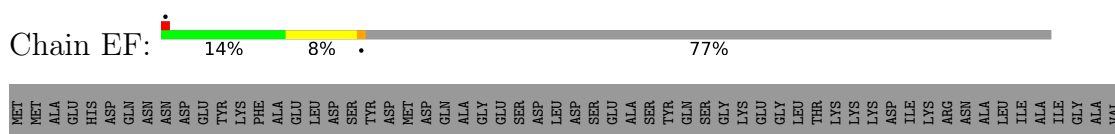
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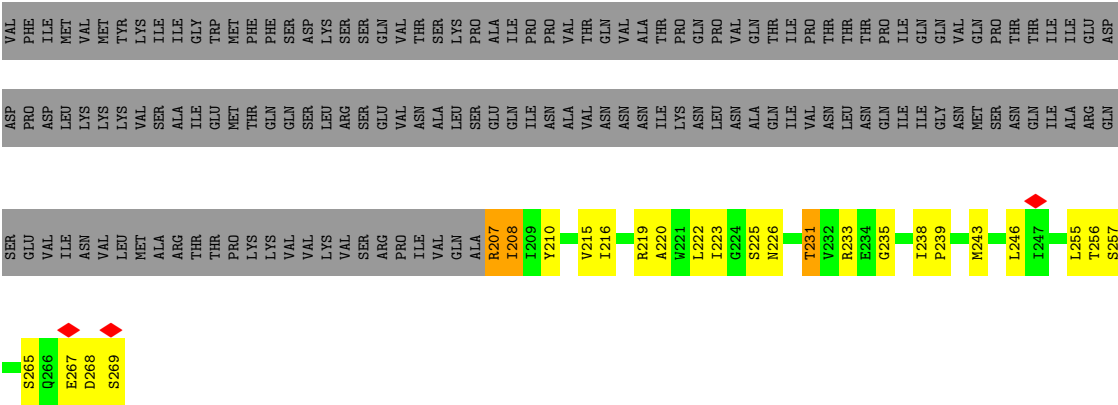


- Molecule 3: DotF

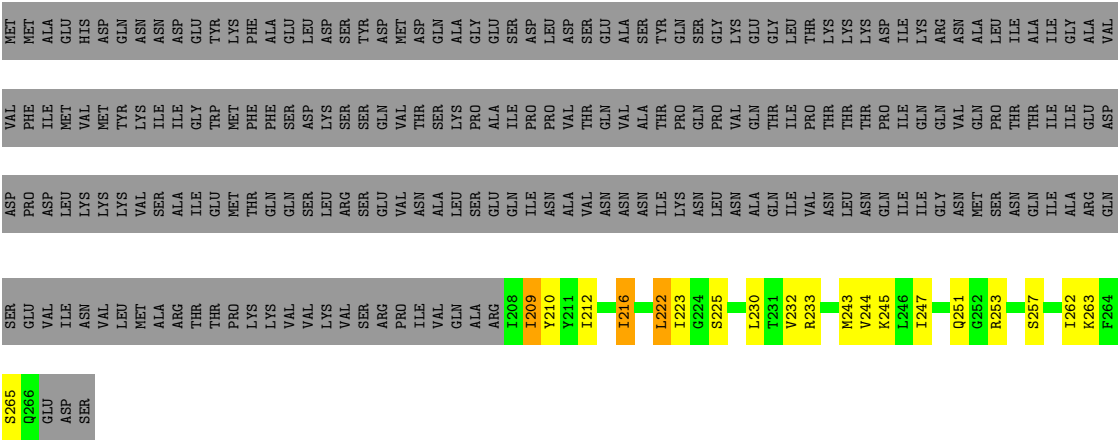


- Molecule 3: DotF

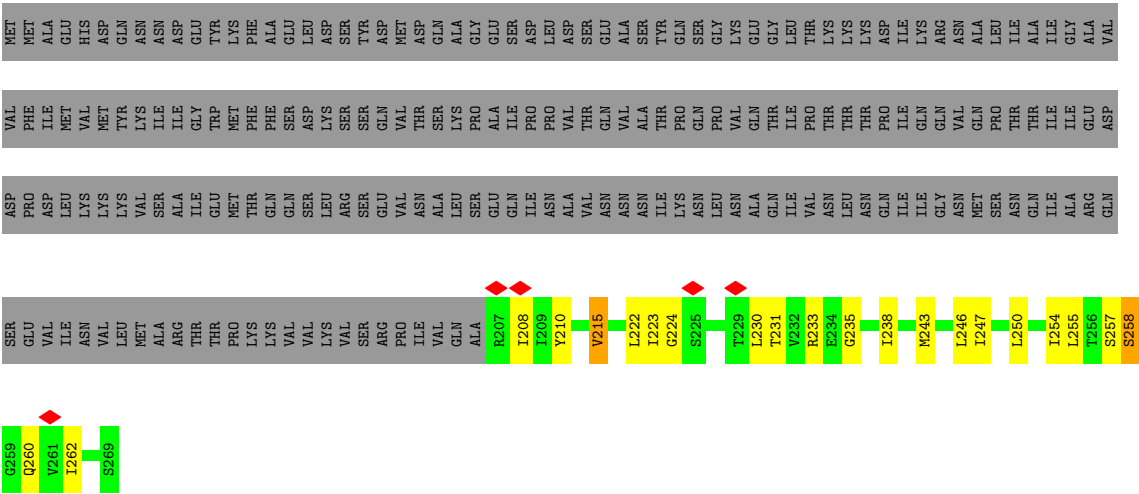




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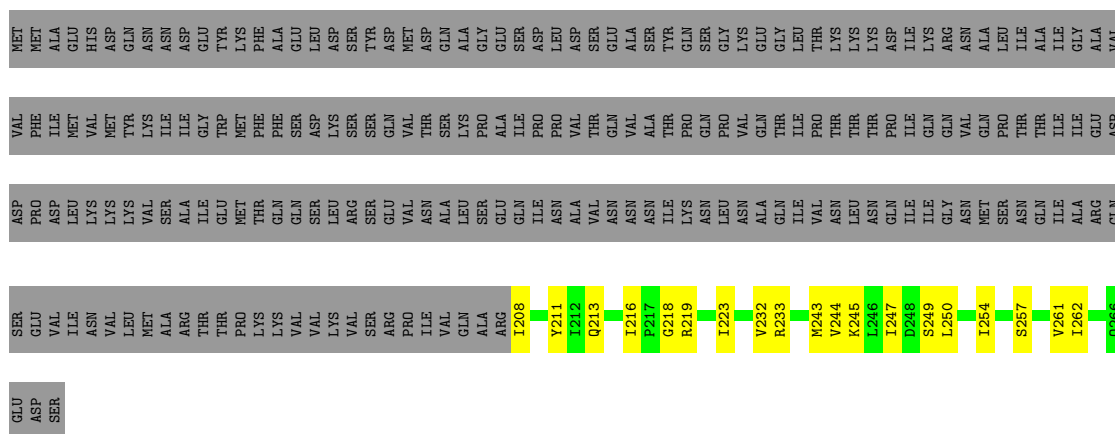


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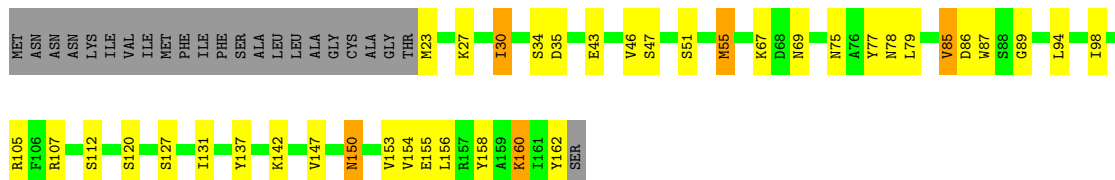


• Molecule 3: DotF

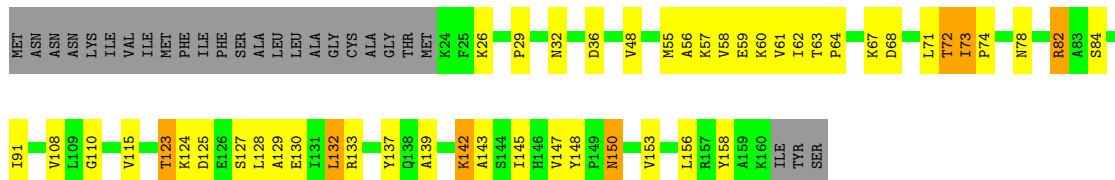




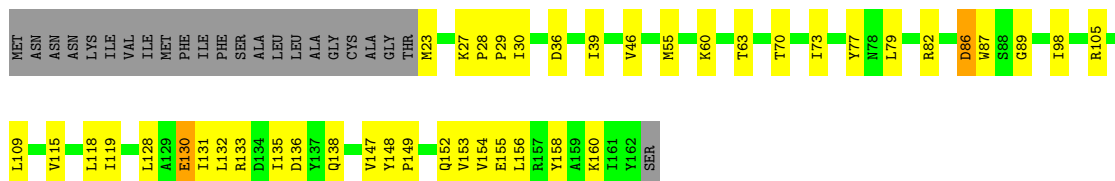
- Molecule 4: DotD



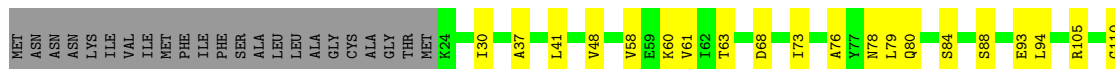
- Molecule 4: DotD



- Molecule 4: DotD

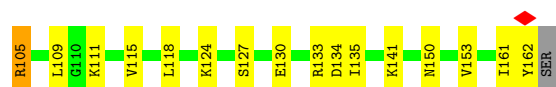


- Molecule 4: DotD

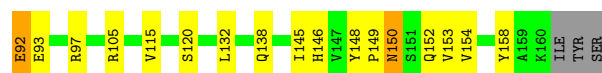




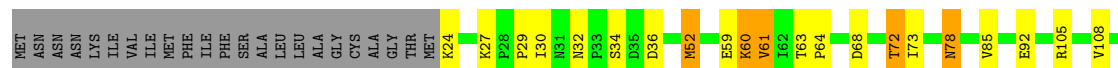
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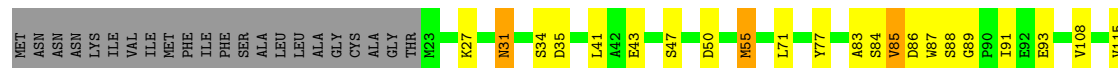
- Molecule 4: DotD



- Molecule 4: DotD

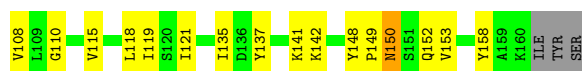


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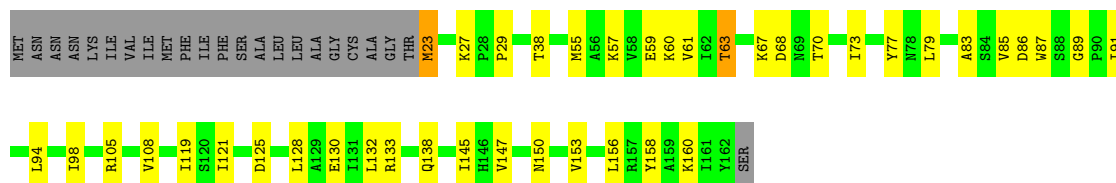


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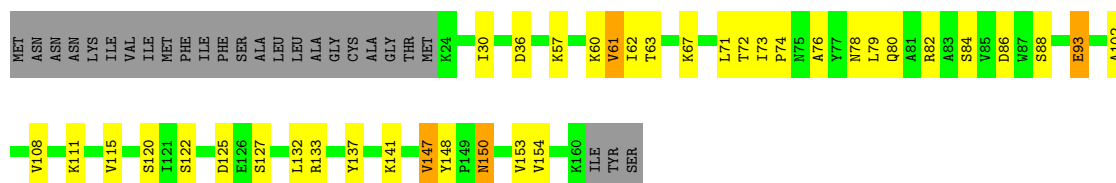




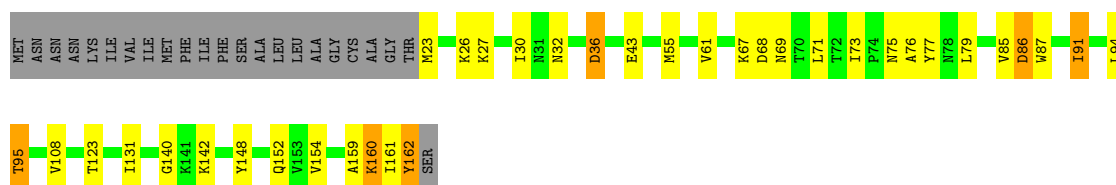
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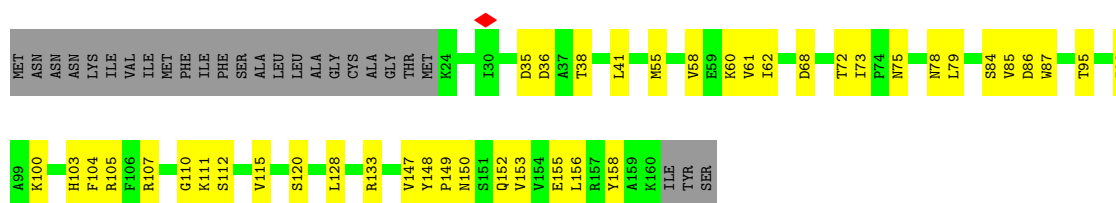
• Molecule 4: DotD



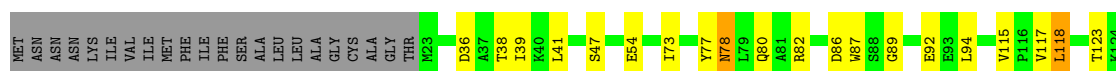
• Molecule 4: DotD



• Molecule 4: DotD

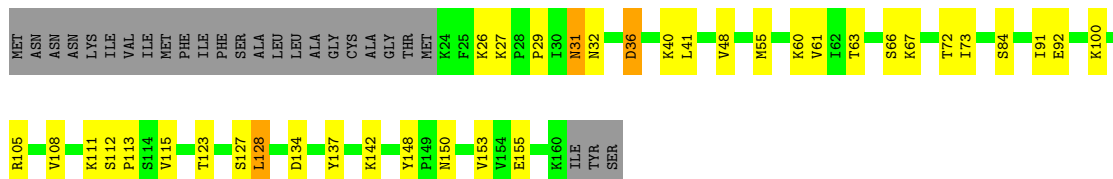


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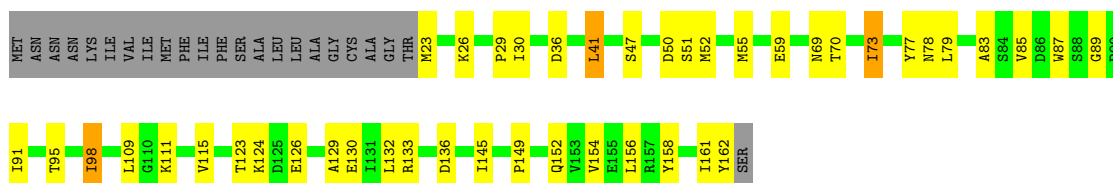




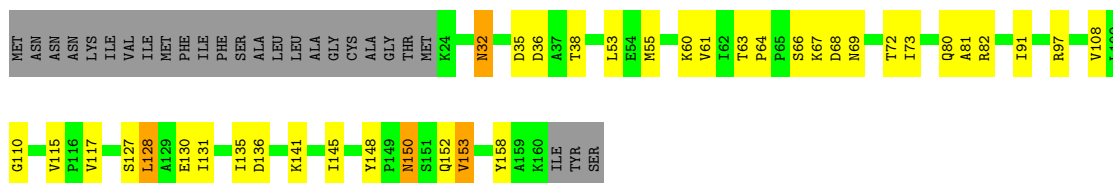
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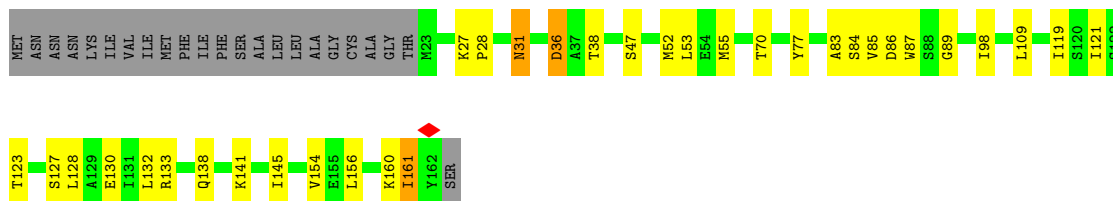
• Molecule 4: DotD



• Molecule 4: DotD

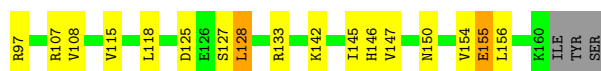


• Molecule 4: DotD

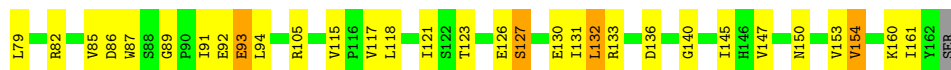
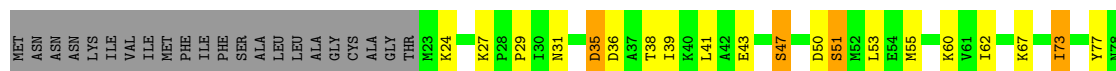


• Molecule 4: DotD

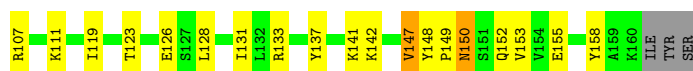
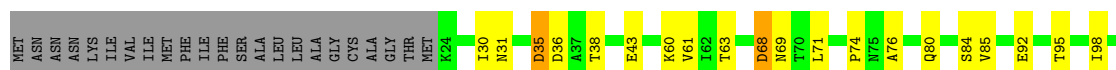




• Molecule 4: DotD



• Molecule 4: DotD



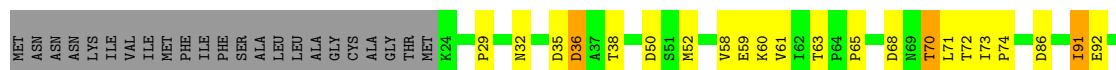
• Molecule 4: DotD



• Molecule 4: DotD



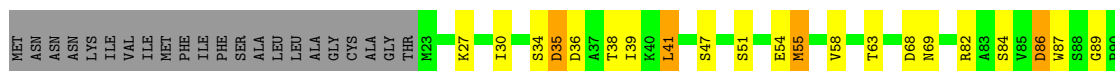
• Molecule 4: DotD





• Molecule 4: DotD

Chain FD: 61% 21% 14%



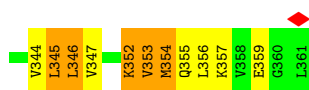
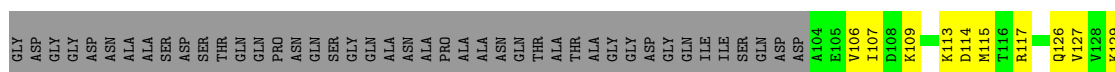
• Molecule 4: DotD

Chain Fd: 66% 15% 16%



• Molecule 5: Type IV secretion protein IcmK

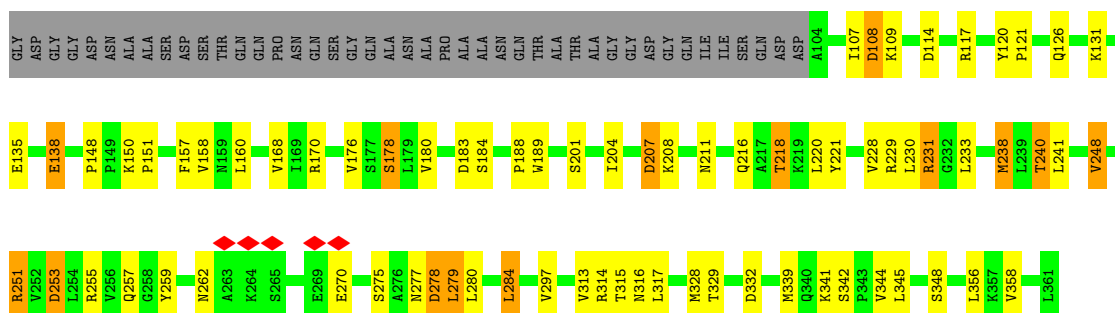
Chain GH: 45% 22% 29%



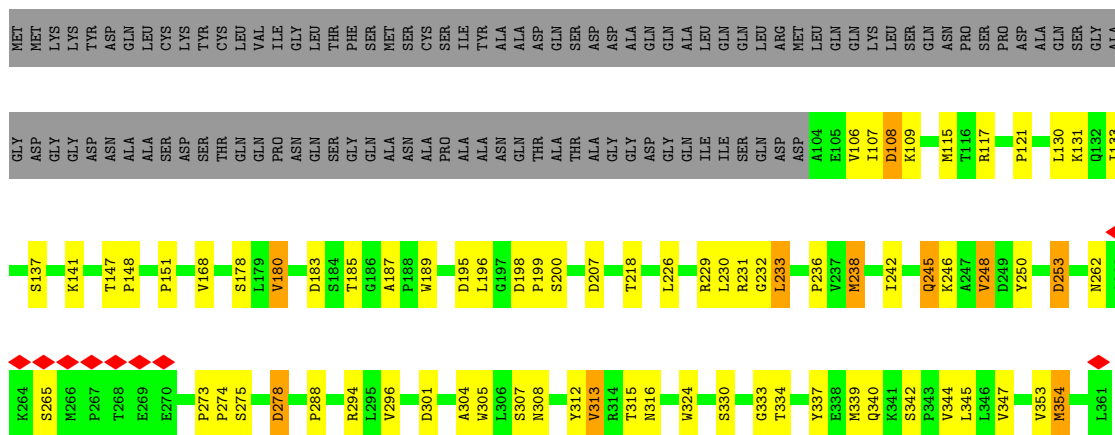
• Molecule 5: Type IV secretion protein IcmK

Chain HH: 51% 17% 29%

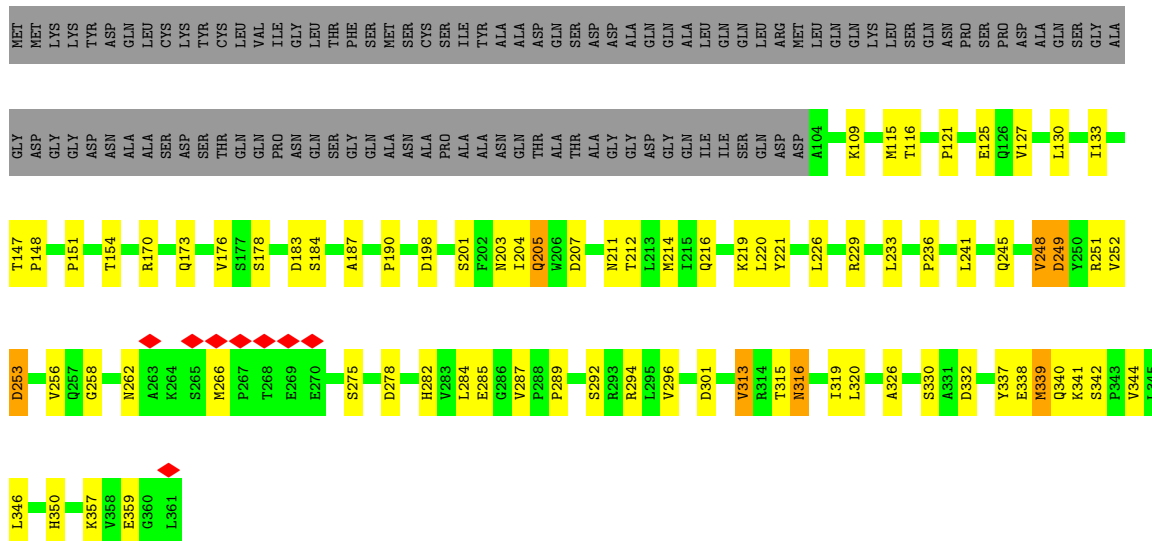




- Molecule 5: Type IV secretion protein IcmK

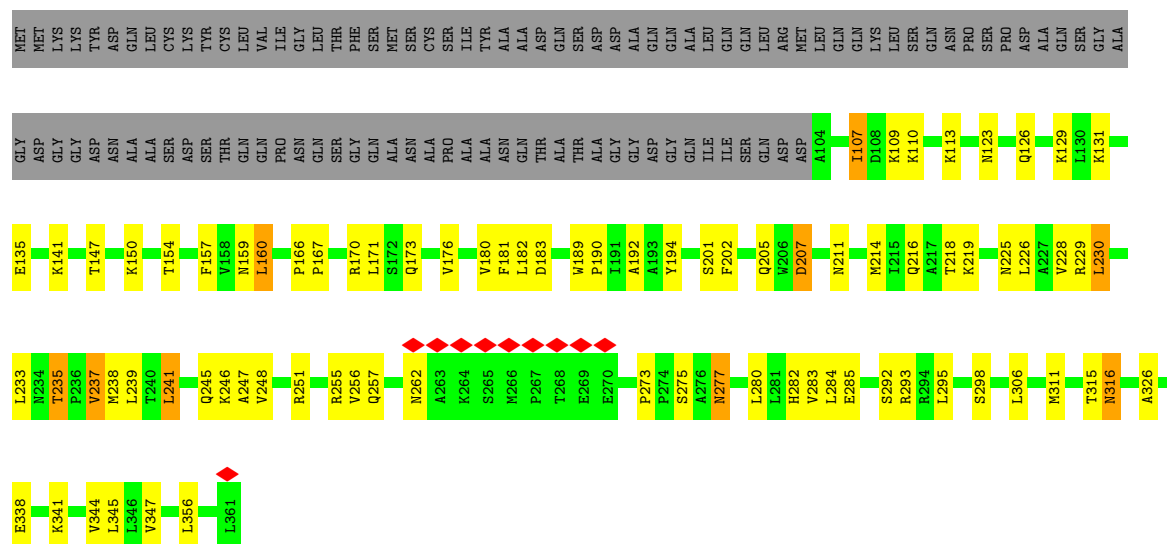


- Molecule 5: Type IV secretion protein IcmK

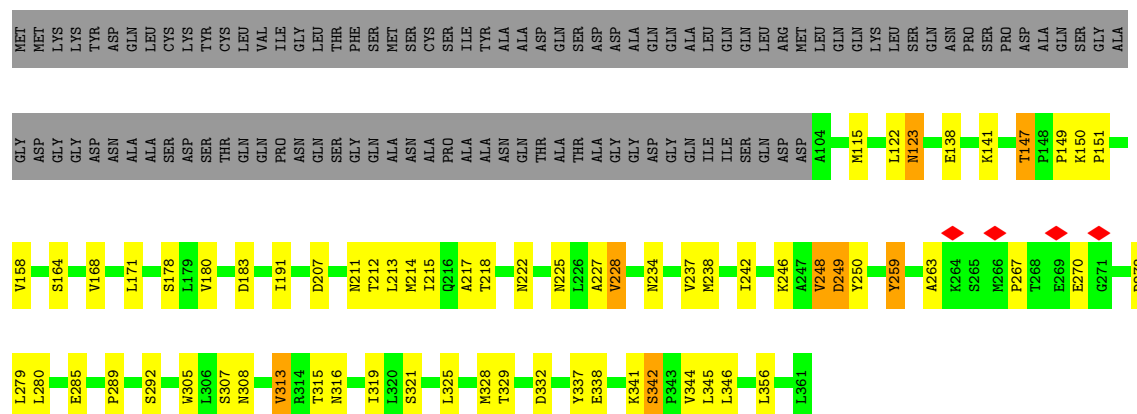


- Molecule 5: Type IV secretion protein IcmK





• Molecule 5: Type IV secretion protein IcmK



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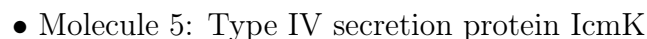


• Molecule 5: Type IV secretion protein IcmK

Frequency	Percentage
Daily	49%
Weekly	20%
Monthly	29%
Other	2%



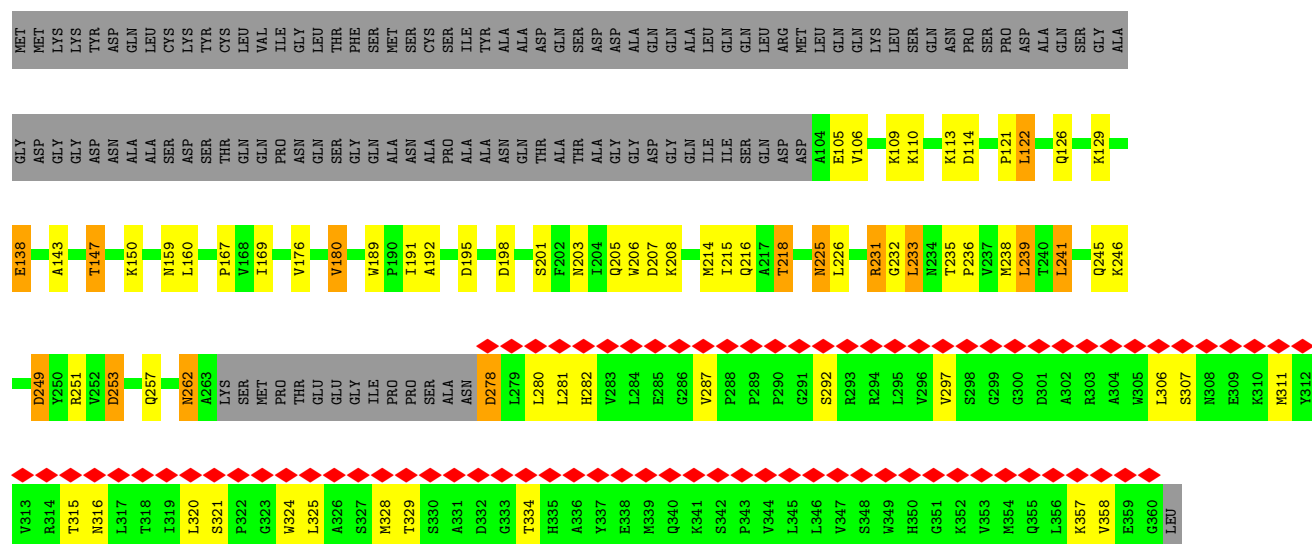
Frequency	Percentage
7%	7%
46%	46%
19%	19%
33%	33%



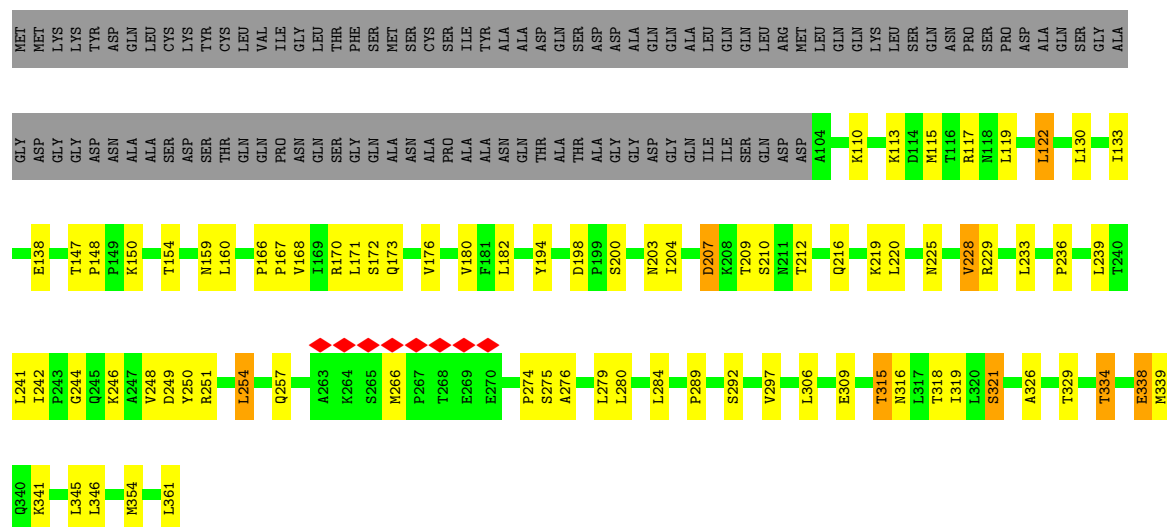
Frequency	Percentage
Daily	14%
Often	51%
Sometimes	15%
Never	33%



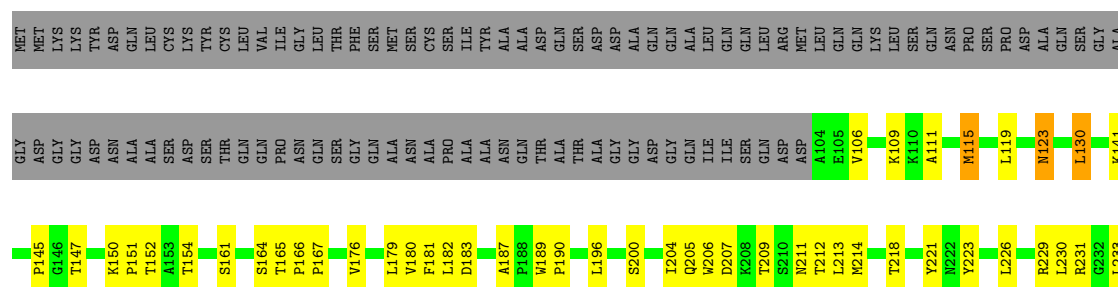


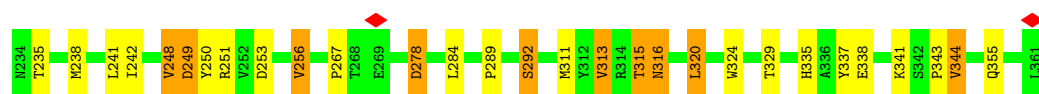


• Molecule 5: Type IV secretion protein IcmK

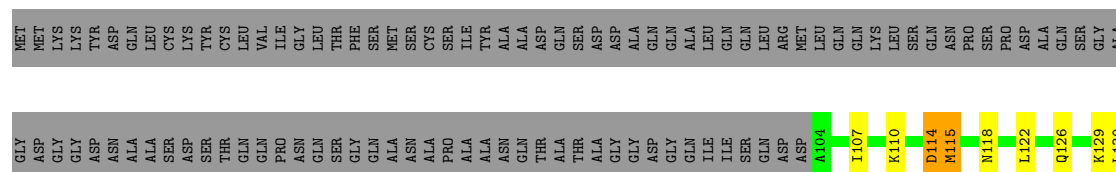


• Molecule 5: Type IV secretion protein IcmK

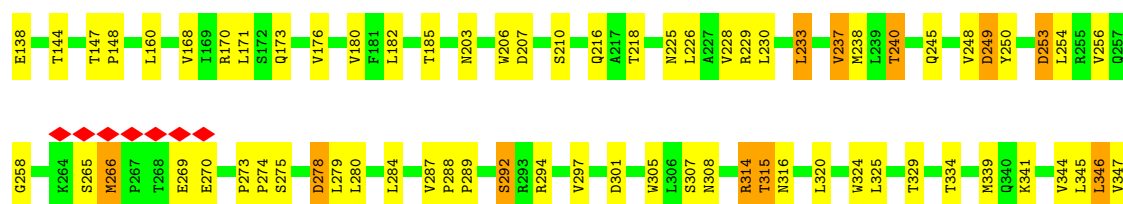
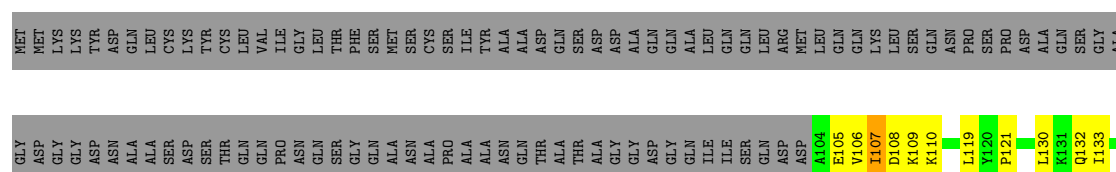




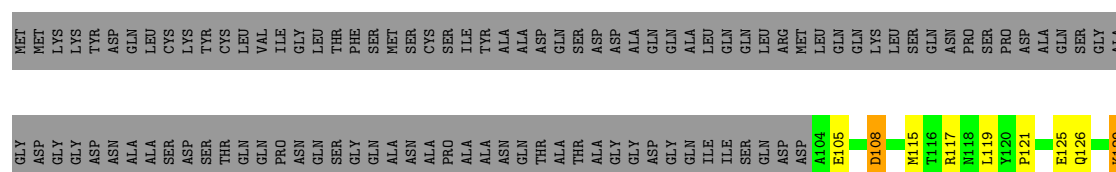
• Molecule 5: Type IV secretion protein IcmK

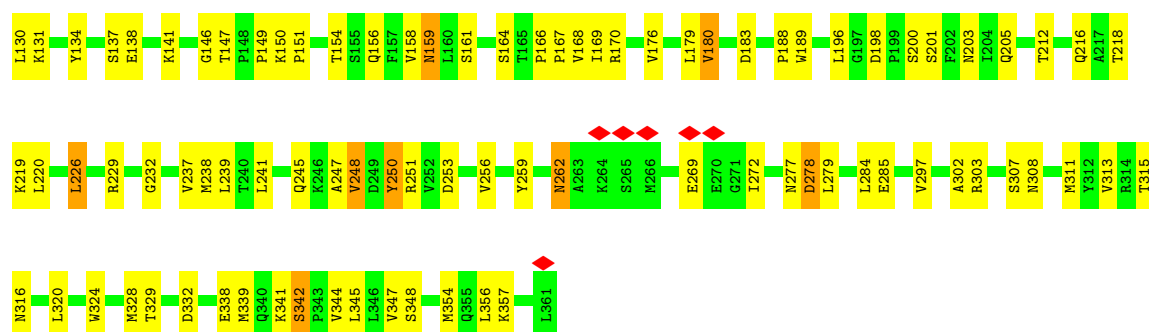


• Molecule 5: Type IV secretion protein IcmK

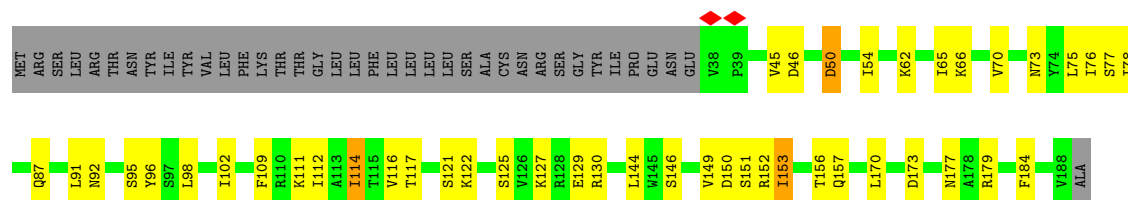


• Molecule 5: Type IV secretion protein IcmK

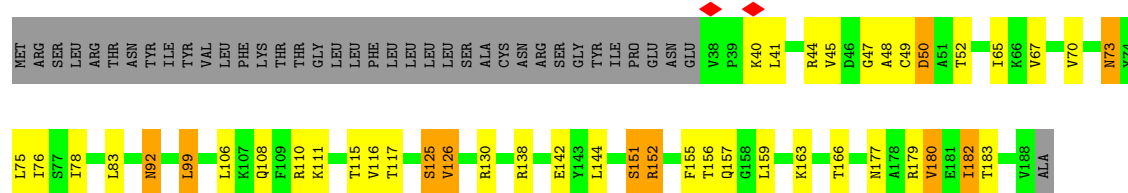




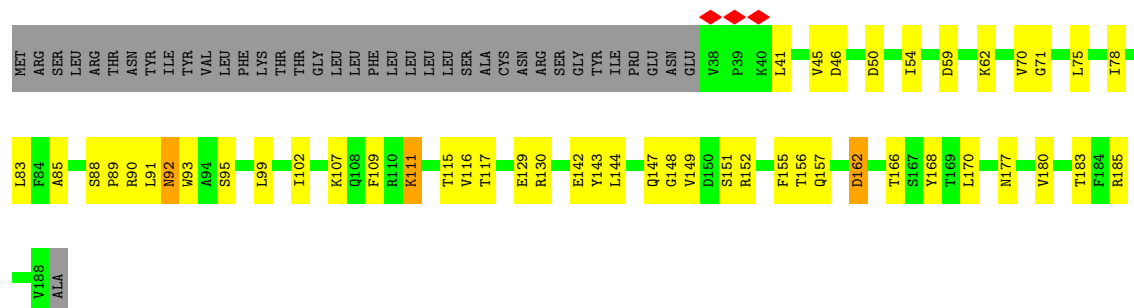
• Molecule 6: Inner membrane lipoprotein YiaD



• Molecule 6: Inner membrane lipoprotein YiaD

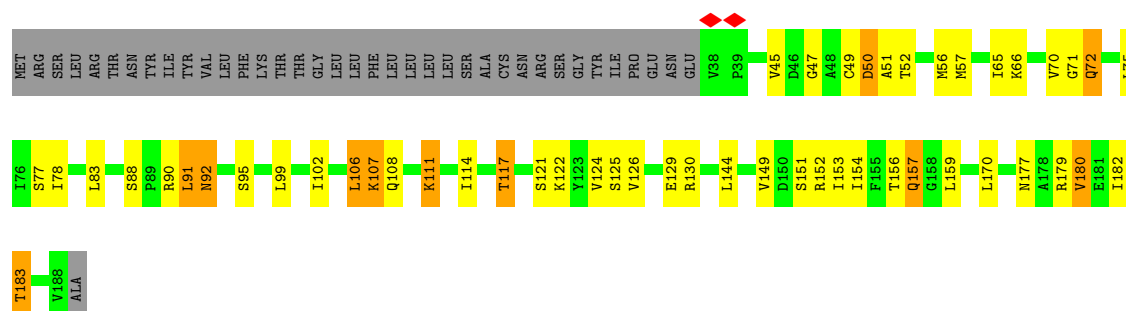


• Molecule 6: Inner membrane lipoprotein YiaD

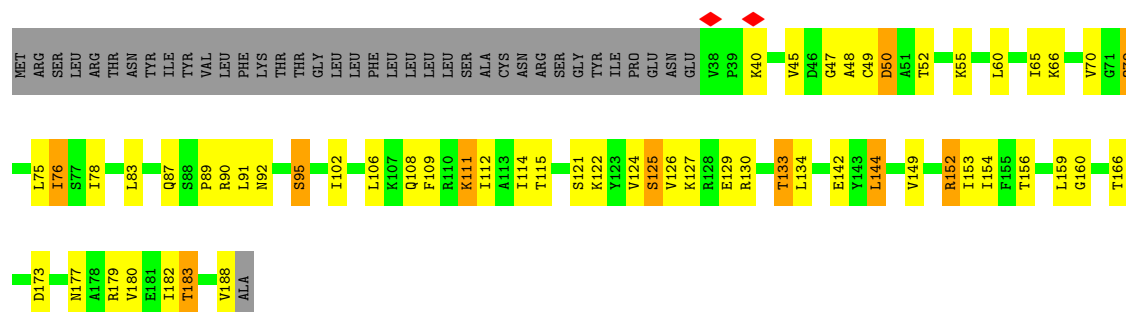


• Molecule 6: Inner membrane lipoprotein YiaD

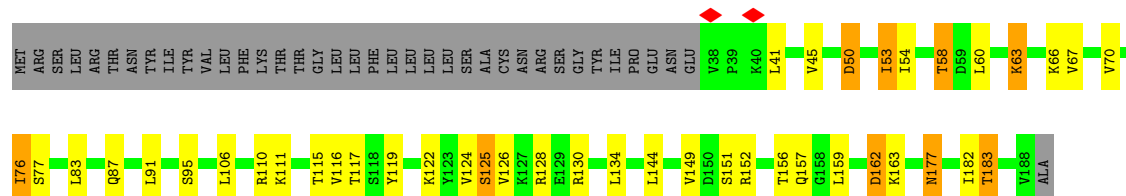




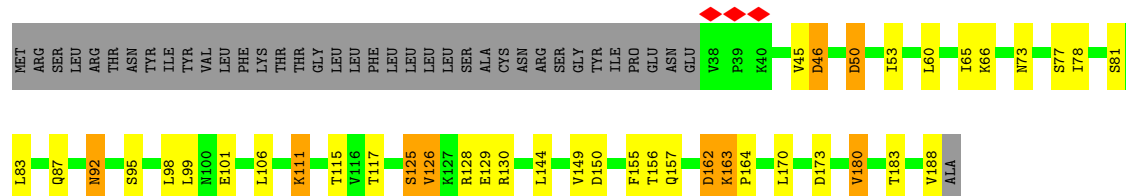
- Molecule 6: Inner membrane lipoprotein YiaD



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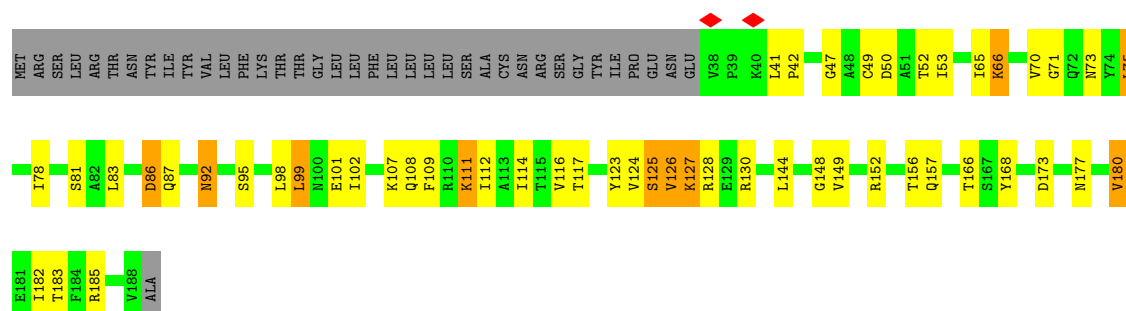


- Molecule 6: Inner membrane lipoprotein YiaD

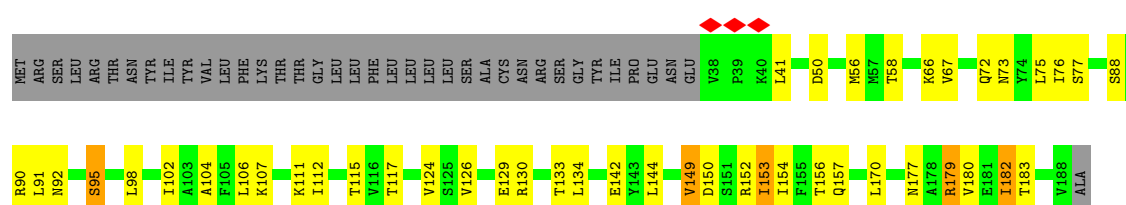


- Molecule 6: Inner membrane lipoprotein YiaD

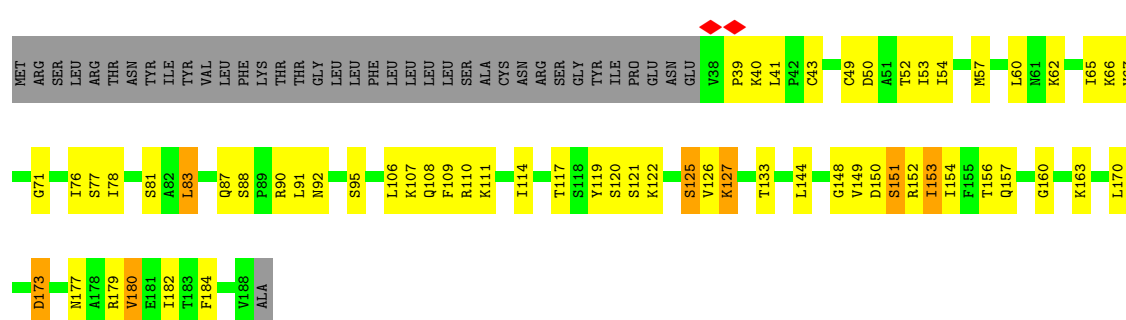




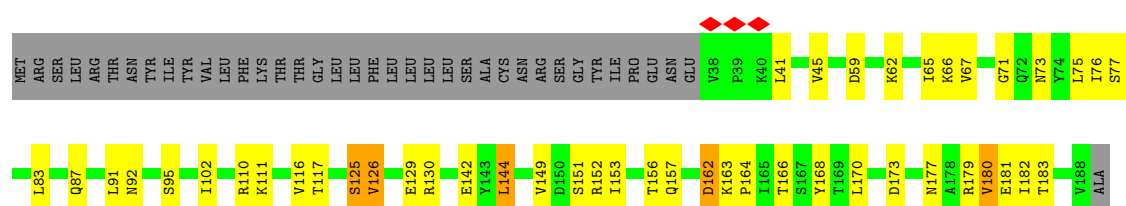
- Molecule 6: Inner membrane lipoprotein YiaD



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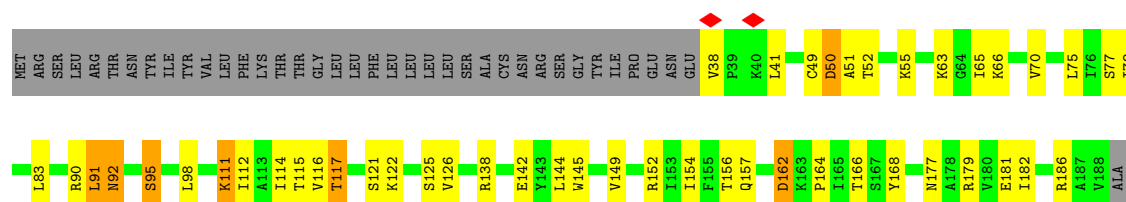


- Molecule 6: Inner membrane lipoprotein YiaD

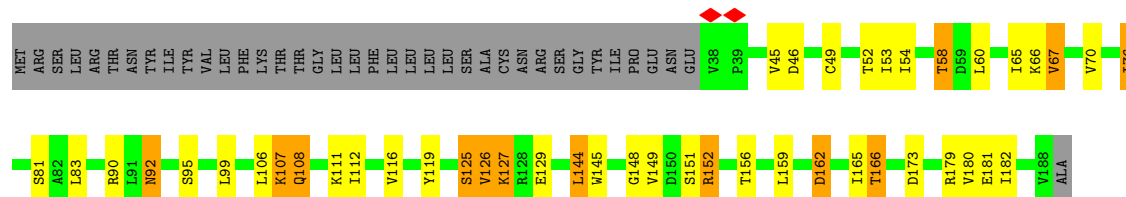


- Molecule 6: Inner membrane lipoprotein YiaD

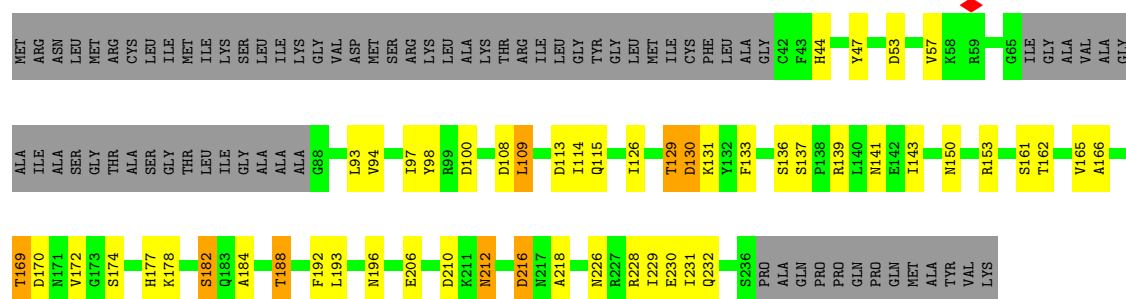




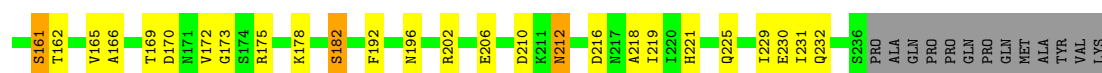
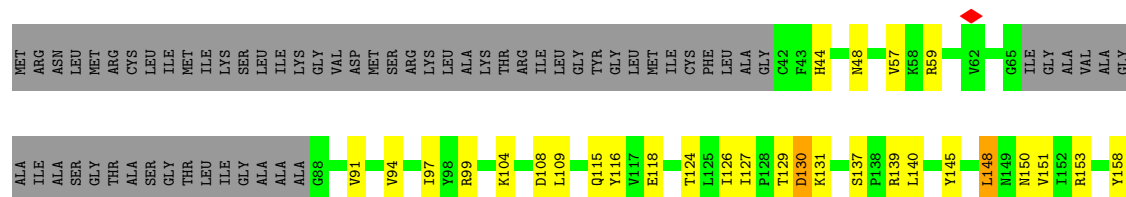
• Molecule 6: Inner membrane lipoprotein YiaD



• Molecule 7: Outer membrane protein, OmpA family protein

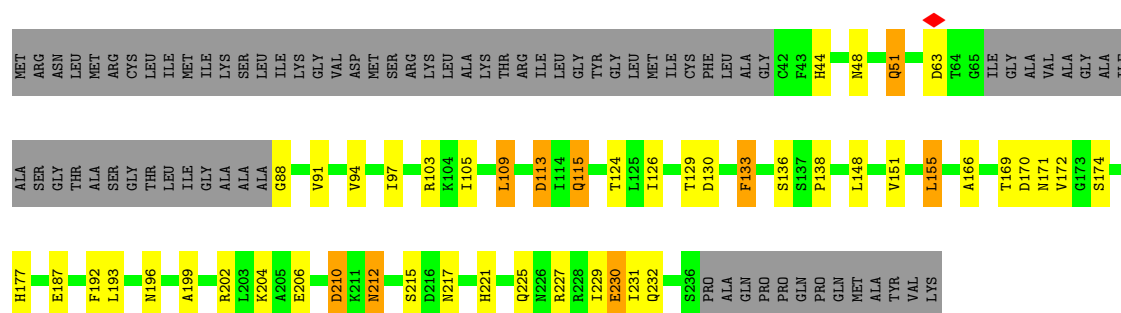


• Molecule 7: Outer membrane protein, OmpA family protein

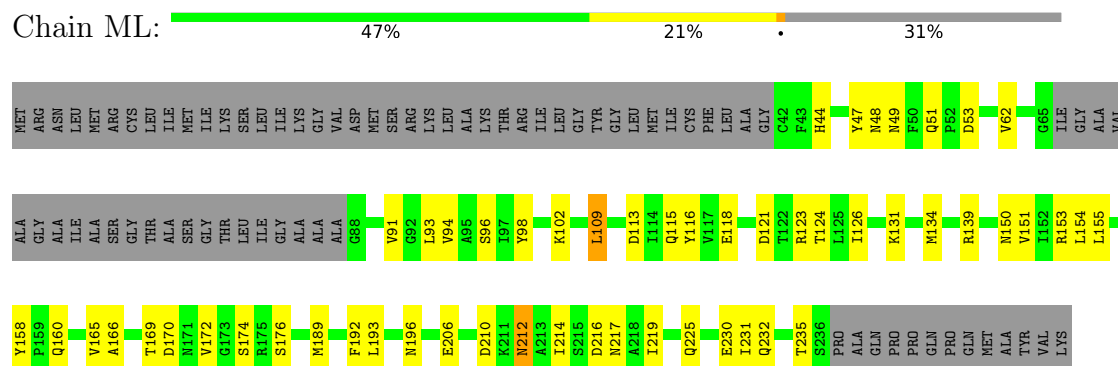


• Molecule 7: Outer membrane protein, OmpA family protein

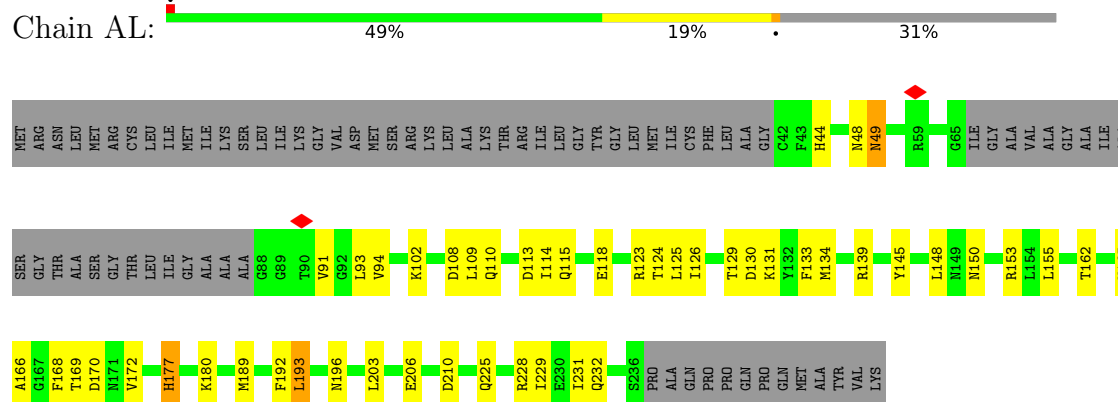




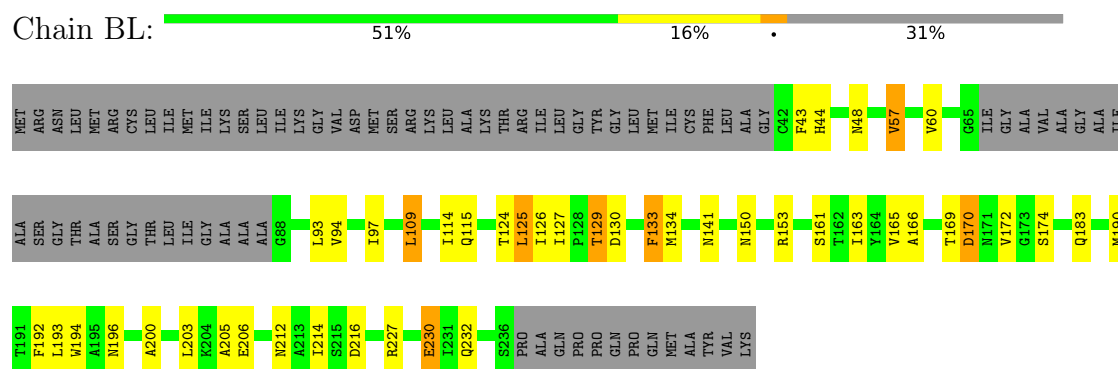
• Molecule 7: Outer membrane protein, OmpA family protein



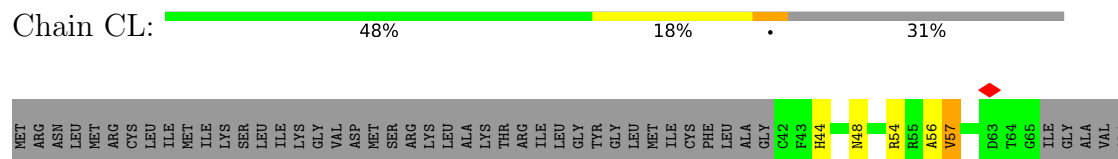
• Molecule 7: Outer membrane protein, OmpA family protein

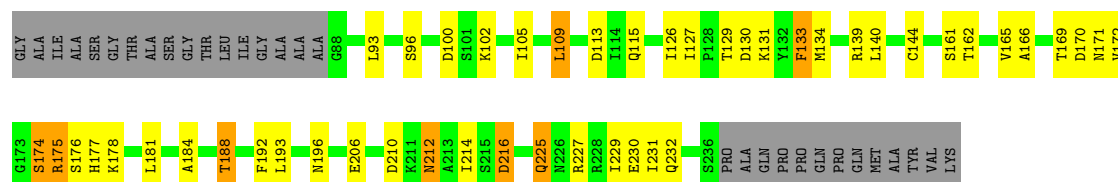


• Molecule 7: Outer membrane protein, OmpA family protein

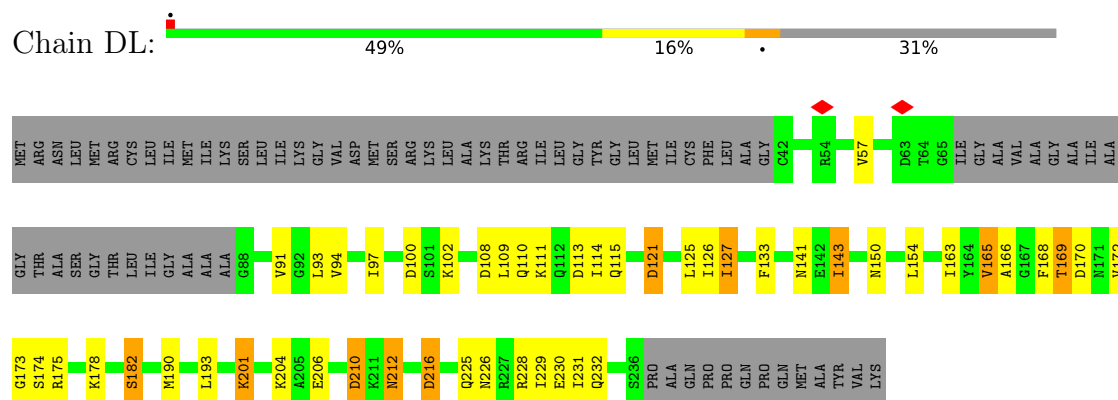


• Molecule 7: Outer membrane protein, OmpA family protein

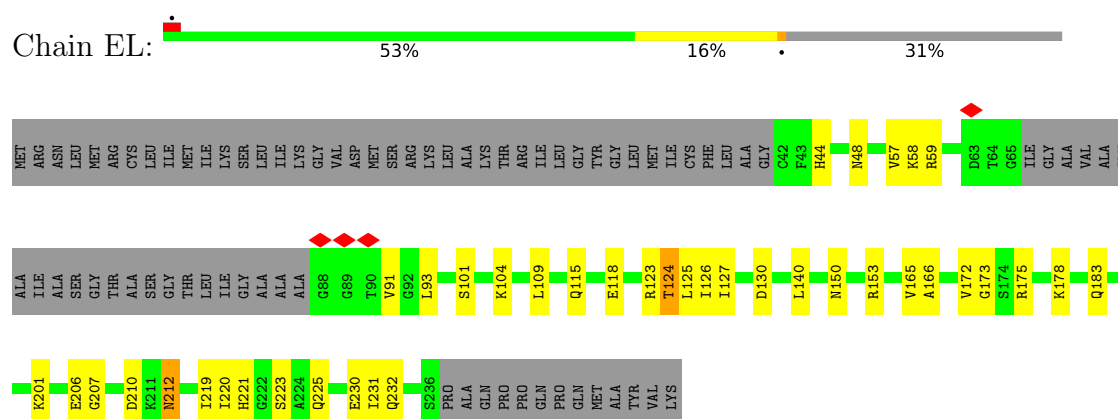




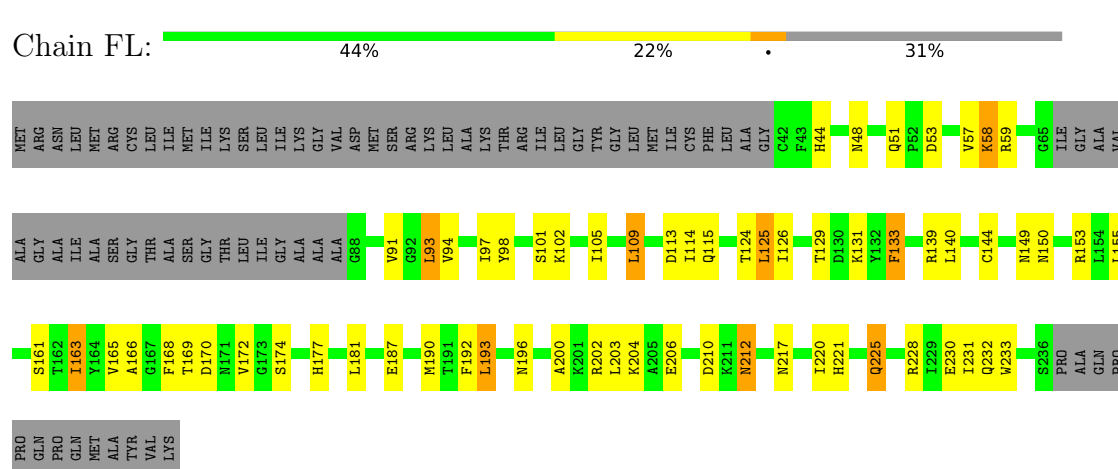
- Molecule 7: Outer membrane protein, OmpA family protein



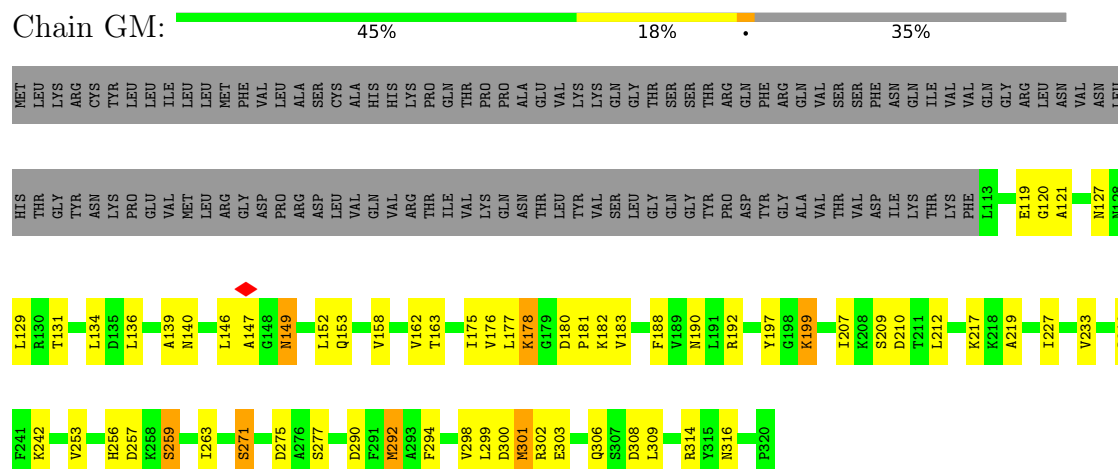
- Molecule 7: Outer membrane protein, OmpA family protein



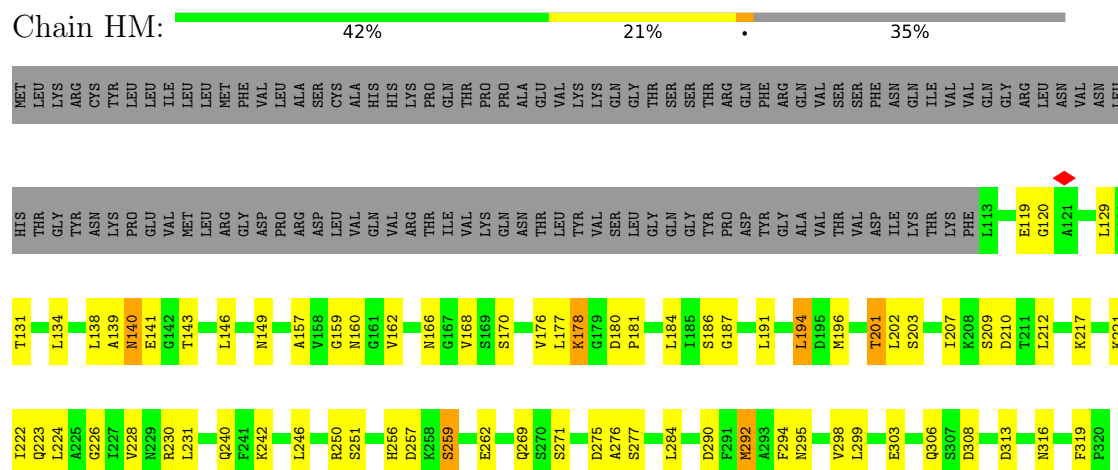
- Molecule 7: Outer membrane protein, OmpA family protein



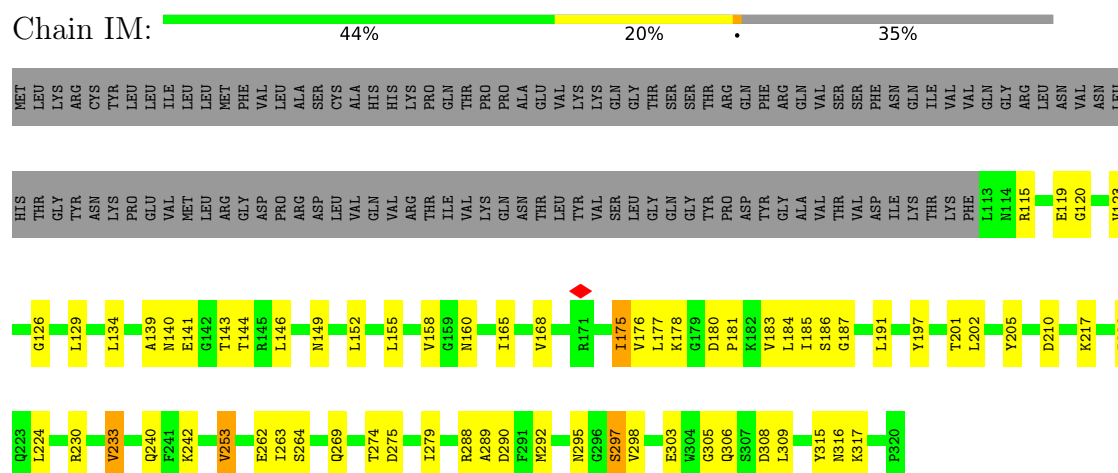
- Molecule 8: DUF2807 domain-containing protein



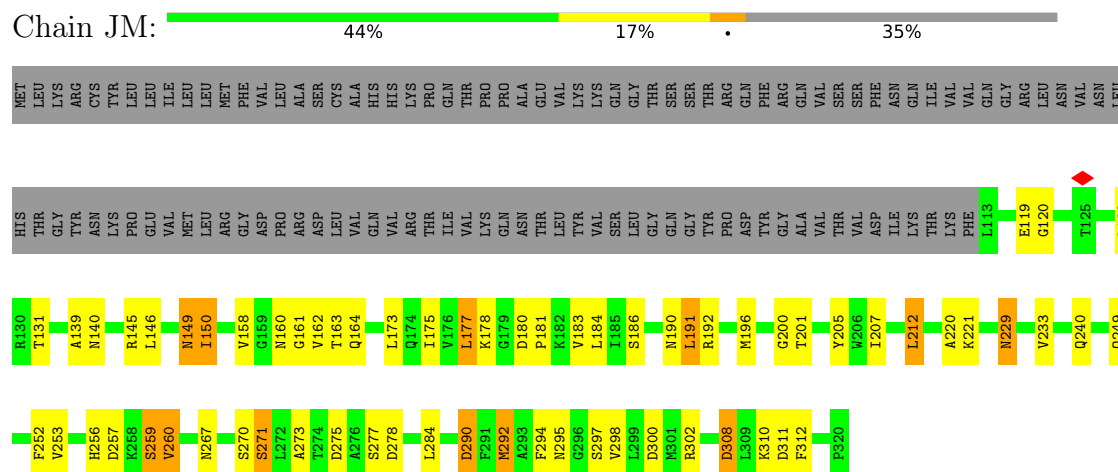
- Molecule 8: DUF2807 domain-containing protein



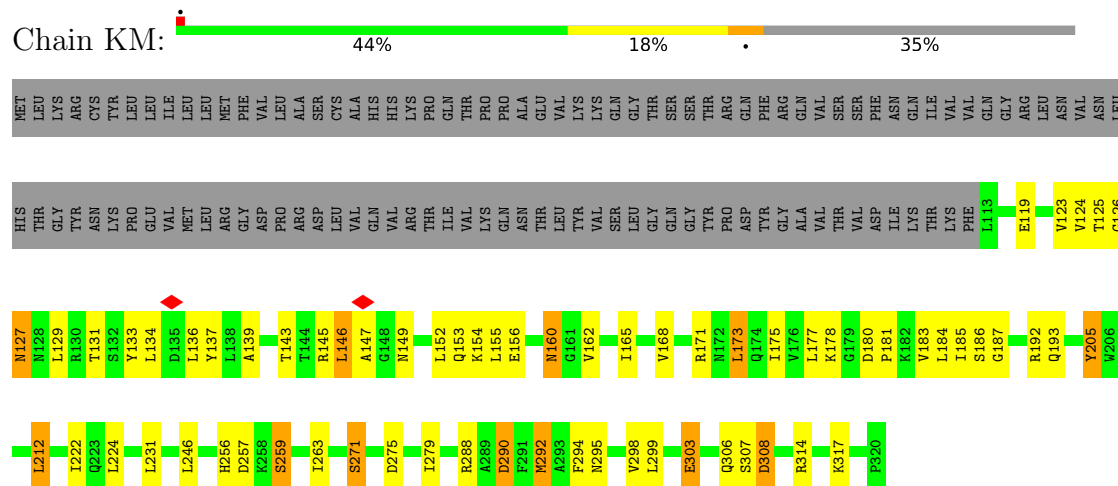
- Molecule 8: DUF2807 domain-containing protein



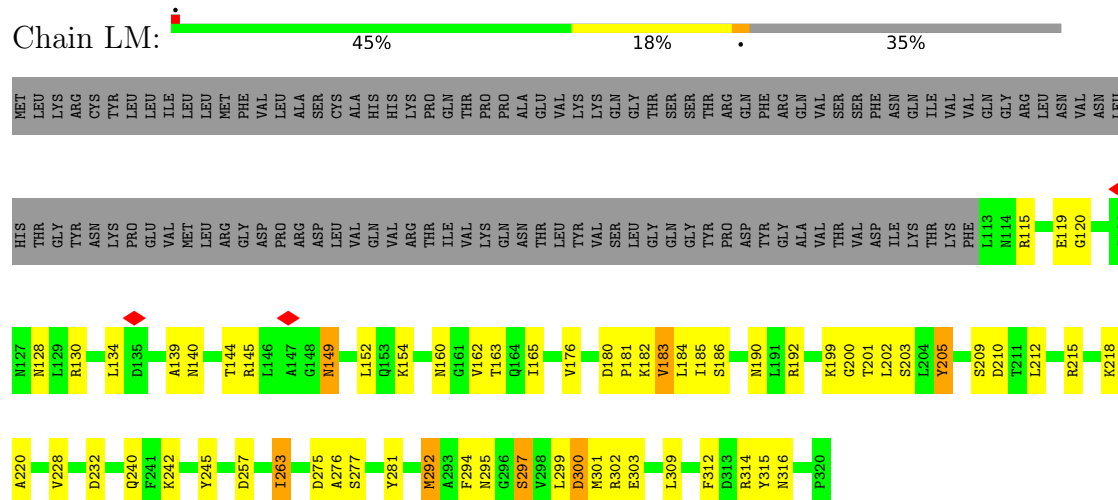
- Molecule 8: DUF2807 domain-containing protein



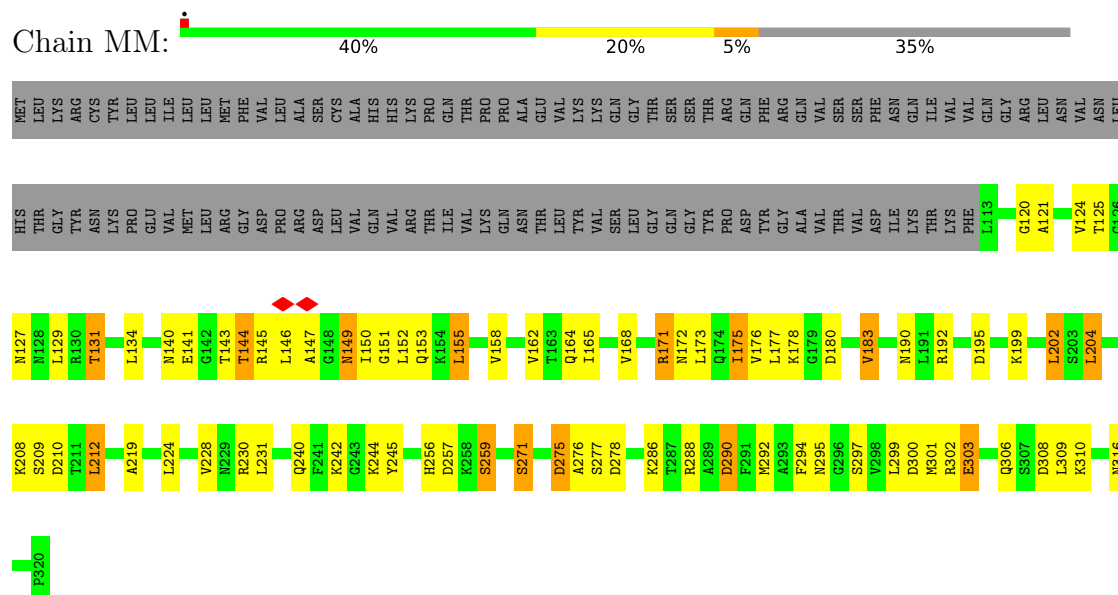
- Molecule 8: DUF2807 domain-containing protein



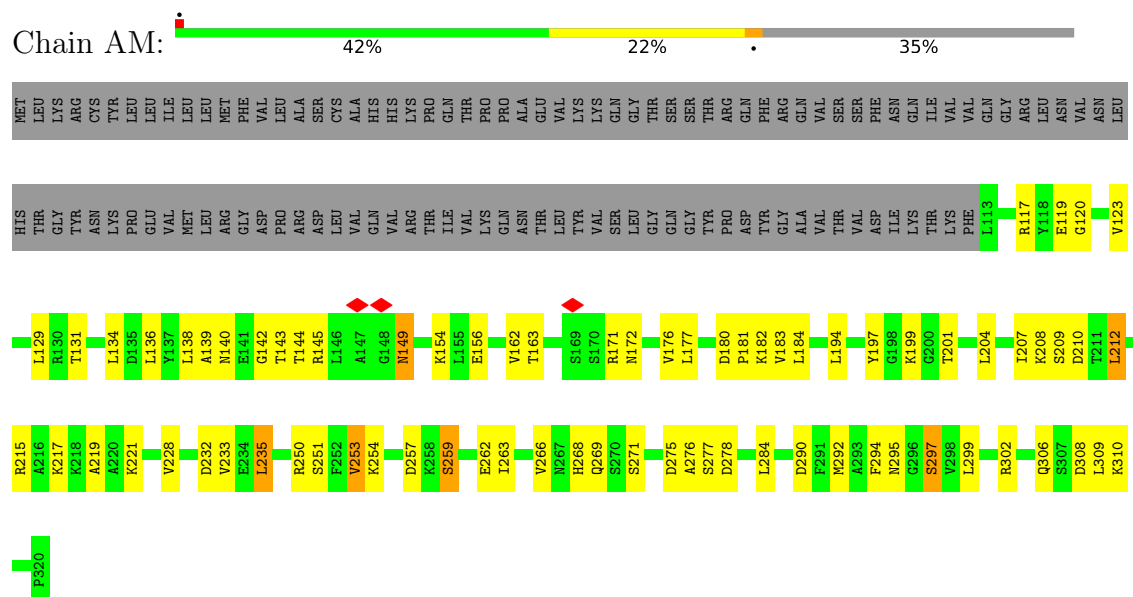
- Molecule 8: DUF2807 domain-containing protein



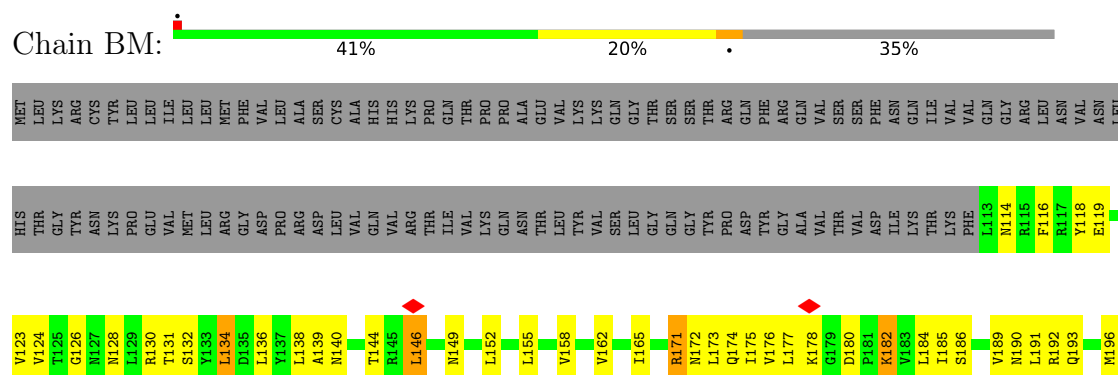
- Molecule 8: DUF2807 domain-containing protein

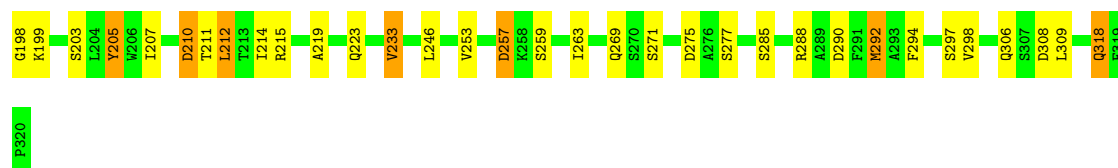


- Molecule 8: DUF2807 domain-containing protein



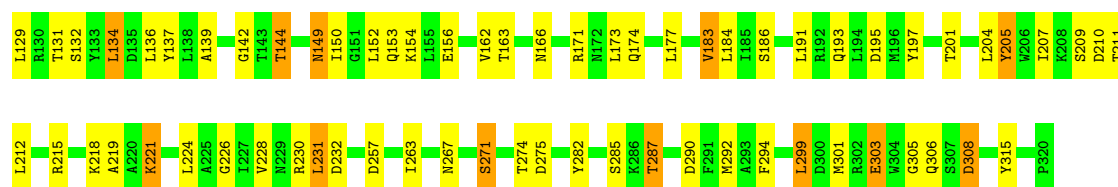
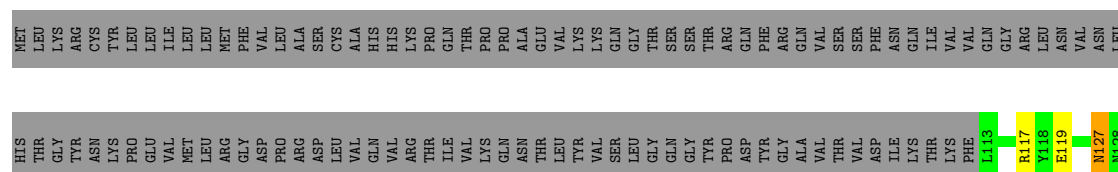
- Molecule 8: DUF2807 domain-containing protein





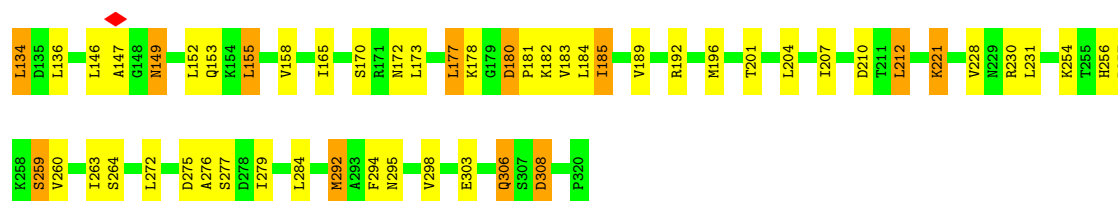
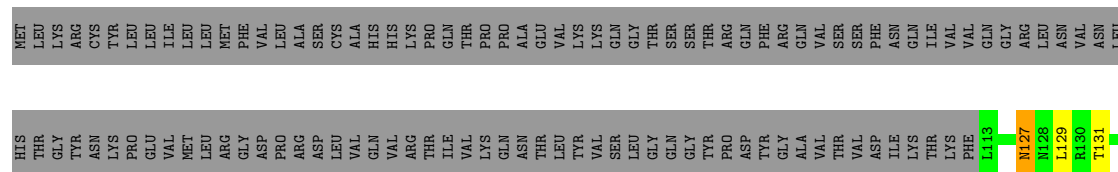
- Molecule 8: DUF2807 domain-containing protein

Chain CM: 43% 18% 35%



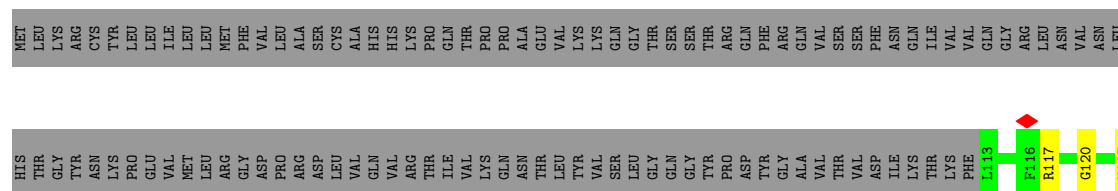
- Molecule 8: DUF2807 domain-containing protein

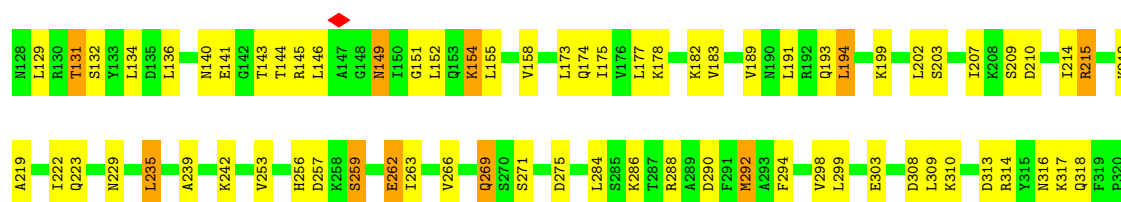
Chain DM: 48% 13% 35%



- Molecule 8: DUF2807 domain-containing protein

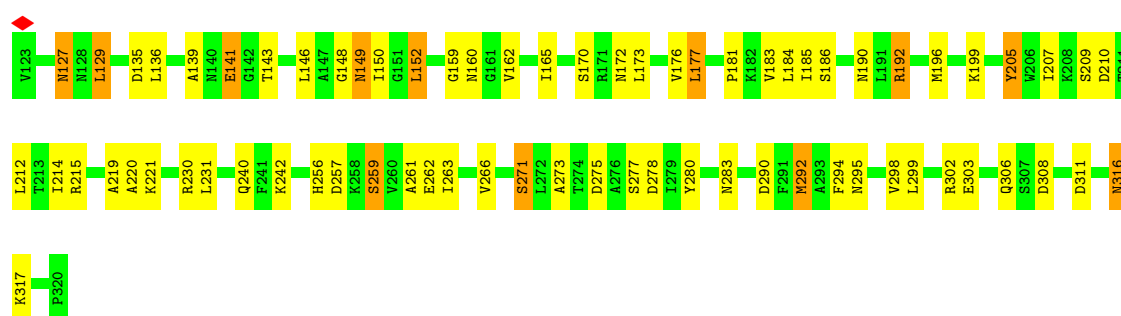
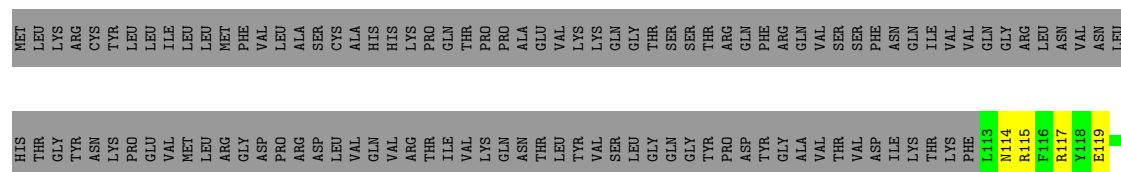
Chain EM: 42% 20% 35%





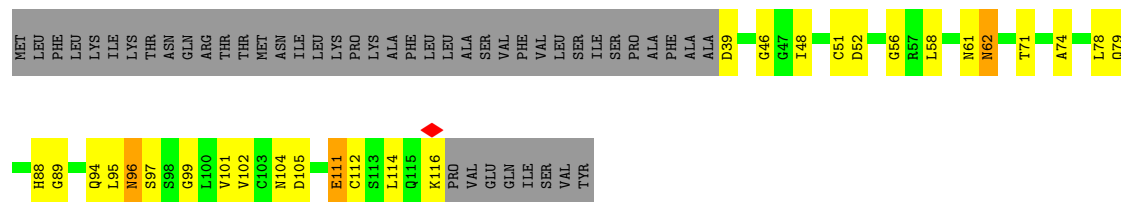
• Molecule 8: DUF2807 domain-containing protein

Chain FM: 42% 20% 35%



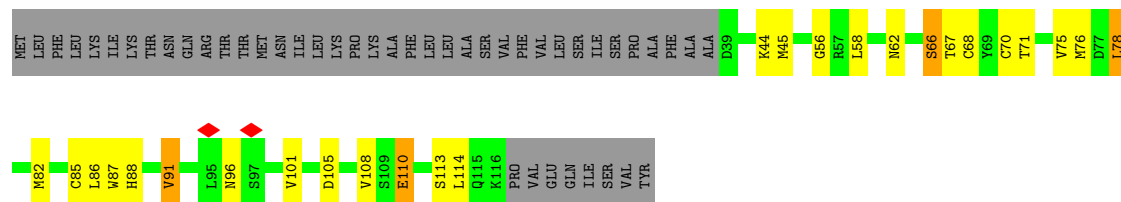
• Molecule 9: Neurogenic locus notch

Chain GN: 40% 20% 37%

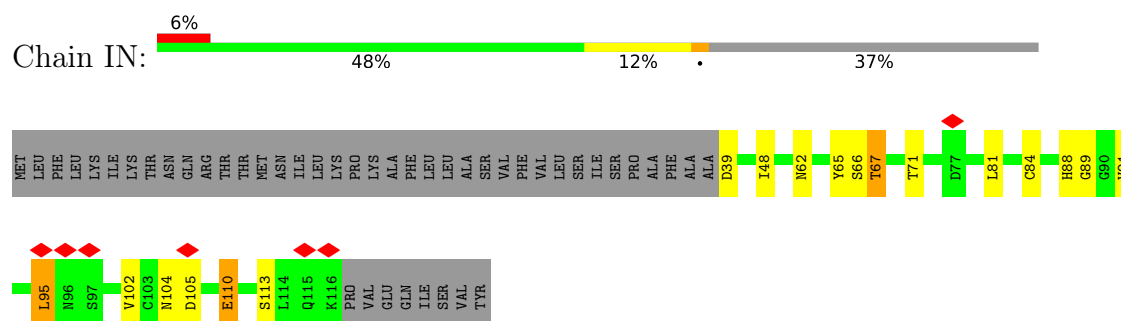


• Molecule 9: Neurogenic locus notch

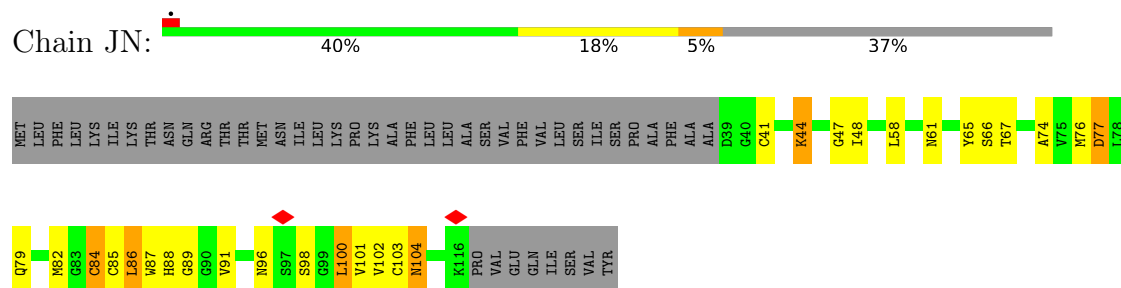
Chain HN: 42% 18% 37%



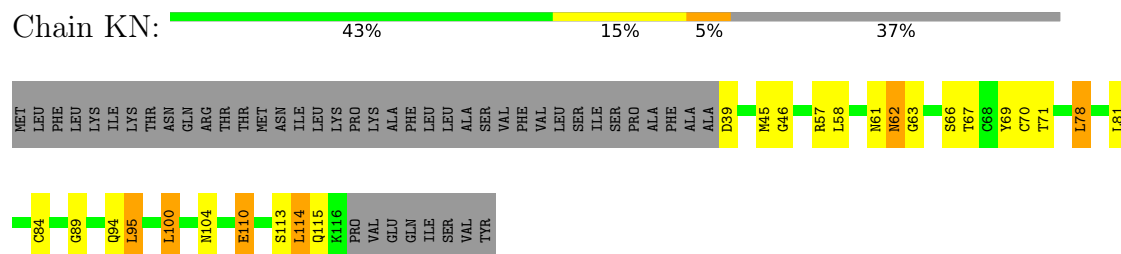
• Molecule 9: Neurogenic locus notch



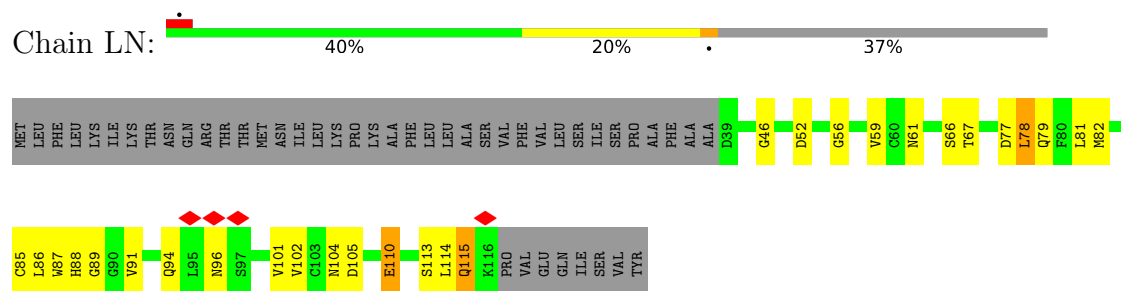
- Molecule 9: Neurogenic locus notch



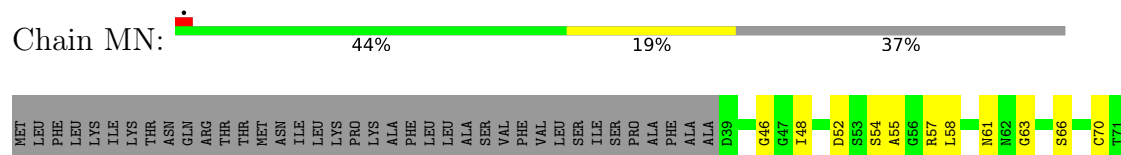
- Molecule 9: Neurogenic locus notch

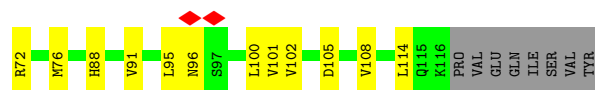


- Molecule 9: Neurogenic locus notch

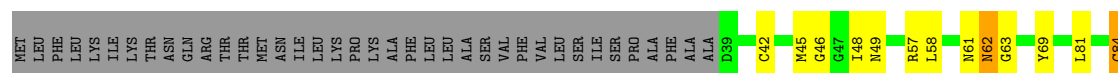


- Molecule 9: Neurogenic locus notch

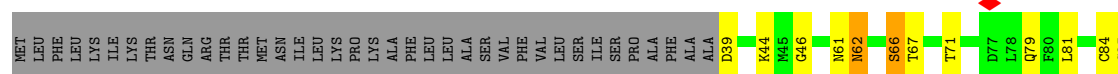




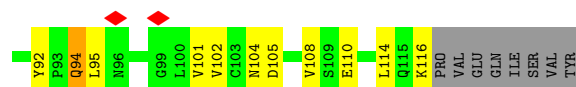
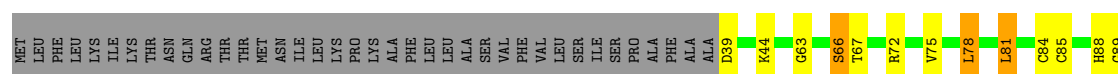
- Molecule 9: Neurogenic locus notch



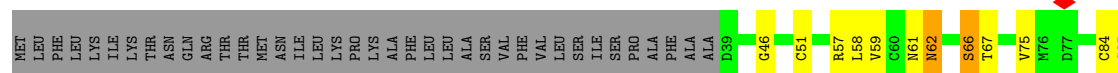
- Molecule 9: Neurogenic locus notch



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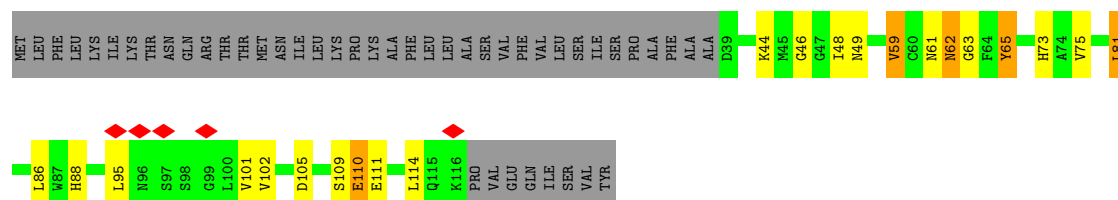


- Molecule 9: Neurogenic locus notch

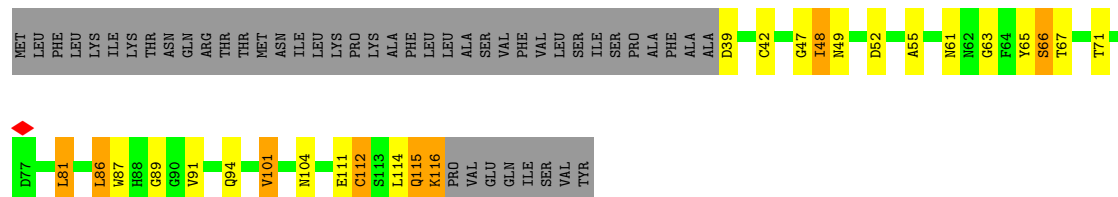


- Molecule 9: Neurogenic locus notch





- Molecule 9: Neurogenic locus notch



- Molecule 10: Unknown protein fragment



There are no outlier residues recorded for this chain.

- Molecule 10: Unknown protein fragment



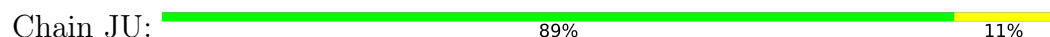
There are no outlier residues recorded for this chain.

- Molecule 10: Unknown protein fragment



There are no outlier residues recorded for this chain.

- Molecule 10: Unknown protein fragment



- Molecule 10: Unknown protein fragment



There are no outlier residues recorded for this chain.

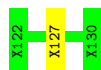
- Molecule 10: Unknown protein fragment





- Molecule 10: Unknown protein fragment

Chain MU: 89% 11%



- Molecule 10: Unknown protein fragment

Chain AU: 100%

There are no outlier residues recorded for this chain.

- Molecule 10: Unknown protein fragment

Chain BU: 100%

There are no outlier residues recorded for this chain.

- Molecule 10: Unknown protein fragment

Chain CU: 100%

There are no outlier residues recorded for this chain.

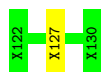
- Molecule 10: Unknown protein fragment

Chain DU: 100%

There are no outlier residues recorded for this chain.

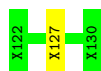
- Molecule 10: Unknown protein fragment

Chain EU: 89% 11%



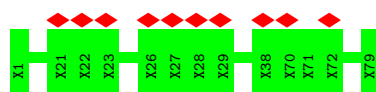
- Molecule 10: Unknown protein fragment

Chain FU: 89% 11%

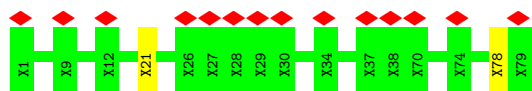


- Molecule 11: Unknown protein fragment

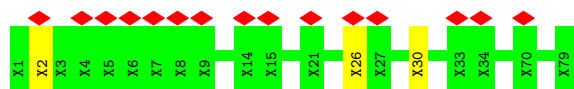
Chain GX: 21% 100%



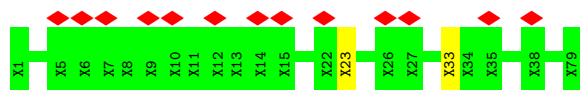
- Molecule 11: Unknown protein fragment



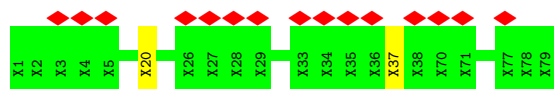
- Molecule 11: Unknown protein fragment



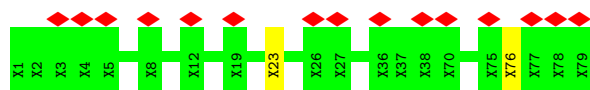
- Molecule 11: Unknown protein fragment



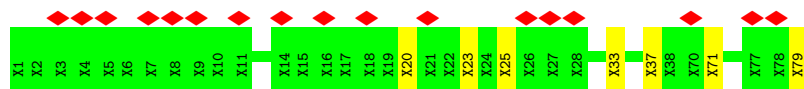
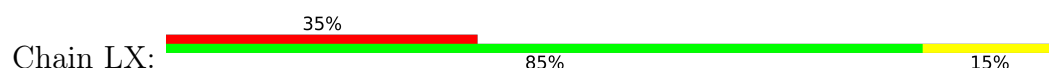
- Molecule 11: Unknown protein fragment



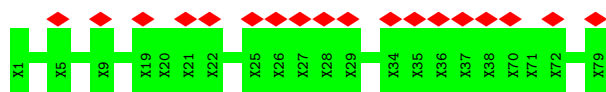
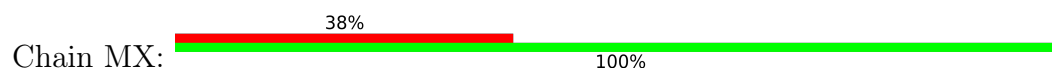
- Molecule 11: Unknown protein fragment



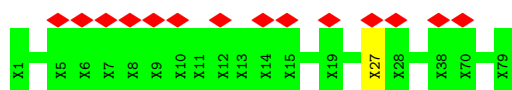
- Molecule 11: Unknown protein fragment



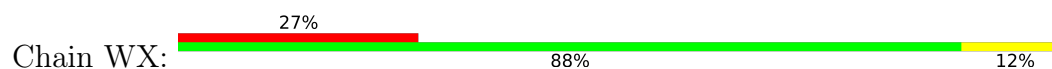
- Molecule 11: Unknown protein fragment



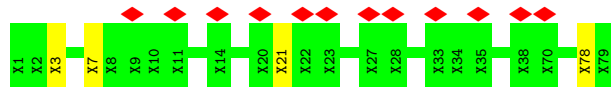
- Molecule 11: Unknown protein fragment



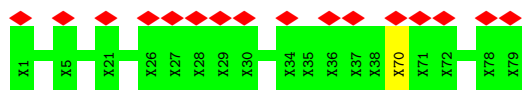
- Molecule 11: Unknown protein fragment



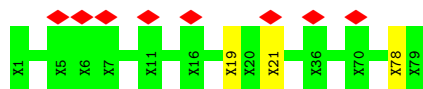
- Molecule 11: Unknown protein fragment



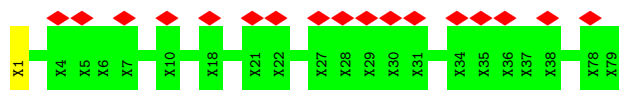
- Molecule 11: Unknown protein fragment



- Molecule 11: Unknown protein fragment

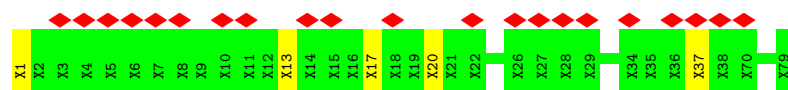


- Molecule 11: Unknown protein fragment

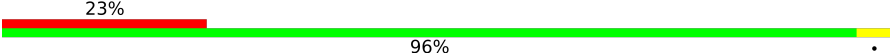


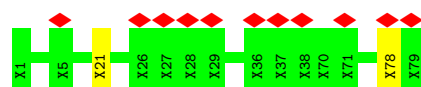
- Molecule 11: Unknown protein fragment

Chain BX: 

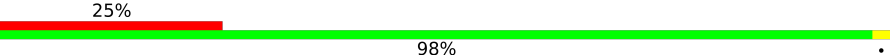


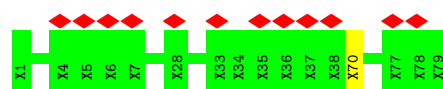
- Molecule 11: Unknown protein fragment

Chain CX: 

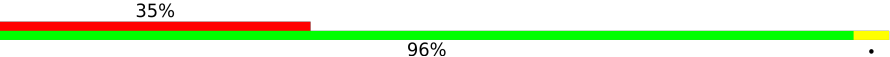


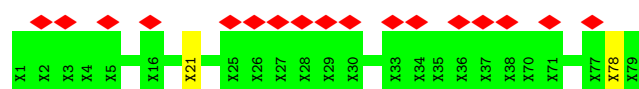
- Molecule 11: Unknown protein fragment

Chain EX: 



- Molecule 11: Unknown protein fragment

Chain FX: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	79720	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	9.547	Depositor
Minimum map value	-4.150	Depositor
Average map value	0.089	Depositor
Map value standard deviation	0.575	Depositor
Recommended contour level	2.25	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 [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AG	0.26	0/1250	0.58	0/1699
1	Ag	0.22	0/278	0.37	0/377
1	BG	0.27	0/1250	0.59	0/1699
1	Bg	0.23	0/278	0.43	0/377
1	CG	0.27	0/1250	0.58	1/1699 (0.1%)
1	Cg	0.21	0/278	0.36	0/377
1	DG	0.26	0/1250	0.57	0/1699
1	Dg	0.20	0/278	0.36	0/377
1	EG	0.25	0/1250	0.55	0/1699
1	Eg	0.23	0/278	0.38	0/377
1	FG	0.24	0/1250	0.54	0/1699
1	Fg	0.21	0/278	0.41	0/377
1	GG	0.26	0/1250	0.55	0/1699
1	Gg	0.23	0/278	0.38	0/377
1	HG	0.25	0/1250	0.58	0/1699
1	Hg	0.22	0/278	0.37	0/377
1	IG	0.27	0/1250	0.58	0/1699
1	Ig	0.25	0/278	0.39	0/377
1	JG	0.27	0/1250	0.59	0/1699
1	Jg	0.23	0/278	0.41	0/377
1	KG	0.27	0/1250	0.60	2/1699 (0.1%)
1	Kg	0.23	0/278	0.38	0/377
1	LG	0.28	0/1250	0.58	0/1699
1	Lg	0.22	0/278	0.38	0/377
1	MG	0.27	0/1250	0.58	0/1699
1	Mg	0.24	0/278	0.38	0/377
1	NG	0.28	0/1250	0.60	0/1699
1	OG	0.28	0/1250	0.61	1/1699 (0.1%)
1	PG	0.27	0/1250	0.59	0/1699
1	VG	0.22	0/278	0.49	0/377
1	WG	0.22	0/278	0.40	0/377
1	XG	0.24	0/278	0.45	0/377
1	YG	0.24	0/278	0.42	0/377
1	ZG	0.21	0/278	0.46	0/377

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	AC	0.33	0/1702	0.48	0/2315
2	BC	0.32	0/1702	0.48	0/2315
2	CC	0.33	0/1702	0.50	0/2315
2	DC	0.31	0/1957	0.46	0/2651
2	EC	0.32	0/1702	0.45	0/2315
2	FC	0.33	0/1702	0.48	0/2315
2	GC	0.33	0/1702	0.47	0/2315
2	HC	0.31	0/1957	0.45	0/2651
2	IC	0.30	0/1957	0.45	0/2651
2	JC	0.33	0/1702	0.48	0/2315
2	KC	0.34	0/1702	0.49	0/2315
2	LC	0.31	0/1957	0.45	0/2651
2	MC	0.31	0/1957	0.45	0/2651
3	AF	0.19	0/490	0.43	0/660
3	Af	0.22	0/456	0.40	0/615
3	BF	0.18	0/490	0.34	0/660
3	Bf	0.19	0/456	0.34	0/615
3	CF	0.17	0/490	0.36	0/660
3	Cf	0.21	0/456	0.39	0/615
3	DF	0.18	0/490	0.36	0/660
3	Df	0.21	0/456	0.39	0/615
3	EF	0.16	0/490	0.40	0/660
3	Ef	0.20	0/456	0.42	0/615
3	FF	0.18	0/490	0.38	0/660
3	Ff	0.22	0/456	0.38	0/615
3	GF	0.20	0/490	0.41	0/660
3	Gf	0.19	0/456	0.37	0/615
3	HF	0.17	0/490	0.38	0/660
3	Hf	0.20	0/456	0.39	0/615
3	IF	0.19	0/490	0.35	0/660
3	If	0.22	0/456	0.43	0/615
3	JF	0.18	0/490	0.35	0/660
3	Jf	0.22	0/456	0.41	0/615
3	KF	0.17	0/490	0.40	0/660
3	Kf	0.21	0/456	0.38	0/615
3	LF	0.17	0/490	0.35	0/660
3	Lf	0.20	0/456	0.35	0/615
3	MF	0.16	0/490	0.32	0/660
3	Mf	0.21	0/456	0.44	0/615
3	VF	0.17	0/490	0.35	0/660
3	WF	0.20	0/490	0.44	0/660
3	XF	0.18	0/490	0.37	0/660
3	YF	0.17	0/490	0.39	0/660

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	ZF	0.18	0/490	0.37	0/660
4	AD	0.31	0/1107	0.54	0/1502
4	Ad	0.29	0/1078	0.43	0/1463
4	BD	0.31	0/1107	0.56	0/1502
4	Bd	0.29	0/1078	0.48	0/1463
4	CD	0.31	0/1107	0.56	0/1502
4	Cd	0.28	0/1078	0.49	0/1463
4	DD	0.32	0/1107	0.55	0/1502
4	Dd	0.28	0/1078	0.47	0/1463
4	ED	0.31	0/1107	0.55	0/1502
4	Ed	0.27	0/1078	0.45	0/1463
4	FD	0.31	0/1107	0.54	0/1502
4	Fd	0.27	0/1078	0.46	0/1463
4	GD	0.30	0/1107	0.55	0/1502
4	Gd	0.29	0/1078	0.44	0/1463
4	HD	0.32	0/1107	0.54	0/1502
4	Hd	0.28	0/1078	0.44	0/1463
4	ID	0.31	0/1107	0.55	2/1502 (0.1%)
4	Id	0.29	0/1078	0.48	0/1463
4	JD	0.31	0/1107	0.54	0/1502
4	Jd	0.28	0/1078	0.43	0/1463
4	KD	0.33	0/1107	0.53	0/1502
4	Kd	0.28	0/1078	0.44	0/1463
4	LD	0.30	0/1107	0.54	0/1502
4	Ld	0.28	0/1078	0.48	0/1463
4	MD	0.31	0/1107	0.55	0/1502
4	Md	0.28	0/1078	0.44	0/1463
5	AH	0.27	0/2033	0.46	0/2775
5	BH	0.27	0/2033	0.46	0/2775
5	CH	0.27	0/2033	0.46	0/2775
5	DH	0.27	0/2033	0.42	0/2775
5	EH	0.26	0/2033	0.45	0/2775
5	FH	0.26	0/2033	0.46	0/2775
5	GH	0.27	0/2033	0.44	0/2775
5	HH	0.27	0/2033	0.45	0/2775
5	IH	0.26	0/2033	0.43	0/2775
5	JH	0.27	0/2033	0.45	0/2775
5	KH	0.26	0/2033	0.47	0/2775
5	LH	0.28	0/2033	0.46	0/2775
5	MH	0.27	0/2033	0.45	0/2775
5	VH	0.20	0/1921	0.41	0/2620
5	WH	0.19	0/1921	0.41	0/2620
5	XH	0.19	0/1921	0.40	0/2620

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
5	YH	0.21	0/1921	0.41	0/2620
5	ZH	0.20	0/1921	0.43	0/2620
6	AK	0.33	0/1195	0.49	0/1616
6	BK	0.33	0/1195	0.48	0/1616
6	CK	0.32	0/1195	0.47	0/1616
6	DK	0.32	0/1195	0.46	0/1616
6	EK	0.32	0/1195	0.51	0/1616
6	FK	0.31	0/1195	0.46	0/1616
6	GK	0.32	0/1195	0.48	0/1616
6	HK	0.33	0/1195	0.48	0/1616
6	IK	0.32	0/1195	0.47	0/1616
6	JK	0.33	0/1195	0.49	0/1616
6	KK	0.34	0/1195	0.46	0/1616
6	LK	0.31	0/1195	0.47	0/1616
6	MK	0.32	0/1195	0.48	0/1616
7	AL	0.30	0/1417	0.49	0/1912
7	BL	0.29	0/1417	0.50	0/1912
7	CL	0.30	0/1417	0.52	0/1912
7	DL	0.30	0/1417	0.51	0/1912
7	EL	0.30	0/1417	0.53	0/1912
7	FL	0.31	0/1417	0.52	0/1912
7	GL	0.30	0/1417	0.50	0/1912
7	HL	0.30	0/1417	0.51	0/1912
7	IL	0.30	0/1417	0.55	0/1912
7	JL	0.31	0/1417	0.51	0/1912
7	KL	0.30	0/1417	0.54	0/1912
7	LL	0.31	0/1417	0.51	0/1912
7	ML	0.29	0/1417	0.53	0/1912
8	AM	0.27	0/1678	0.48	0/2262
8	BM	0.27	0/1678	0.49	0/2262
8	CM	0.27	0/1678	0.51	0/2262
8	DM	0.25	0/1678	0.45	0/2262
8	EM	0.26	0/1678	0.47	0/2262
8	FM	0.26	0/1678	0.46	0/2262
8	GM	0.26	0/1678	0.49	2/2262 (0.1%)
8	HM	0.26	0/1678	0.45	0/2262
8	IM	0.27	0/1678	0.49	0/2262
8	JM	0.27	0/1678	0.50	0/2262
8	KM	0.26	0/1678	0.47	0/2262
8	LM	0.26	0/1678	0.45	0/2262
8	MM	0.25	0/1678	0.46	0/2262
9	AN	0.30	0/593	0.43	0/799
9	BN	0.31	0/593	0.54	0/799

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
9	CN	0.32	0/593	0.46	0/799
9	DN	0.31	0/593	0.46	0/799
9	EN	0.31	0/593	0.47	0/799
9	FN	0.30	0/593	0.47	0/799
9	GN	0.31	0/593	0.47	0/799
9	HN	0.30	0/593	0.49	0/799
9	IN	0.29	0/593	0.42	0/799
9	JN	0.30	0/593	0.49	0/799
9	KN	0.33	0/593	0.54	0/799
9	LN	0.34	0/593	0.49	0/799
9	MN	0.29	0/593	0.47	0/799
All	All	0.28	0/191071	0.48	8/258997 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	LC	0	1
5	CH	0	1
All	All	0	2

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	ID	77	TYR	CA-C-N	5.28	129.62	122.07
4	ID	77	TYR	C-N-CA	5.28	129.62	122.07
1	CG	939	THR	N-CA-C	-5.27	106.79	113.43
1	KG	1009	ALA	CA-C-N	-5.26	113.90	122.26
1	KG	1009	ALA	C-N-CA	-5.26	113.90	122.26
1	OG	939	THR	N-CA-C	-5.25	108.14	114.75
8	GM	121	ALA	CA-C-N	-5.22	118.58	122.18
8	GM	121	ALA	C-N-CA	-5.22	118.58	122.18

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	CH	320	LEU	Peptide

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Mol	Chain	Res	Type	Group
2	LC	30	GLY	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AG	1229	0	1231	39	0
1	Ag	276	0	263	8	0
1	BG	1229	0	1231	37	0
1	Bg	276	0	263	5	0
1	CG	1229	0	1231	41	0
1	Cg	276	0	263	9	0
1	DG	1229	0	1231	41	0
1	Dg	276	0	263	9	0
1	EG	1229	0	1231	33	0
1	Eg	276	0	263	9	0
1	FG	1229	0	1231	38	0
1	Fg	276	0	263	5	0
1	GG	1229	0	1231	37	0
1	Gg	276	0	263	9	0
1	HG	1229	0	1231	31	0
1	Hg	276	0	263	11	0
1	IG	1229	0	1231	33	0
1	Ig	276	0	263	8	0
1	JG	1229	0	1231	29	0
1	Jg	276	0	263	7	0
1	KG	1229	0	1231	29	0
1	Kg	276	0	263	7	0
1	LG	1229	0	1231	30	0
1	Lg	276	0	263	10	0
1	MG	1229	0	1231	34	0
1	Mg	276	0	263	7	0
1	NG	1229	0	1231	38	0
1	OG	1229	0	1231	39	0
1	PG	1229	0	1231	42	0
1	VG	276	0	263	2	0
1	WG	276	0	263	1	0
1	XG	276	0	263	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	YG	276	0	263	4	0
1	ZG	276	0	263	4	0
2	AC	1667	0	1682	33	0
2	BC	1667	0	1682	31	0
2	CC	1667	0	1682	43	0
2	DC	1921	0	1952	26	0
2	EC	1667	0	1682	37	0
2	FC	1667	0	1682	42	0
2	GC	1667	0	1682	42	0
2	HC	1921	0	1952	34	0
2	IC	1921	0	1952	39	0
2	JC	1667	0	1682	37	0
2	KC	1667	0	1682	45	0
2	LC	1921	0	1952	32	0
2	MC	1921	0	1952	36	0
3	AF	483	0	502	13	0
3	Af	449	0	474	5	0
3	BF	483	0	502	9	0
3	Bf	449	0	474	6	0
3	CF	483	0	502	11	0
3	Cf	449	0	474	15	0
3	DF	483	0	502	15	0
3	Df	449	0	474	14	0
3	EF	483	0	502	13	0
3	Ef	449	0	474	10	0
3	FF	483	0	502	11	0
3	Ff	449	0	474	6	0
3	GF	483	0	502	15	0
3	Gf	449	0	474	4	0
3	HF	483	0	502	14	0
3	Hf	449	0	474	8	0
3	IF	483	0	502	16	0
3	If	449	0	474	11	0
3	JF	483	0	502	13	0
3	Jf	449	0	474	10	0
3	KF	483	0	502	15	0
3	Kf	449	0	474	8	0
3	LF	483	0	502	14	0
3	Lf	449	0	474	8	0
3	MF	483	0	502	16	0
3	Mf	449	0	474	5	0
3	VF	483	0	502	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	WF	483	0	502	16	0
3	XF	483	0	502	15	0
3	YF	483	0	502	11	0
3	ZF	483	0	502	11	0
4	AD	1086	0	1121	31	0
4	Ad	1058	0	1092	21	0
4	BD	1086	0	1121	17	0
4	Bd	1058	0	1092	16	0
4	CD	1086	0	1121	20	0
4	Cd	1058	0	1092	18	0
4	DD	1086	0	1121	22	0
4	Dd	1058	0	1092	16	0
4	ED	1086	0	1121	21	0
4	Ed	1058	0	1092	21	0
4	FD	1086	0	1121	23	0
4	Fd	1058	0	1092	12	0
4	GD	1086	0	1121	24	0
4	Gd	1058	0	1092	28	0
4	HD	1086	0	1121	27	0
4	Hd	1058	0	1092	17	0
4	ID	1086	0	1121	25	0
4	Id	1058	0	1092	16	0
4	JD	1086	0	1121	20	0
4	Jd	1058	0	1092	19	0
4	KD	1086	0	1121	29	0
4	Kd	1058	0	1092	19	0
4	LD	1086	0	1121	19	0
4	Ld	1058	0	1092	22	0
4	MD	1086	0	1121	23	0
4	Md	1058	0	1092	17	0
5	AH	1983	0	2009	45	0
5	BH	1983	0	2009	47	0
5	CH	1983	0	2009	45	0
5	DH	1983	0	2009	40	0
5	EH	1983	0	2009	45	0
5	FH	1983	0	2009	54	0
5	GH	1983	0	2009	60	0
5	HH	1983	0	2009	47	0
5	IH	1983	0	2009	42	0
5	JH	1983	0	2009	48	0
5	KH	1983	0	2009	37	0
5	LH	1983	0	2009	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	MH	1983	0	2009	44	0
5	VH	1875	0	1900	45	0
5	WH	1875	0	1900	32	0
5	XH	1875	0	1900	38	0
5	YH	1875	0	1900	47	0
5	ZH	1875	0	1900	41	0
6	AK	1175	0	1221	21	0
6	BK	1175	0	1221	24	0
6	CK	1175	0	1221	35	0
6	DK	1175	0	1221	28	0
6	EK	1175	0	1221	22	0
6	FK	1175	0	1221	25	0
6	GK	1175	0	1221	26	0
6	HK	1175	0	1221	26	0
6	IK	1175	0	1221	26	0
6	JK	1175	0	1221	31	0
6	KK	1175	0	1221	31	0
6	LK	1175	0	1221	22	0
6	MK	1175	0	1221	31	0
7	AL	1388	0	1378	23	0
7	BL	1388	0	1378	24	0
7	CL	1388	0	1378	31	0
7	DL	1388	0	1378	26	0
7	EL	1388	0	1378	22	0
7	FL	1388	0	1378	36	0
7	GL	1388	0	1378	30	0
7	HL	1388	0	1378	35	0
7	IL	1388	0	1378	29	0
7	JL	1388	0	1378	27	0
7	KL	1388	0	1378	32	0
7	LL	1388	0	1378	29	0
7	ML	1388	0	1378	26	0
8	AM	1650	0	1658	39	0
8	BM	1650	0	1658	36	0
8	CM	1650	0	1658	34	0
8	DM	1650	0	1658	28	0
8	EM	1650	0	1658	35	0
8	FM	1650	0	1658	40	0
8	GM	1650	0	1658	29	0
8	HM	1650	0	1658	30	0
8	IM	1650	0	1658	32	0
8	JM	1650	0	1658	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	KM	1650	0	1658	36	0
8	LM	1650	0	1658	32	0
8	MM	1650	0	1658	45	0
9	AN	582	0	530	14	0
9	BN	582	0	530	8	0
9	CN	582	0	530	13	0
9	DN	582	0	530	12	0
9	EN	582	0	530	12	0
9	FN	582	0	530	15	0
9	GN	582	0	530	12	0
9	HN	582	0	530	14	0
9	IN	582	0	530	6	0
9	JN	582	0	530	15	0
9	KN	582	0	530	15	0
9	LN	582	0	530	15	0
9	MN	582	0	530	10	0
10	AU	45	0	12	0	0
10	BU	45	0	12	0	0
10	CU	45	0	12	0	0
10	DU	45	0	12	0	0
10	EU	45	0	12	1	0
10	FU	45	0	13	1	0
10	GU	45	0	12	0	0
10	HU	45	0	13	0	0
10	IU	45	0	13	0	0
10	JU	45	0	12	1	0
10	KU	45	0	12	0	0
10	LU	45	0	13	1	0
10	MU	45	0	12	1	0
11	AX	240	0	56	1	0
11	BX	240	0	55	3	0
11	CX	240	0	55	1	0
11	DX	240	0	58	1	0
11	EX	240	0	55	1	0
11	FX	240	0	54	2	0
11	GX	240	0	55	0	0
11	HX	240	0	56	2	0
11	IX	240	0	54	1	0
11	JX	240	0	55	1	0
11	KX	240	0	59	1	0
11	LX	240	0	56	4	0
11	MX	240	0	56	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	VX	240	0	56	1	0
11	WX	240	0	56	3	0
11	XX	240	0	58	2	0
11	YX	240	0	56	1	0
11	ZX	240	0	57	2	0
All	All	192370	0	190628	3726	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 (3726) 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)
7:BL:129:THR:O	7:BL:133:PHE:HB2	1.64	0.97
7:BL:166:ALA:HA	7:BL:206:GLU:O	1.72	0.90
7:IL:166:ALA:HA	7:IL:206:GLU:O	1.71	0.89
7:AL:166:ALA:HA	7:AL:206:GLU:O	1.75	0.86
7:JL:166:ALA:HA	7:JL:206:GLU:O	1.76	0.85
7:FL:129:THR:O	7:FL:133:PHE:HB2	1.81	0.80
7:FL:166:ALA:HA	7:FL:206:GLU:O	1.83	0.78
7:LL:166:ALA:HA	7:LL:206:GLU:O	1.83	0.77
7:EL:166:ALA:HA	7:EL:206:GLU:O	1.86	0.76
7:DL:166:ALA:HA	7:DL:206:GLU:O	1.85	0.75
7:GL:166:ALA:HA	7:GL:206:GLU:O	1.87	0.74
1:AG:876:SER:HB2	1:AG:1033:SER:HB3	1.68	0.73
7:KL:166:ALA:HA	7:KL:206:GLU:O	1.89	0.72
7:ML:166:ALA:HA	7:ML:206:GLU:O	1.90	0.71
8:FM:306:GLN:HG2	8:FM:308:ASP:H	1.57	0.70
7:CL:129:THR:O	7:CL:133:PHE:HB2	1.91	0.70
2:BC:92:ILE:HG13	4:Gd:48:VAL:HG11	1.74	0.69
7:IL:129:THR:O	7:IL:133:PHE:HB2	1.92	0.69
2:MC:56:ARG:HH22	1:PG:1036:GLY:H	1.40	0.69
8:MM:275:ASP:HB3	8:MM:294:PHE:HB2	1.76	0.68
5:LH:235:THR:HG23	5:MH:251:ARG:HH12	1.60	0.67
7:FL:115:GLN:HB3	7:FL:126:ILE:HB	1.76	0.67
7:EL:115:GLN:HB3	7:EL:126:ILE:HB	1.76	0.67
1:AG:886:LEU:HD21	1:BG:1040:LEU:HB2	1.77	0.67
1:Gg:801:MET:HB3	5:HH:121:PRO:HB2	1.77	0.67
6:MK:127:LYS:H	6:MK:127:LYS:HZ2	1.41	0.67
5:GH:115:MET:HE3	1:Fg:801:MET:HB3	1.77	0.66
8:LM:302:ARG:HH11	8:LM:309:LEU:HD11	1.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:MG:872:VAL:HA	1:MG:1036:GLY:HA2	1.77	0.66
4:LD:76:ALA:H	4:LD:79:LEU:HD12	1.60	0.66
5:VH:131:LYS:HB3	5:CH:145:PRO:HG3	1.78	0.66
5:CH:183:ASP:HA	5:CH:256:VAL:HG12	1.78	0.66
1:PG:912:MET:HB3	1:PG:944:LEU:HB2	1.78	0.66
4:LD:36:ASP:OD1	4:LD:36:ASP:N	2.28	0.66
1:IG:876:SER:HB3	1:JG:941:ARG:HG2	1.77	0.65
3:Df:218:GLY:H	3:Df:247:ILE:HD11	1.62	0.65
4:ID:29:PRO:HG2	7:IL:225:GLN:HA	1.78	0.65
5:XH:183:ASP:HA	5:XH:256:VAL:HG12	1.78	0.65
7:IL:177:HIS:HD1	8:IM:315:TYR:HH	1.40	0.65
1:FG:899:LEU:HD13	1:FG:919:MET:HG2	1.79	0.65
2:IC:147:THR:OG1	2:IC:148:TRP:N	2.30	0.65
6:EK:117:THR:HA	6:EK:157:GLN:O	1.96	0.65
4:Id:29:PRO:HB2	4:Id:32:ASN:HB2	1.78	0.65
7:KL:115:GLN:HB3	7:KL:126:ILE:HB	1.79	0.65
8:GM:120:GLY:H	8:GM:140:ASN:HB2	1.63	0.64
5:HH:238:MET:N	5:HH:238:MET:SD	2.70	0.64
8:FM:115:ARG:HG3	8:FM:135:ASP:HB3	1.79	0.64
5:IH:229:ARG:HG2	5:IH:236:PRO:HB3	1.79	0.64
1:CG:912:MET:HB3	1:CG:944:LEU:HB2	1.80	0.64
1:KG:1005:VAL:O	1:KG:1009:ALA:HB2	1.98	0.64
8:HM:306:GLN:HG2	8:HM:308:ASP:H	1.62	0.64
3:MF:250:LEU:HD12	3:MF:251:GLN:HG3	1.79	0.64
8:BM:292:MET:N	8:BM:292:MET:SD	2.71	0.64
4:Gd:108:VAL:HG12	4:Gd:156:LEU:HB3	1.80	0.64
4:Hd:84:SER:H	2:DC:268:ALA:HB3	1.62	0.64
1:CG:884:PRO:HB2	1:DG:1040:LEU:HD11	1.79	0.64
2:GC:146:THR:OG1	2:GC:147:TRP:N	2.29	0.64
1:OG:876:SER:HB2	1:OG:1033:SER:HB3	1.79	0.64
7:HL:166:ALA:HA	7:HL:206:GLU:O	1.97	0.64
6:EK:50:ASP:OD1	6:EK:50:ASP:N	2.29	0.64
8:JM:308:ASP:OD1	8:JM:308:ASP:N	2.31	0.63
1:DG:937:PRO:HD3	1:DG:1037:LEU:HA	1.79	0.63
6:LK:177:ASN:OD1	6:LK:177:ASN:N	2.31	0.63
1:IG:972:PHE:HB3	1:IG:1005:VAL:HG22	1.79	0.63
5:VH:256:VAL:HG12	5:VH:258:GLY:H	1.64	0.63
4:CD:130:GLU:OE2	4:CD:133:ARG:NH1	2.32	0.63
3:ZF:208:ILE:HG13	3:ZF:225:SER:H	1.64	0.63
2:FC:145:THR:OG1	2:FC:146:TRP:N	2.29	0.63
8:AM:163:THR:HB	8:AM:183:VAL:HG12	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:CK:49:CYS:HG	6:CK:52:THR:HG1	1.46	0.63
3:DF:250:LEU:HD12	3:DF:251:GLN:HG3	1.79	0.63
9:IN:110:GLU:HA	9:IN:113:SER:HB2	1.80	0.63
7:KL:130:ASP:OD1	7:KL:130:ASP:N	2.32	0.63
5:FH:183:ASP:HB2	5:FH:259:TYR:HA	1.81	0.63
8:EM:292:MET:SD	8:EM:292:MET:N	2.72	0.63
1:MG:931:SER:H	1:MG:1043:GLN:HE22	1.47	0.63
4:Jd:78:ASN:HD21	4:Jd:103:HIS:HB2	1.63	0.63
5:YH:183:ASP:HB2	5:YH:259:TYR:HA	1.81	0.62
5:FH:324:TRP:HB3	5:FH:339:MET:HE2	1.81	0.62
6:GK:117:THR:HA	6:GK:157:GLN:O	1.99	0.62
4:Hd:48:VAL:HG21	2:CC:93:ILE:HG13	1.81	0.62
6:EK:162:ASP:OD1	6:EK:162:ASP:N	2.27	0.62
3:Jf:210:TYR:HB3	3:Jf:222:LEU:HD12	1.80	0.62
5:VH:344:VAL:HG13	5:VH:355:GLN:HE21	1.62	0.62
1:CG:911:LYS:HA	1:CG:943:ALA:HA	1.80	0.62
5:YH:238:MET:N	5:YH:238:MET:SD	2.71	0.62
5:DH:189:TRP:HE1	5:DH:232:GLY:H	1.46	0.62
6:FK:162:ASP:OD1	6:FK:162:ASP:N	2.31	0.62
6:FK:127:LYS:HZ2	6:FK:127:LYS:H	1.47	0.62
2:LC:147:THR:OG1	2:LC:148:TRP:N	2.32	0.62
2:EC:146:THR:OG1	2:EC:147:TRP:N	2.30	0.62
8:HM:120:GLY:H	8:HM:140:ASN:HB2	1.64	0.62
3:IF:208:ILE:HG13	3:IF:225:SER:H	1.65	0.62
8:LM:119:GLU:HG3	8:LM:139:ALA:HB3	1.82	0.62
8:LM:120:GLY:H	8:LM:140:ASN:HB2	1.65	0.62
7:CL:166:ALA:HA	7:CL:206:GLU:O	1.99	0.62
1:LG:899:LEU:HD13	1:LG:919:MET:HG2	1.80	0.62
5:DH:183:ASP:HA	5:DH:256:VAL:HG12	1.82	0.62
5:BH:225:ASN:HD21	5:CH:176:VAL:H	1.46	0.62
7:BL:115:GLN:HB3	7:BL:126:ILE:HB	1.82	0.61
2:GC:263:ARG:HH11	2:GC:264:ALA:H	1.46	0.61
2:BC:145:THR:OG1	2:BC:146:TRP:N	2.31	0.61
1:Gg:811:ASP:HA	1:Gg:814:GLN:HE22	1.65	0.61
8:MM:240:GLN:HB3	8:MM:242:LYS:HE3	1.83	0.61
5:VH:284:LEU:HD21	5:VH:330:SER:HB3	1.82	0.61
3:Bf:223:ILE:HG13	3:Bf:229:THR:HG22	1.82	0.61
7:CL:54:ARG:HH21	7:CL:57:VAL:HG13	1.65	0.61
4:Cd:84:SER:H	2:LC:268:ALA:HB3	1.65	0.61
1:GG:969:GLY:HA3	1:GG:1009:ALA:HB2	1.82	0.61
1:OG:899:LEU:HD13	1:OG:919:MET:HG2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:JK:106:LEU:O	6:JK:111:LYS:NZ	2.32	0.61
7:JL:224:ALA:HA	7:JL:227:ARG:HH11	1.65	0.61
7:AL:129:THR:O	7:AL:133:PHE:HB2	1.99	0.61
8:KM:306:GLN:HG2	8:KM:308:ASP:H	1.64	0.61
3:MF:254:ILE:O	3:MF:261:VAL:HA	2.00	0.61
5:ZH:189:TRP:HE1	5:ZH:232:GLY:H	1.48	0.61
8:AM:306:GLN:HB3	8:AM:309:LEU:HB2	1.83	0.61
6:BK:117:THR:HA	6:BK:157:GLN:O	2.01	0.61
7:BL:130:ASP:N	7:BL:130:ASP:OD1	2.33	0.61
7:CL:115:GLN:HB3	7:CL:126:ILE:HB	1.82	0.61
7:DL:212:ASN:N	7:DL:212:ASN:OD1	2.33	0.61
1:OG:872:VAL:HA	1:OG:1036:GLY:HA2	1.83	0.61
7:IL:192:PHE:O	7:IL:196:ASN:ND2	2.33	0.61
5:LH:171:LEU:HD11	5:LH:241:LEU:HB2	1.82	0.61
5:EH:320:LEU:HB2	5:EH:346:LEU:HB3	1.82	0.61
2:AC:145:THR:OG1	2:AC:146:TRP:N	2.32	0.61
1:FG:886:LEU:HA	1:FG:899:LEU:O	2.01	0.61
3:Cf:221:TRP:HE1	3:Cf:229:THR:HB	1.65	0.61
5:DH:238:MET:N	5:DH:238:MET:SD	2.74	0.61
1:CG:876:SER:HB2	1:CG:1033:SER:HB3	1.83	0.61
6:HK:117:THR:HA	6:HK:157:GLN:O	2.01	0.61
5:MH:154:THR:HB	5:MH:156:GLN:HE22	1.66	0.61
2:KC:99:LEU:HB3	2:KC:209:MET:HE2	1.82	0.61
4:DD:75:ASN:ND2	4:DD:80:GLN:OE1	2.34	0.61
5:FH:108:ASP:N	5:FH:108:ASP:OD1	2.34	0.61
1:ZG:806:THR:O	1:ZG:810:GLN:NE2	2.34	0.60
1:GG:867:ASP:OD1	1:GG:867:ASP:N	2.34	0.60
7:FL:44:HIS:HB2	7:FL:48:ASN:HA	1.83	0.60
8:FM:196:MET:HE2	8:FM:220:ALA:HB2	1.83	0.60
5:IH:278:ASP:N	5:IH:278:ASP:OD1	2.33	0.60
8:MM:303:GLU:HG2	3:Mf:251:GLN:HE21	1.66	0.60
5:YH:229:ARG:HG2	5:YH:236:PRO:HB3	1.82	0.60
3:Df:243:MET:O	3:Df:245:LYS:NZ	2.34	0.60
8:BM:173:LEU:HD22	8:BM:175:ILE:HD11	1.83	0.60
10:EU:127:UNK:O	7:FL:232:GLN:NE2	2.34	0.60
5:LH:324:TRP:HA	5:LH:339:MET:HB3	1.83	0.60
5:MH:326:ALA:HB3	5:MH:338:GLU:HB3	1.83	0.60
7:FL:163:ILE:HG23	7:FL:233:TRP:HB3	1.84	0.60
2:BC:128:ASP:N	2:BC:128:ASP:OD1	2.33	0.60
9:GN:62:ASN:OD1	9:GN:62:ASN:N	2.32	0.60
4:ID:105:ARG:HB3	4:ID:153:VAL:HG12	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:LL:210:ASP:OD1	7:LL:210:ASP:N	2.34	0.60
1:EG:898:LYS:HE3	1:FG:865:THR:HB	1.83	0.60
2:FC:220:VAL:HG12	2:FC:254:LEU:HD23	1.84	0.60
1:OG:898:LYS:HD3	1:PG:866:GLY:HA3	1.84	0.60
7:HL:212:ASN:OD1	7:HL:212:ASN:N	2.33	0.60
8:IM:240:GLN:HB3	8:IM:242:LYS:HE3	1.84	0.60
4:KD:98:ILE:HD11	4:KD:128:LEU:HD22	1.83	0.60
6:LK:87:GLN:OE1	6:LK:128:ARG:NH1	2.34	0.60
1:MG:1003:ASN:HA	1:MG:1006:ILE:HD12	1.84	0.60
5:HH:189:TRP:HE1	5:HH:231:ARG:H	1.48	0.60
3:Hf:254:ILE:HB	3:Hf:262:ILE:HG23	1.83	0.60
7:JL:170:ASP:OD2	7:JL:227:ARG:NH2	2.35	0.60
4:CD:73:ILE:O	4:CD:133:ARG:NH2	2.35	0.60
2:IC:102:LEU:HB2	2:IC:106:ILE:HG23	1.84	0.60
7:ML:115:GLN:HB3	7:ML:126:ILE:HB	1.83	0.60
5:XH:193:ALA:HB3	5:XH:229:ARG:HD3	1.82	0.60
3:BF:231:THR:HG23	5:CH:150:LYS:HE3	1.83	0.60
5:IH:315:THR:OG1	5:IH:316:ASN:N	2.35	0.60
7:JL:115:GLN:HB3	7:JL:126:ILE:HB	1.83	0.60
6:LK:151:SER:OG	6:LK:152:ARG:N	2.35	0.60
7:AL:115:GLN:HB3	7:AL:126:ILE:HB	1.84	0.60
8:DM:308:ASP:OD1	8:DM:308:ASP:N	2.32	0.60
4:Dd:132:LEU:HD11	4:Dd:145:ILE:HG12	1.82	0.60
2:CC:146:THR:OG1	2:CC:147:TRP:N	2.33	0.60
1:JG:899:LEU:HD13	1:JG:919:MET:HG2	1.84	0.60
1:OG:912:MET:HB3	1:OG:944:LEU:HB2	1.82	0.60
3:Kf:254:ILE:O	3:Kf:261:VAL:HA	2.02	0.60
1:KG:944:LEU:HD21	1:KG:1031:VAL:HG12	1.84	0.60
5:GH:208:LYS:NZ	1:Hg:822:GLU:O	2.33	0.59
6:GK:146:SER:HB2	4:Gd:29:PRO:HG3	1.83	0.59
7:GL:130:ASP:N	7:GL:130:ASP:OD1	2.35	0.59
5:AH:292:SER:OG	5:AH:293:ARG:N	2.35	0.59
4:Ld:79:LEU:HG	4:Ld:128:LEU:HB2	1.85	0.59
5:DH:345:LEU:HB2	5:DH:356:LEU:HB2	1.84	0.59
1:OG:891:THR:OG1	1:OG:892:GLY:N	2.33	0.59
2:HC:147:THR:OG1	2:HC:148:TRP:N	2.34	0.59
1:BG:935:ILE:HG23	1:BG:1040:LEU:HD22	1.84	0.59
5:LH:326:ALA:HB3	5:LH:338:GLU:HB3	1.83	0.59
6:LK:117:THR:HA	6:LK:157:GLN:O	2.03	0.59
6:MK:71:GLY:O	4:AD:27:LYS:NZ	2.35	0.59
3:Ff:243:MET:H	3:Ff:257:SER:HB3	1.65	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:HK:73:ASN:N	6:HK:73:ASN:OD1	2.33	0.59
4:Ld:98:ILE:HD11	4:Ld:128:LEU:HD22	1.82	0.59
4:CD:162:TYR:O	2:KC:245:ARG:NH1	2.35	0.59
1:FG:951:HIS:H	1:FG:1027:THR:HG22	1.66	0.59
1:GG:955:ARG:NH1	1:GG:1023:PHE:O	2.35	0.59
1:MG:944:LEU:HD11	1:MG:1031:VAL:HA	1.83	0.59
1:AG:910:ASP:OD1	1:AG:910:ASP:N	2.36	0.59
6:HK:92:ASN:N	6:HK:92:ASN:OD1	2.35	0.59
7:JL:230:GLU:OE2	7:JL:232:GLN:NE2	2.34	0.59
6:AK:111:LYS:NZ	6:AK:150:ASP:O	2.33	0.59
7:ML:165:VAL:HG12	7:ML:231:ILE:HG12	1.82	0.59
5:YH:183:ASP:O	5:YH:255:ARG:NH1	2.35	0.59
2:GC:117:LEU:HB2	2:GC:127:ILE:HG13	1.85	0.59
2:JC:257:ASN:O	2:JC:261:TRP:NE1	2.34	0.59
6:CK:125:SER:OG	6:CK:127:LYS:NZ	2.36	0.59
4:GD:67:LYS:HB2	4:Gd:62:ILE:HD11	1.83	0.59
1:Hg:802:LEU:HG	5:IH:115:MET:HG2	1.84	0.59
3:If:212:ILE:HD12	3:If:254:ILE:HD11	1.83	0.59
9:KN:89:GLY:HA3	9:KN:104:ASN:HB2	1.84	0.59
7:ML:192:PHE:O	7:ML:196:ASN:ND2	2.32	0.59
7:CL:216:ASP:N	7:CL:216:ASP:OD1	2.35	0.59
8:EM:275:ASP:HB3	8:EM:294:PHE:HB2	1.82	0.59
1:HG:937:PRO:HD3	1:HG:1037:LEU:HA	1.85	0.59
5:HH:108:ASP:OD1	5:HH:108:ASP:N	2.34	0.59
5:HH:284:LEU:O	5:HH:314:ARG:NH2	2.35	0.59
8:HM:203:SER:HA	8:HM:223:GLN:O	2.03	0.59
4:Ld:87:TRP:O	4:Ld:120:SER:HA	2.02	0.59
6:AK:50:ASP:N	6:AK:50:ASP:OD1	2.33	0.59
5:MH:126:GLN:HA	5:MH:129:LYS:HE3	1.85	0.59
3:Gf:218:GLY:H	3:Gf:247:ILE:HD11	1.67	0.59
4:ID:141:LYS:NZ	4:Id:59:GLU:O	2.36	0.59
7:KL:212:ASN:OD1	7:KL:212:ASN:N	2.36	0.59
6:LK:76:ILE:HG13	6:LK:182:ILE:HB	1.85	0.59
8:CM:149:ASN:OD1	8:CM:149:ASN:N	2.36	0.59
2:AC:230:LEU:HB2	2:AC:243:ASP:HB2	1.85	0.59
1:BG:886:LEU:HD21	1:CG:1040:LEU:HB2	1.85	0.59
4:Jd:78:ASN:ND2	4:Jd:102:ALA:O	2.34	0.59
4:KD:119:ILE:HG23	4:KD:138:GLN:HG2	1.85	0.59
2:FC:262:ARG:NH1	2:FC:263:ALA:O	2.36	0.59
1:MG:874:ASP:N	1:MG:874:ASP:OD1	2.36	0.59
6:CK:90:ARG:NH2	6:CK:92:ASN:OD1	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:FH:201:SER:OG	5:FH:219:LYS:NZ	2.35	0.59
4:GD:150:ASN:OD1	4:GD:150:ASN:N	2.35	0.59
9:GN:88:HIS:ND1	9:GN:105:ASP:OD2	2.36	0.59
6:KK:152:ARG:HB2	6:KK:153:ILE:HD12	1.84	0.59
9:LN:79:GLN:O	2:GC:84:ASN:ND2	2.36	0.59
4:Cd:68:ASP:N	4:Cd:68:ASP:OD1	2.36	0.59
1:PG:972:PHE:O	1:PG:976:ASN:ND2	2.35	0.59
8:IM:288:ARG:NH2	8:IM:316:ASN:O	2.36	0.58
6:AK:163:LYS:NZ	6:AK:164:PRO:O	2.36	0.58
1:AG:899:LEU:HD13	1:AG:919:MET:HG2	1.85	0.58
4:ID:73:ILE:O	4:ID:133:ARG:NH2	2.37	0.58
5:LH:315:THR:OG1	5:LH:316:ASN:N	2.35	0.58
8:MM:146:LEU:HD23	8:MM:165:ILE:HG12	1.84	0.58
5:BH:315:THR:OG1	5:BH:316:ASN:N	2.35	0.58
1:LG:891:THR:OG1	1:LG:892:GLY:N	2.36	0.58
5:GH:352:LYS:NZ	5:GH:354:MET:SD	2.75	0.58
4:Jd:150:ASN:OD1	4:Jd:150:ASN:N	2.36	0.58
5:BH:173:GLN:NE2	5:BH:219:LYS:O	2.36	0.58
1:HG:899:LEU:HD13	1:HG:919:MET:HG2	1.84	0.58
8:FM:117:ARG:NH2	8:FM:119:GLU:OE2	2.37	0.58
2:BC:141:THR:HG23	2:BC:142:THR:HG22	1.85	0.58
4:GD:105:ARG:HB2	4:GD:153:VAL:HG22	1.86	0.58
5:MH:301:ASP:OD1	5:MH:301:ASP:N	2.36	0.58
2:JC:145:THR:OG1	2:JC:146:TRP:N	2.36	0.58
1:HG:1011:VAL:HG12	1:IG:963:SER:HB2	1.86	0.58
4:HD:73:ILE:O	4:HD:133:ARG:NH2	2.35	0.58
7:IL:115:GLN:HB3	7:IL:126:ILE:HB	1.84	0.58
4:CD:23:MET:N	4:CD:23:MET:SD	2.77	0.58
7:BL:183:GLN:HE22	7:BL:206:GLU:HA	1.68	0.58
4:AD:130:GLU:OE2	4:AD:133:ARG:NH1	2.36	0.58
5:EH:249:ASP:N	5:EH:249:ASP:OD1	2.33	0.58
4:ID:124:LYS:O	8:IM:317:LYS:NZ	2.36	0.58
6:KK:76:ILE:HG13	6:KK:182:ILE:HB	1.85	0.58
8:KM:119:GLU:HG3	8:KM:139:ALA:HB3	1.86	0.58
3:LF:235:GLY:HA2	3:LF:243:MET:HE1	1.84	0.58
8:LM:128:ASN:HB3	8:LM:130:ARG:HH12	1.68	0.58
7:FL:165:VAL:HG12	7:FL:231:ILE:HG12	1.85	0.58
2:EC:91:ASP:HB3	2:EC:147:TRP:HE1	1.68	0.58
5:IH:148:PRO:O	5:IH:246:LYS:NZ	2.37	0.58
8:JM:201:THR:HG22	8:JM:221:LYS:HB2	1.86	0.58
7:LL:113:ASP:OD1	7:LL:113:ASP:N	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Md:26:LYS:NZ	4:Md:27:LYS:O	2.36	0.58
5:EH:106:VAL:HA	5:EH:109:LYS:HE2	1.85	0.58
5:EH:278:ASP:OD1	5:EH:278:ASP:N	2.35	0.58
1:NG:972:PHE:HB3	1:NG:1005:VAL:HG22	1.86	0.58
1:Hg:810:GLN:NE2	1:Hg:811:ASP:OD1	2.37	0.58
4:KD:55:MET:O	2:FC:213:LYS:NZ	2.34	0.58
7:LL:170:ASP:OD2	7:LL:227:ARG:NH2	2.37	0.58
4:Bd:78:ASN:OD1	4:Bd:78:ASN:N	2.37	0.58
5:EH:229:ARG:NH2	5:FH:212:THR:OG1	2.36	0.58
8:FM:129:LEU:HB2	8:FM:150:ILE:HD11	1.85	0.58
2:EC:109:VAL:HG23	2:EC:208:GLY:HA3	1.85	0.58
5:WH:250:TYR:HD2	5:FH:238:MET:HB3	1.69	0.58
2:FC:149:TYR:O	2:FC:197:ASN:ND2	2.37	0.58
4:ED:77:TYR:O	4:ED:78:ASN:ND2	2.36	0.58
6:EK:116:VAL:HG22	6:EK:182:ILE:HG22	1.86	0.58
6:EK:138:ARG:NH2	8:EM:318:GLN:O	2.36	0.58
1:IG:874:ASP:OD1	1:IG:874:ASP:N	2.37	0.58
7:FL:131:LYS:NZ	7:FL:144:CYS:SG	2.75	0.58
5:AH:315:THR:OG1	5:AH:316:ASN:N	2.33	0.58
9:LN:82:MET:N	9:LN:82:MET:SD	2.77	0.58
11:WX:20:UNK:HA	11:WX:79:UNK:HA	1.86	0.58
1:EG:917:ASN:HA	1:EG:931:SER:HA	1.86	0.58
7:CL:192:PHE:O	7:CL:196:ASN:ND2	2.37	0.58
8:CM:306:GLN:HG2	8:CM:308:ASP:H	1.68	0.58
6:DK:163:LYS:NZ	6:DK:164:PRO:O	2.37	0.58
3:AF:210:TYR:HB3	3:AF:222:LEU:HB3	1.86	0.57
7:HL:127:ILE:HB	7:HL:229:ILE:HB	1.85	0.57
1:BG:972:PHE:O	1:BG:976:ASN:ND2	2.36	0.57
4:KD:60:LYS:O	4:KD:60:LYS:NZ	2.38	0.57
4:Md:66:SER:OG	4:Md:67:LYS:NZ	2.37	0.57
6:IK:162:ASP:OD1	6:IK:162:ASP:N	2.36	0.57
8:IM:120:GLY:H	8:IM:140:ASN:HB2	1.67	0.57
5:JH:176:VAL:HG22	5:JH:216:GLN:HB2	1.86	0.57
5:AH:273:PRO:O	2:IC:127:ARG:NH1	2.37	0.57
9:DN:84:CYS:SG	9:DN:85:CYS:N	2.77	0.57
1:OG:871:ALA:HB2	1:OG:889:ILE:HD13	1.86	0.57
8:IM:316:ASN:N	8:IM:316:ASN:OD1	2.38	0.57
6:JK:92:ASN:N	6:JK:92:ASN:OD1	2.37	0.57
5:AH:275:SER:HA	2:IC:127:ARG:HD3	1.85	0.57
4:Kd:71:LEU:O	4:Kd:133:ARG:NH1	2.38	0.57
2:GC:231:LEU:HB2	2:GC:244:ASP:HB3	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Cd:149:PRO:O	4:Cd:152:GLN:NE2	2.37	0.57
4:DD:119:ILE:HD11	4:DD:138:GLN:HB3	1.86	0.57
5:EH:315:THR:OG1	5:EH:316:ASN:N	2.35	0.57
2:HC:117:THR:HB	2:HC:129:SER:HB2	1.86	0.57
3:HF:235:GLY:HA2	3:HF:243:MET:HE1	1.86	0.57
5:HH:229:ARG:NH2	5:XH:212:THR:OG1	2.36	0.57
1:CG:1044:ASP:OD1	1:CG:1044:ASP:N	2.37	0.57
3:VF:265:SER:HB3	3:VF:268:ASP:HB2	1.87	0.57
4:AD:73:ILE:O	4:AD:133:ARG:NH2	2.37	0.57
2:FC:156:LYS:NZ	2:FC:157:PRO:O	2.36	0.57
4:ED:36:ASP:OD1	4:ED:36:ASP:N	2.37	0.57
3:FF:254:ILE:HB	3:FF:262:ILE:HB	1.86	0.57
1:NG:891:THR:OG1	1:NG:892:GLY:N	2.36	0.57
1:AG:899:LEU:HA	1:AG:918:THR:O	2.04	0.57
5:AH:131:LYS:NZ	5:ZH:143:ALA:O	2.37	0.57
7:KL:54:ARG:HE	7:KL:57:VAL:HG13	1.69	0.57
9:KN:100:LEU:HA	9:KN:113:SER:HB3	1.86	0.57
7:LL:136:SER:OG	8:LM:314:ARG:NH1	2.37	0.57
8:MM:306:GLN:HG2	8:MM:308:ASP:H	1.69	0.57
4:Md:31:ASN:OD1	4:Md:31:ASN:N	2.34	0.57
5:XH:207:ASP:N	5:XH:207:ASP:OD1	2.37	0.57
8:AM:306:GLN:NE2	8:AM:308:ASP:OD1	2.36	0.57
1:Dg:818:GLN:NE2	5:DH:205:GLN:OE1	2.38	0.57
3:DF:220:ALA:O	3:DF:231:THR:HA	2.03	0.57
5:EH:284:LEU:O	5:EH:314:ARG:NH2	2.36	0.57
5:FH:278:ASP:N	5:FH:278:ASP:OD1	2.37	0.57
1:OG:898:LYS:HE3	1:PG:865:THR:HB	1.87	0.57
5:JH:316:ASN:OD1	5:JH:316:ASN:N	2.37	0.57
2:CC:119:LEU:HA	2:CC:125:ILE:HG22	1.86	0.57
1:EG:972:PHE:HB3	1:EG:1005:VAL:HG22	1.85	0.57
5:BH:130:LEU:HD23	5:BH:133:ILE:HD11	1.87	0.57
8:BM:165:ILE:HB	8:BM:185:ILE:HG23	1.87	0.57
3:DF:219:ARG:NH1	3:EF:269:SER:O	2.38	0.57
7:EL:165:VAL:HG12	7:EL:231:ILE:HG12	1.86	0.57
7:HL:124:THR:HG22	7:HL:232:GLN:HG2	1.87	0.57
5:JH:315:THR:OG1	5:JH:316:ASN:N	2.36	0.57
1:Mg:811:ASP:O	1:Mg:814:GLN:NE2	2.38	0.57
5:MH:315:THR:OG1	5:MH:316:ASN:N	2.38	0.57
5:MH:324:TRP:HB3	5:MH:339:MET:HG2	1.87	0.57
4:Md:111:LYS:NZ	4:Md:112:SER:O	2.38	0.57
3:Df:210:TYR:HB3	3:Df:222:LEU:HD11	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:DC:90:ASN:N	2:DC:90:ASN:OD1	2.36	0.57
5:BH:203:ASN:ND2	5:BH:216:GLN:OE1	2.37	0.57
8:CM:154:LYS:NZ	8:CM:156:GLU:OE2	2.37	0.57
9:DN:57:ARG:HH21	9:DN:67:THR:HA	1.69	0.57
8:FM:119:GLU:HG3	8:FM:139:ALA:HB3	1.85	0.57
4:Hd:155:GLU:OE2	4:Hd:157:ARG:NH2	2.38	0.57
5:AH:192:ALA:HB3	5:AH:229:ARG:HG2	1.86	0.57
7:KL:108:ASP:OD2	7:KL:150:ASN:ND2	2.38	0.57
5:LH:236:PRO:O	5:MH:251:ARG:NH2	2.37	0.57
7:LL:124:THR:HA	7:LL:231:ILE:O	2.03	0.57
3:YF:266:GLN:HG3	3:YF:267:GLU:HG2	1.86	0.57
2:MC:246:ARG:HB2	2:AC:126:ILE:HG12	1.86	0.57
9:EN:62:ASN:OD1	9:EN:62:ASN:N	2.37	0.57
8:GM:275:ASP:HB3	8:GM:294:PHE:HB2	1.85	0.57
5:HH:207:ASP:N	5:HH:207:ASP:OD1	2.37	0.57
8:HM:166:ASN:HA	8:HM:186:SER:HB3	1.87	0.57
5:JH:326:ALA:HB3	5:JH:338:GLU:HB3	1.85	0.57
8:LM:210:ASP:OD1	8:LM:210:ASP:N	2.37	0.57
2:FC:175:TRP:O	2:FC:179:THR:OG1	2.23	0.57
5:FH:315:THR:OG1	5:FH:316:ASN:N	2.36	0.57
1:KG:867:ASP:OD1	1:KG:867:ASP:N	2.37	0.57
7:HL:165:VAL:HG12	7:HL:231:ILE:HG12	1.87	0.57
4:JD:31:ASN:N	4:JD:31:ASN:OD1	2.37	0.57
1:CG:899:LEU:HD13	1:CG:919:MET:HG2	1.86	0.57
2:CC:147:TRP:HB2	2:CC:151:LEU:HB2	1.87	0.57
9:LN:52:ASP:O	9:LN:56:GLY:N	2.37	0.57
7:AL:169:THR:OG1	7:AL:170:ASP:N	2.36	0.57
3:ZF:233:ARG:HG2	3:ZF:236:SER:HB2	1.87	0.57
3:BF:246:LEU:HB2	3:BF:255:LEU:HB2	1.87	0.57
8:BM:290:ASP:N	8:BM:290:ASP:OD1	2.37	0.57
3:Bf:243:MET:O	3:Bf:245:LYS:NZ	2.38	0.57
3:Cf:245:LYS:NZ	3:Cf:255:LEU:O	2.36	0.57
1:PG:951:HIS:H	1:PG:1027:THR:HG22	1.69	0.57
2:BC:108:VAL:HG23	2:BC:207:GLY:HA3	1.86	0.56
6:GK:177:ASN:O	6:GK:179:ARG:NH1	2.37	0.56
5:HH:160:LEU:HD22	5:HH:257:GLN:HB2	1.87	0.56
1:BG:874:ASP:OD1	1:BG:874:ASP:N	2.39	0.56
9:MN:57:ARG:NH1	9:MN:66:SER:O	2.38	0.56
7:BL:230:GLU:OE2	7:BL:232:GLN:NE2	2.37	0.56
4:Bd:71:LEU:O	4:Bd:133:ARG:NH1	2.38	0.56
1:JG:1003:ASN:HA	1:JG:1006:ILE:HD12	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:FL:210:ASP:OD1	7:FL:210:ASP:N	2.36	0.56
8:FM:273:ALA:HB1	8:FM:277:SER:HB2	1.86	0.56
1:AG:928:ILE:HD12	1:AG:1045:VAL:HG11	1.87	0.56
5:VH:238:MET:N	5:VH:238:MET:SD	2.78	0.56
5:VH:303:ARG:O	5:VH:313:VAL:HA	2.05	0.56
1:FG:972:PHE:O	1:FG:976:ASN:ND2	2.37	0.56
5:EH:170:ARG:HH21	5:EH:245:GLN:HB3	1.69	0.56
5:FH:347:VAL:HG23	5:FH:354:MET:HB3	1.86	0.56
1:KG:899:LEU:HD13	1:KG:919:MET:HG2	1.87	0.56
9:FN:89:GLY:O	9:FN:104:ASN:ND2	2.38	0.56
4:HD:136:ASP:O	4:Hd:60:LYS:NZ	2.38	0.56
4:ID:23:MET:N	4:ID:23:MET:SD	2.78	0.56
3:IF:243:MET:N	3:IF:243:MET:SD	2.78	0.56
2:CC:61:GLU:HA	2:CC:64:LEU:HD12	1.86	0.56
3:KF:220:ALA:O	3:KF:231:THR:HA	2.05	0.56
4:MD:118:LEU:O	2:HC:98:ASN:ND2	2.38	0.56
10:MU:127:UNK:O	7:AL:232:GLN:NE2	2.38	0.56
5:YH:226:LEU:HD13	5:YH:241:LEU:HD13	1.86	0.56
5:YH:315:THR:OG1	5:YH:316:ASN:N	2.38	0.56
2:MC:127:ARG:NH1	5:EH:273:PRO:O	2.39	0.56
5:DH:315:THR:OG1	5:DH:316:ASN:N	2.37	0.56
1:KG:950:HIS:HB2	1:KG:1027:THR:HG22	1.88	0.56
8:FM:240:GLN:HB3	8:FM:242:LYS:HE3	1.86	0.56
6:HK:47:GLY:O	6:HK:108:GLN:NE2	2.37	0.56
5:KH:227:ALA:HB2	5:KH:238:MET:HE3	1.87	0.56
1:YG:818:GLN:NE2	5:YH:203:ASN:OD1	2.36	0.56
5:ZH:147:THR:O	5:ZH:246:LYS:NZ	2.35	0.56
8:AM:276:ALA:H	8:AM:295:ASN:HB2	1.71	0.56
7:CL:131:LYS:NZ	7:CL:144:CYS:SG	2.75	0.56
7:CL:230:GLU:OE2	7:CL:232:GLN:NE2	2.38	0.56
4:DD:73:ILE:O	4:DD:133:ARG:NH2	2.38	0.56
7:DL:210:ASP:OD1	7:DL:210:ASP:N	2.39	0.56
1:HG:972:PHE:HB3	1:HG:1005:VAL:HG22	1.86	0.56
1:MG:910:ASP:OD1	1:MG:910:ASP:N	2.34	0.56
6:GK:109:PHE:O	6:GK:111:LYS:NZ	2.38	0.56
7:HL:230:GLU:OE2	7:HL:232:GLN:NE2	2.39	0.56
4:Jd:65:PRO:HA	4:Jd:68:ASP:HB2	1.88	0.56
5:AH:150:LYS:H	5:AH:247:ALA:HA	1.71	0.56
4:Ed:70:THR:OG1	4:Ed:71:LEU:N	2.38	0.56
1:KG:1003:ASN:HA	1:KG:1006:ILE:HD12	1.88	0.56
1:OG:1005:VAL:O	1:OG:1009:ALA:HB2	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:LC:111:LEU:HD23	2:LC:213:TYR:HB2	1.88	0.56
2:AC:90:ASP:HB3	2:AC:146:TRP:HE1	1.71	0.56
2:BC:229:ASP:N	2:BC:229:ASP:OD1	2.38	0.56
3:LF:265:SER:HB3	3:LF:268:ASP:HB3	1.87	0.56
5:LH:106:VAL:HA	5:LH:109:LYS:HE2	1.86	0.56
5:WH:168:VAL:HA	5:WH:240:THR:O	2.05	0.56
5:ZH:169:ILE:HB	5:ZH:241:LEU:HB3	1.86	0.56
4:AD:105:ARG:HB2	4:AD:153:VAL:HG12	1.88	0.56
4:Cd:36:ASP:N	4:Cd:36:ASP:OD1	2.35	0.56
5:DH:311:MET:HE3	5:DH:341:LYS:HA	1.87	0.56
7:EL:130:ASP:N	7:EL:130:ASP:OD1	2.37	0.56
4:KD:23:MET:N	4:KD:23:MET:SD	2.79	0.56
6:KK:50:ASP:OD1	6:KK:50:ASP:N	2.39	0.56
7:LL:169:THR:OG1	7:LL:170:ASP:N	2.39	0.56
7:LL:212:ASN:N	7:LL:212:ASN:OD1	2.38	0.56
7:ML:210:ASP:OD1	7:ML:210:ASP:N	2.37	0.56
4:BD:77:TYR:OH	6:BK:130:ARG:NH1	2.39	0.56
3:BF:213:GLN:O	5:BH:170:ARG:NH1	2.39	0.56
5:BH:354:MET:N	5:BH:354:MET:SD	2.79	0.56
5:CH:315:THR:OG1	5:CH:316:ASN:N	2.37	0.56
6:CK:90:ARG:NH1	6:CK:91:LEU:O	2.38	0.56
4:FD:124:LYS:O	8:FM:317:LYS:NZ	2.38	0.56
6:FK:92:ASN:OD1	6:FK:92:ASN:N	2.38	0.56
2:HC:231:ASP:N	2:HC:231:ASP:OD1	2.37	0.56
8:FM:316:ASN:OD1	8:FM:316:ASN:N	2.38	0.56
4:Dd:72:THR:OG1	4:Dd:73:ILE:N	2.39	0.56
6:JK:177:ASN:O	6:JK:179:ARG:NH1	2.39	0.56
8:JM:229:ASN:N	8:JM:229:ASN:OD1	2.39	0.56
9:LN:46:GLY:O	9:LN:61:ASN:ND2	2.39	0.56
5:MH:160:LEU:HD21	5:MH:257:GLN:HB3	1.87	0.56
5:WH:178:SER:HA	5:WH:213:LEU:O	2.06	0.56
5:YH:301:ASP:N	5:YH:301:ASP:OD1	2.38	0.56
8:BM:306:GLN:HB2	8:BM:309:LEU:HG	1.86	0.56
8:CM:166:ASN:HA	8:CM:186:SER:HB3	1.87	0.56
5:DH:328:MET:SD	2:LC:117:THR:OG1	2.63	0.56
6:FK:125:SER:OG	6:FK:126:VAL:N	2.37	0.56
1:MG:898:LYS:HD3	1:NG:866:GLY:HA3	1.88	0.56
5:GH:236:PRO:O	5:HH:251:ARG:NH1	2.38	0.56
5:GH:315:THR:OG1	5:GH:316:ASN:N	2.39	0.56
7:IL:108:ASP:OD2	7:IL:150:ASN:ND2	2.39	0.56
5:AH:229:ARG:NH2	5:BH:212:THR:OG1	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CC:243:ASP:N	2:CC:243:ASP:OD1	2.36	0.56
5:LH:158:VAL:HB	5:LH:256:VAL:HA	1.88	0.56
8:LM:186:SER:HA	8:LM:205:TYR:HB2	1.87	0.56
1:DG:886:LEU:HD21	1:EG:1040:LEU:HB2	1.87	0.56
4:Cd:148:TYR:HB2	4:Cd:153:VAL:HG12	1.88	0.56
4:FD:162:TYR:O	2:AC:244:ARG:NH2	2.39	0.56
3:AF:213:GLN:HG3	5:AH:170:ARG:HH12	1.71	0.55
9:JN:66:SER:OG	9:JN:67:THR:N	2.38	0.55
5:AH:171:LEU:HD11	5:AH:241:LEU:HB2	1.87	0.55
2:CC:109:VAL:HG13	2:CC:208:GLY:HA3	1.88	0.55
3:LF:269:SER:OG	3:YF:233:ARG:NH1	2.39	0.55
5:MH:157:PHE:HA	5:MH:255:ARG:HB3	1.88	0.55
4:CD:77:TYR:O	4:CD:78:ASN:ND2	2.39	0.55
5:YH:249:ASP:OD1	5:YH:249:ASP:N	2.38	0.55
2:DC:28:ASP:OD1	2:DC:28:ASP:N	2.38	0.55
8:DM:153:GLN:NE2	8:DM:172:ASN:OD1	2.38	0.55
4:Ed:36:ASP:N	4:Ed:36:ASP:OD1	2.37	0.55
1:LG:972:PHE:O	1:LG:976:ASN:ND2	2.38	0.55
1:PG:874:ASP:N	1:PG:874:ASP:OD1	2.39	0.55
7:GL:230:GLU:OE2	7:GL:232:GLN:NE2	2.39	0.55
8:GM:177:LEU:HD13	8:GM:181:PRO:HG2	1.88	0.55
1:Bg:810:GLN:OE1	1:Bg:814:GLN:NE2	2.40	0.55
4:Id:78:ASN:N	4:Id:78:ASN:OD1	2.38	0.55
8:JM:190:ASN:HD21	8:JM:192:ARG:HH21	1.52	0.55
7:KL:210:ASP:N	7:KL:210:ASP:OD1	2.37	0.55
8:KM:125:THR:HG23	8:KM:145:ARG:HB2	1.88	0.55
5:LH:339:MET:N	5:LH:339:MET:SD	2.79	0.55
8:MM:302:ARG:HH11	8:MM:309:LEU:HD11	1.71	0.55
5:WH:301:ASP:OD1	5:WH:301:ASP:N	2.39	0.55
3:Af:251:GLN:OE1	3:Af:253:ARG:NH1	2.39	0.55
1:Dg:797:ARG:NH2	5:EH:121:PRO:O	2.38	0.55
5:DH:221:TYR:HE2	5:EH:138:GLU:HG3	1.72	0.55
3:GF:253:ARG:HH22	3:GF:255:LEU:HD12	1.71	0.55
5:GH:147:THR:O	5:GH:246:LYS:NZ	2.39	0.55
3:HF:207:ARG:NH2	3:HF:208:ILE:O	2.40	0.55
5:HH:315:THR:OG1	5:HH:316:ASN:N	2.38	0.55
1:BG:1005:VAL:O	1:BG:1009:ALA:HB2	2.05	0.55
6:KK:177:ASN:O	6:KK:179:ARG:NH1	2.36	0.55
7:ML:169:THR:OG1	7:ML:170:ASP:N	2.40	0.55
1:FG:1005:VAL:O	1:FG:1009:ALA:HB2	2.07	0.55
7:BL:170:ASP:OD2	7:BL:227:ARG:NH2	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:ED:140:GLY:O	4:Ed:60:LYS:NZ	2.34	0.55
7:EL:221:HIS:ND1	7:EL:225:GLN:OE1	2.39	0.55
1:HG:946:SER:OG	1:HG:1030:GLU:O	2.22	0.55
1:LG:955:ARG:NH1	1:LG:1023:PHE:O	2.39	0.55
1:MG:950:HIS:HB2	1:MG:1027:THR:HG22	1.88	0.55
7:FL:102:LYS:HA	7:FL:105:ILE:HD12	1.88	0.55
1:AG:1033:SER:OG	1:BG:941:ARG:NH1	2.39	0.55
8:GM:149:ASN:OD1	8:GM:149:ASN:N	2.39	0.55
9:GN:99:GLY:HA3	9:GN:114:LEU:HB3	1.87	0.55
4:HD:60:LYS:O	4:HD:60:LYS:NZ	2.39	0.55
4:HD:86:ASP:OD1	2:CC:88:ARG:NH1	2.36	0.55
5:HH:117:ARG:NH1	5:HH:120:TYR:O	2.40	0.55
4:ID:52:MET:HE2	4:Id:52:MET:HG2	1.88	0.55
5:WH:324:TRP:HA	5:WH:339:MET:HB3	1.89	0.55
2:IC:155:ASP:OD1	2:IC:155:ASP:N	2.38	0.55
2:KC:64:LEU:HB2	2:KC:179:TYR:HB3	1.89	0.55
6:DK:71:GLY:O	4:ED:27:LYS:NZ	2.38	0.55
7:DL:178:LYS:O	7:DL:182:SER:OG	2.22	0.55
8:EM:120:GLY:H	8:EM:140:ASN:HB2	1.71	0.55
1:HG:886:LEU:HA	1:HG:899:LEU:O	2.06	0.55
6:JK:51:ALA:O	9:JN:44:LYS:NZ	2.39	0.55
7:LL:230:GLU:OE2	7:LL:232:GLN:NE2	2.40	0.55
8:MM:288:ARG:NH2	8:MM:316:ASN:O	2.40	0.55
5:VH:330:SER:HA	5:CH:267:PRO:HB3	1.88	0.55
2:MC:199:ASN:OD1	2:MC:202:ARG:NH1	2.39	0.55
8:DM:127:ASN:HB3	8:DM:147:ALA:HB3	1.88	0.55
5:EH:185:THR:HB	5:EH:265:SER:HB3	1.89	0.55
5:EH:230:LEU:HB2	5:EH:233:LEU:HB2	1.89	0.55
7:EL:212:ASN:N	7:EL:212:ASN:OD1	2.37	0.55
1:JG:891:THR:OG1	1:JG:892:GLY:N	2.38	0.55
1:MG:886:LEU:HA	1:MG:899:LEU:O	2.06	0.55
1:MG:899:LEU:HA	1:MG:918:THR:O	2.05	0.55
8:FM:257:ASP:OD1	8:FM:257:ASP:N	2.40	0.55
2:LC:177:TRP:O	2:LC:181:THR:OG1	2.24	0.55
7:GL:178:LYS:O	7:GL:182:SER:OG	2.24	0.55
4:Gd:82:ARG:NH1	4:Gd:125:ASP:OD1	2.36	0.55
1:BG:877:VAL:H	1:BG:1031:VAL:HG22	1.72	0.55
4:ID:118:LEU:O	2:DC:98:ASN:ND2	2.40	0.55
8:JM:284:LEU:HB3	8:JM:310:LYS:HE3	1.87	0.55
3:MF:231:THR:HG23	5:ZH:150:LYS:HZ2	1.71	0.55
7:ML:150:ASN:OD1	7:ML:153:ARG:NH2	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Ad:148:TYR:HB2	4:Ad:153:VAL:HG12	1.89	0.55
3:CF:246:LEU:HB2	3:CF:255:LEU:HD12	1.89	0.55
2:MC:106:ILE:HD11	2:MC:139:ALA:HB1	1.89	0.55
7:CL:177:HIS:HD1	8:CM:315:TYR:HH	1.53	0.55
5:DH:256:VAL:HG13	5:DH:258:GLY:H	1.71	0.55
7:EL:219:ILE:O	7:EL:223:SER:HB2	2.06	0.55
5:FH:262:ASN:OD1	5:FH:262:ASN:N	2.40	0.55
1:KG:874:ASP:N	1:KG:874:ASP:OD1	2.40	0.55
4:Fd:82:ARG:NH2	4:Fd:83:ALA:O	2.34	0.55
1:AG:865:THR:HB	1:PG:898:LYS:HE3	1.88	0.55
2:BC:96:ASN:OD1	2:BC:96:ASN:N	2.33	0.55
6:GK:114:ILE:HG23	6:GK:184:PHE:HB3	1.89	0.55
8:HM:119:GLU:HG3	8:HM:139:ALA:HB3	1.88	0.55
8:LM:257:ASP:N	8:LM:257:ASP:OD1	2.38	0.55
5:VH:279:LEU:HD11	5:VH:289:PRO:HB3	1.89	0.55
6:BK:150:ASP:O	6:BK:152:ARG:NH1	2.39	0.55
2:GC:150:TYR:O	2:GC:198:ASN:ND2	2.40	0.55
2:IC:48:LYS:O	1:KG:938:ASN:ND2	2.39	0.55
2:KC:110:LEU:HD23	2:KC:212:TYR:HB2	1.89	0.55
8:EM:308:ASP:OD1	8:EM:308:ASP:N	2.37	0.55
1:HG:912:MET:HB3	1:HG:944:LEU:HB2	1.88	0.55
1:PG:931:SER:H	1:PG:1043:GLN:HE22	1.55	0.55
7:FL:221:HIS:O	7:FL:225:GLN:NE2	2.40	0.55
1:Gg:818:GLN:HE21	5:GH:205:GLN:HG3	1.72	0.55
4:JD:86:ASP:OD2	6:JK:152:ARG:NH2	2.40	0.55
8:JM:131:THR:HG22	8:JM:150:ILE:HG22	1.87	0.55
5:ZH:262:ASN:OD1	5:ZH:262:ASN:N	2.40	0.55
3:CF:230:LEU:HA	5:CH:165:THR:HG21	1.87	0.55
6:DK:151:SER:OG	6:DK:152:ARG:N	2.40	0.55
1:IG:871:ALA:HB2	1:IG:889:ILE:HD13	1.88	0.55
1:IG:937:PRO:HD3	1:IG:1037:LEU:HA	1.88	0.55
2:LC:113:GLU:OE2	2:LC:131:ARG:NH1	2.40	0.55
5:JH:205:GLN:HB2	5:JH:214:MET:HE2	1.89	0.55
5:YH:297:VAL:HG11	5:YH:302:ALA:HB3	1.87	0.55
1:FG:867:ASP:OD1	1:FG:867:ASP:N	2.40	0.55
2:FC:153:ASP:OD1	2:FC:153:ASP:N	2.40	0.55
4:DD:150:ASN:OD1	4:DD:150:ASN:N	2.39	0.55
6:DK:177:ASN:OD1	6:DK:177:ASN:N	2.39	0.55
4:ED:124:LYS:O	8:EM:317:LYS:NZ	2.39	0.55
3:AF:241:TYR:HB3	3:AF:256:THR:HG21	1.89	0.55
4:GD:158:TYR:O	4:Gd:137:TYR:OH	2.24	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:GL:113:ASP:OD1	7:GL:113:ASP:N	2.37	0.55
4:HD:149:PRO:O	4:HD:152:GLN:NE2	2.40	0.55
9:HN:76:MET:HE2	9:HN:78:LEU:HD21	1.89	0.55
1:CG:1003:ASN:HA	1:CG:1006:ILE:HD12	1.89	0.55
4:Jd:36:ASP:OD1	4:Jd:36:ASP:N	2.38	0.55
5:KH:228:VAL:HG13	5:KH:237:VAL:HB	1.88	0.55
1:DG:874:ASP:OD1	1:DG:874:ASP:N	2.39	0.55
6:AK:87:GLN:NE2	6:AK:173:ASP:OD1	2.40	0.55
6:AK:115:THR:HG22	6:AK:155:PHE:HB2	1.88	0.55
1:FG:955:ARG:NH1	1:FG:1023:PHE:O	2.38	0.55
7:BL:192:PHE:O	7:BL:196:ASN:ND2	2.38	0.55
1:GG:1003:ASN:HA	1:GG:1006:ILE:HD12	1.88	0.55
8:DM:149:ASN:OD1	8:DM:149:ASN:N	2.40	0.55
9:DN:62:ASN:OD1	9:DN:62:ASN:N	2.32	0.55
5:EH:270:GLU:OE2	2:LC:249:ARG:NH2	2.40	0.55
4:FD:84:SER:HB2	4:FD:124:LYS:HD3	1.88	0.55
7:HL:139:ARG:HD2	8:HM:319:PHE:H	1.72	0.54
8:HM:313:ASP:HB2	8:HM:316:ASN:HD21	1.70	0.54
7:JL:169:THR:OG1	7:JL:170:ASP:N	2.39	0.54
5:AH:159:ASN:ND2	5:AH:257:GLN:OE1	2.38	0.54
5:AH:326:ALA:HB3	5:AH:338:GLU:HB3	1.89	0.54
8:LM:199:LYS:HA	8:LM:219:ALA:O	2.08	0.54
9:LN:66:SER:OG	9:LN:67:THR:N	2.39	0.54
7:AL:145:TYR:HA	7:AL:148:LEU:HD12	1.89	0.54
11:ZX:19:UNK:O	11:AX:1:UNK:N	2.40	0.54
6:BK:177:ASN:O	6:BK:179:ARG:NH1	2.37	0.54
2:IC:102:LEU:HG	2:IC:108:PRO:HG3	1.89	0.54
2:JC:145:THR:O	2:JC:148:GLN:NE2	2.40	0.54
8:EM:214:ILE:O	8:EM:215:ARG:NH1	2.39	0.54
1:MG:867:ASP:OD1	1:MG:867:ASP:N	2.40	0.54
7:FL:212:ASN:OD1	7:FL:212:ASN:N	2.39	0.54
4:GD:27:LYS:HB2	9:FN:63:GLY:HA3	1.88	0.54
3:JF:233:ARG:NH1	3:KF:269:SER:OG	2.40	0.54
1:CG:999:SER:OG	1:CG:1000:THR:N	2.41	0.54
2:CC:188:ILE:O	2:CC:192:ASN:ND2	2.39	0.54
1:Kg:800:ASP:N	1:Kg:800:ASP:OD1	2.39	0.54
5:LH:207:ASP:OD1	5:LH:207:ASP:N	2.38	0.54
7:LL:44:HIS:HB2	7:LL:48:ASN:HA	1.88	0.54
4:Ld:105:ARG:HB3	4:Ld:153:VAL:HG23	1.89	0.54
6:AK:66:LYS:HB3	6:AK:77:SER:HB2	1.89	0.54
6:MK:73:ASN:HD21	6:MK:185:ARG:HH21	1.55	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:XF:233:ARG:NE	3:XF:235:GLY:O	2.40	0.54
3:XF:241:TYR:HB3	3:XF:256:THR:HG21	1.89	0.54
2:MC:128:ILE:HG13	2:LC:246:ARG:HB2	1.89	0.54
5:FH:176:VAL:HG22	5:FH:216:GLN:HB3	1.88	0.54
5:FH:188:PRO:HG2	5:FH:262:ASN:HD22	1.72	0.54
1:HG:931:SER:O	1:HG:1042:THR:OG1	2.25	0.54
1:LG:1003:ASN:HA	1:LG:1006:ILE:HD12	1.89	0.54
1:NG:910:ASP:OD1	1:NG:910:ASP:N	2.40	0.54
7:FL:192:PHE:O	7:FL:196:ASN:ND2	2.34	0.54
5:GH:316:ASN:N	5:GH:316:ASN:OD1	2.40	0.54
8:GM:316:ASN:N	8:GM:316:ASN:OD1	2.40	0.54
1:BG:891:THR:OG1	1:BG:892:GLY:N	2.40	0.54
5:LH:273:PRO:O	2:GC:126:ARG:NH1	2.41	0.54
4:MD:73:ILE:O	4:MD:133:ARG:NH2	2.40	0.54
6:MK:109:PHE:O	6:MK:111:LYS:NZ	2.40	0.54
7:ML:230:GLU:OE2	7:ML:232:GLN:NE2	2.39	0.54
4:Ad:55:MET:HG3	4:AD:55:MET:HE1	1.88	0.54
5:CH:316:ASN:N	5:CH:316:ASN:OD1	2.37	0.54
1:KG:1011:VAL:HG12	1:LG:963:SER:HB2	1.89	0.54
2:EC:65:SER:O	2:EC:69:GLN:NE2	2.41	0.54
7:HL:173:GLY:O	7:HL:178:LYS:NZ	2.40	0.54
4:Dd:62:ILE:O	4:DD:67:LYS:NZ	2.39	0.54
1:Jg:800:ASP:OD1	1:Jg:800:ASP:N	2.40	0.54
6:JK:71:GLY:O	4:KD:27:LYS:NZ	2.40	0.54
5:XH:180:VAL:HG23	5:XH:212:THR:HG22	1.90	0.54
2:JC:175:TRP:O	2:JC:179:THR:OG1	2.24	0.54
1:GG:899:LEU:HD13	1:GG:919:MET:HG2	1.87	0.54
1:PG:1005:VAL:O	1:PG:1009:ALA:HB2	2.08	0.54
2:LC:231:ASP:OD1	2:LC:231:ASP:N	2.39	0.54
7:GL:169:THR:OG1	7:GL:170:ASP:N	2.40	0.54
7:GL:226:ASN:O	7:GL:228:ARG:NH1	2.39	0.54
5:JH:190:PRO:HA	5:JH:211:ASN:HB3	1.88	0.54
2:CC:166:LEU:O	2:CC:168:LYS:NZ	2.40	0.54
3:LF:248:ASP:OD2	3:LF:253:ARG:NH2	2.41	0.54
7:LL:63:ASP:O	7:LL:88:GLY:N	2.41	0.54
6:AK:78:ILE:HB	6:AK:180:VAL:HG13	1.89	0.54
1:XG:792:GLN:OE1	1:XG:795:GLN:NE2	2.40	0.54
7:AL:134:MET:HB2	7:AL:139:ARG:HB2	1.89	0.54
2:FC:242:ASP:OD1	2:FC:242:ASP:N	2.40	0.54
2:MC:35:LEU:HA	2:MC:38:MET:HG2	1.89	0.54
8:CM:127:ASN:OD1	8:CM:127:ASN:N	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:IG:1011:VAL:HG12	1:JG:963:SER:HB2	1.89	0.54
9:GN:89:GLY:O	9:GN:104:ASN:ND2	2.40	0.54
4:Gd:110:GLY:HA3	4:Gd:158:TYR:HB2	1.88	0.54
5:HH:208:LYS:HE2	1:XG:823:GLY:HA2	1.89	0.54
5:IH:137:SER:OG	5:IH:141:LYS:NZ	2.40	0.54
6:KK:111:LYS:HD3	6:KK:114:ILE:HD11	1.89	0.54
7:KL:113:ASP:OD1	7:KL:113:ASP:N	2.31	0.54
7:AL:150:ASN:OD1	7:AL:153:ARG:NH2	2.39	0.54
2:LC:231:ASP:OD2	2:LC:246:ARG:NH2	2.41	0.54
2:AC:156:LYS:NZ	2:AC:157:PRO:O	2.41	0.54
6:GK:65:ILE:HD12	6:GK:78:ILE:HG12	1.89	0.54
7:GL:165:VAL:HG12	7:GL:231:ILE:HG12	1.89	0.54
8:GM:127:ASN:HB3	8:GM:147:ALA:HB3	1.87	0.54
1:BG:931:SER:O	1:BG:1042:THR:OG1	2.26	0.54
4:MD:36:ASP:OD2	2:HC:193:ASN:ND2	2.40	0.54
4:CD:98:ILE:HG21	4:CD:132:LEU:HD11	1.90	0.54
9:AN:46:GLY:HA3	9:AN:61:ASN:HB2	1.89	0.54
9:AN:62:ASN:OD1	9:AN:62:ASN:N	2.36	0.54
5:CH:278:ASP:N	5:CH:278:ASP:OD1	2.40	0.54
4:DD:36:ASP:OD1	2:LC:76:ARG:NH2	2.41	0.54
9:EN:49:ASN:HB3	9:EN:59:VAL:HG23	1.89	0.54
1:JG:1011:VAL:HG12	1:KG:963:SER:HB2	1.89	0.54
1:NG:903:PHE:HA	1:NG:915:THR:H	1.73	0.54
4:Gd:150:ASN:N	4:Gd:150:ASN:OD1	2.40	0.54
6:HK:110:ARG:NH1	9:HN:75:VAL:O	2.35	0.54
8:HM:276:ALA:H	8:HM:295:ASN:HB2	1.72	0.54
3:IF:210:TYR:HB3	3:IF:222:LEU:HB3	1.89	0.54
1:CG:946:SER:OG	1:CG:1030:GLU:O	2.25	0.54
3:KF:247:ILE:HG12	3:KF:254:ILE:HG23	1.90	0.54
8:KM:127:ASN:HB3	8:KM:147:ALA:HB3	1.90	0.54
6:AK:188:VAL:O	9:AN:57:ARG:NH1	2.39	0.54
4:MD:140:GLY:O	4:Md:60:LYS:NZ	2.41	0.54
6:MK:47:GLY:O	6:MK:108:GLN:NE2	2.41	0.54
1:EG:950:HIS:HB2	1:EG:1027:THR:HG22	1.89	0.54
1:XG:818:GLN:NE2	5:XH:203:ASN:OD1	2.37	0.54
5:XH:183:ASP:OD1	5:XH:187:ALA:N	2.41	0.54
5:XH:278:ASP:OD1	5:XH:278:ASP:N	2.41	0.54
1:NG:900:ILE:HG13	1:NG:918:THR:HB	1.89	0.54
2:AC:153:ASP:OD1	2:AC:153:ASP:N	2.39	0.54
5:GH:106:VAL:HA	5:GH:109:LYS:HE2	1.90	0.54
4:Gd:29:PRO:O	4:Gd:32:ASN:ND2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:HD:132:LEU:HA	4:HD:135:ILE:HD12	1.90	0.54
1:Hg:801:MET:HB3	5:XH:121:PRO:HB2	1.90	0.54
5:HH:278:ASP:N	5:HH:278:ASP:OD1	2.37	0.54
5:IH:294:ARG:NH1	2:DC:198:GLU:OE2	2.41	0.54
5:AH:189:TRP:HE1	5:AH:230:LEU:HD13	1.72	0.54
8:KM:290:ASP:OD1	8:KM:290:ASP:N	2.37	0.54
1:DG:1044:ASP:OD1	1:DG:1044:ASP:N	2.41	0.54
3:WF:269:SER:OG	3:FF:233:ARG:NH1	2.39	0.54
3:XF:222:LEU:HD21	3:XF:254:ILE:HD12	1.90	0.54
3:YF:241:TYR:HB3	3:YF:256:THR:HG21	1.90	0.54
7:AL:108:ASP:OD2	7:AL:150:ASN:ND2	2.40	0.54
1:Fg:820:TYR:HB2	5:FH:205:GLN:HG2	1.90	0.54
1:KG:871:ALA:HB2	1:KG:889:ILE:HD13	1.90	0.54
2:AC:108:VAL:HG23	2:AC:207:GLY:HA3	1.88	0.54
7:GL:53:ASP:OD1	7:GL:53:ASP:N	2.40	0.54
7:GL:136:SER:OG	8:GM:314:ARG:NH2	2.39	0.54
3:JF:210:TYR:HA	3:JF:224:GLY:HA2	1.90	0.54
7:KL:121:ASP:N	7:KL:121:ASP:OD1	2.40	0.54
3:Lf:221:TRP:HE1	3:Lf:229:THR:HB	1.71	0.54
6:AK:73:ASN:ND2	7:BL:214:ILE:O	2.40	0.54
8:MM:300:ASP:OD1	8:MM:302:ARG:NE	2.39	0.54
8:BM:131:THR:OG1	8:BM:132:SER:N	2.41	0.54
8:BM:275:ASP:HB3	8:BM:294:PHE:HB2	1.89	0.54
2:JC:68:GLN:HB3	2:JC:157:PRO:HG2	1.88	0.54
5:FH:311:MET:HG3	5:FH:341:LYS:HA	1.89	0.54
5:GH:131:LYS:NZ	5:WH:141:LYS:O	2.41	0.53
7:GL:192:PHE:O	7:GL:196:ASN:ND2	2.40	0.53
5:JH:313:VAL:HG12	5:JH:337:TYR:HB2	1.89	0.53
7:JL:193:LEU:HB3	7:JL:198:ILE:HD11	1.90	0.53
3:KF:251:GLN:HB2	3:KF:253:ARG:HE	1.72	0.53
4:Kd:60:LYS:NZ	4:Kd:61:VAL:O	2.41	0.53
4:Ld:84:SER:H	2:HC:268:ALA:HB3	1.73	0.53
6:MK:78:ILE:HB	6:MK:180:VAL:HG23	1.89	0.53
3:YF:219:ARG:NH2	3:YF:231:THR:OG1	2.41	0.53
3:CF:226:ASN:ND2	3:CF:228:SER:OG	2.41	0.53
2:GC:169:THR:OG1	2:GC:170:LYS:N	2.38	0.53
6:DK:66:LYS:HB3	6:DK:77:SER:HB3	1.89	0.53
1:JG:950:HIS:HB2	1:JG:1027:THR:HG22	1.90	0.53
1:PG:872:VAL:HA	1:PG:1036:GLY:HA2	1.89	0.53
2:HC:130:ASP:N	2:HC:130:ASP:OD1	2.35	0.53
1:AG:972:PHE:O	1:AG:976:ASN:ND2	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:GD:23:MET:SD	4:GD:23:MET:N	2.81	0.53
3:GF:235:GLY:HA2	3:GF:243:MET:HE1	1.89	0.53
6:HK:49:CYS:O	6:HK:52:THR:OG1	2.26	0.53
7:JL:108:ASP:OD2	7:JL:150:ASN:ND2	2.41	0.53
7:JL:216:ASP:OD1	7:JL:216:ASP:N	2.40	0.53
1:DG:876:SER:HB2	1:DG:1033:SER:HB3	1.89	0.53
5:MH:278:ASP:OD1	5:MH:278:ASP:N	2.40	0.53
1:HG:958:SER:O	1:HG:962:SER:OG	2.26	0.53
9:FN:66:SER:OG	9:FN:67:THR:N	2.36	0.53
3:JF:219:ARG:NH2	3:JF:231:THR:OG1	2.40	0.53
7:JL:44:HIS:N	7:JL:48:ASN:OD1	2.40	0.53
7:JL:212:ASN:N	7:JL:212:ASN:OD1	2.41	0.53
7:KL:136:SER:OG	8:KM:314:ARG:NH1	2.42	0.53
5:MH:180:VAL:HG23	5:MH:212:THR:HG22	1.90	0.53
1:EG:899:LEU:HD13	1:EG:919:MET:HG2	1.91	0.53
5:XH:158:VAL:HB	5:XH:256:VAL:HA	1.90	0.53
8:BM:124:VAL:O	8:BM:144:THR:HA	2.09	0.53
8:CM:267:ASN:O	8:CM:287:THR:OG1	2.24	0.53
1:KG:891:THR:OG1	1:KG:892:GLY:N	2.41	0.53
1:MG:891:THR:OG1	1:MG:892:GLY:N	2.41	0.53
1:NG:972:PHE:O	1:NG:976:ASN:ND2	2.39	0.53
1:NG:1005:VAL:O	1:NG:1009:ALA:HB2	2.09	0.53
2:EC:75:ARG:HB2	2:EC:188:ILE:HG12	1.89	0.53
4:HD:86:ASP:OD2	6:HK:152:ARG:NH2	2.40	0.53
4:HD:130:GLU:OE1	4:HD:133:ARG:NH1	2.41	0.53
9:HN:66:SER:OG	9:HN:67:THR:N	2.39	0.53
1:CG:972:PHE:HB3	1:CG:1005:VAL:HG22	1.89	0.53
1:Kg:810:GLN:HA	1:Kg:813:LYS:HB2	1.89	0.53
4:Kd:78:ASN:ND2	4:Kd:102:ALA:O	2.42	0.53
5:MH:183:ASP:HA	5:MH:256:VAL:HG22	1.89	0.53
4:CD:149:PRO:O	4:CD:152:GLN:NE2	2.42	0.53
4:BD:86:ASP:OD1	2:JC:87:ARG:NH1	2.41	0.53
4:Bd:76:ALA:HB3	4:Bd:79:LEU:HD13	1.91	0.53
1:HG:1003:ASN:HA	1:HG:1006:ILE:HD12	1.90	0.53
1:PG:891:THR:OG1	1:PG:892:GLY:N	2.42	0.53
1:AG:920:SER:HA	1:AG:927:THR:HA	1.91	0.53
2:EC:88:ARG:NH1	4:JD:86:ASP:OD1	2.41	0.53
2:EC:167:PRO:HB2	2:EC:173:LYS:HD3	1.91	0.53
3:AF:266:GLN:OE1	3:ZF:233:ARG:NH2	2.40	0.53
5:GH:229:ARG:NH2	5:HH:211:ASN:OD1	2.42	0.53
3:HF:219:ARG:NH1	3:XF:269:SER:O	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Hd:105:ARG:HB3	4:Hd:153:VAL:HG23	1.89	0.53
7:KL:173:GLY:O	7:KL:178:LYS:NZ	2.41	0.53
1:Ag:800:ASP:OD1	1:Ag:800:ASP:N	2.41	0.53
8:MM:124:VAL:HB	8:MM:144:THR:HG23	1.89	0.53
1:EG:886:LEU:HD21	1:FG:1040:LEU:HB2	1.90	0.53
5:XH:198:ASP:OD2	5:XH:219:LYS:NZ	2.42	0.53
7:BL:44:HIS:HB2	7:BL:48:ASN:HA	1.89	0.53
8:BM:214:ILE:O	8:BM:215:ARG:NH1	2.41	0.53
5:CH:181:PHE:HB2	5:CH:211:ASN:HB2	1.91	0.53
5:GH:114:ASP:OD1	5:GH:117:ARG:NH1	2.42	0.53
8:GM:197:TYR:HA	8:GM:217:LYS:HB3	1.90	0.53
5:HH:183:ASP:HB2	5:HH:259:TYR:HA	1.91	0.53
7:IL:109:LEU:HD12	7:IL:114:ILE:HB	1.90	0.53
4:Jd:110:GLY:HA3	4:Jd:158:TYR:HB2	1.90	0.53
5:MH:229:ARG:NH2	5:ZH:207:ASP:OD2	2.40	0.53
3:YF:210:TYR:HA	3:YF:224:GLY:HA2	1.90	0.53
8:BM:162:VAL:HG12	8:BM:182:LYS:HB2	1.90	0.53
2:IC:244:ASP:O	2:JC:127:SER:HA	2.08	0.53
7:DL:169:THR:OG1	7:DL:170:ASP:N	2.41	0.53
6:EK:121:SER:OG	6:EK:122:LYS:N	2.42	0.53
7:EL:124:THR:HA	7:EL:231:ILE:O	2.09	0.53
4:FD:86:ASP:OD1	2:AC:87:ARG:NH1	2.41	0.53
1:IG:884:PRO:HA	1:IG:901:GLY:O	2.09	0.53
1:IG:1005:VAL:O	1:IG:1009:ALA:HB2	2.08	0.53
7:FL:53:ASP:N	7:FL:53:ASP:OD1	2.41	0.53
8:FM:190:ASN:O	8:FM:192:ARG:NH2	2.41	0.53
4:Fd:76:ALA:O	4:Fd:80:GLN:NE2	2.41	0.53
3:Ff:219:ARG:HE	3:Ff:233:ARG:HH12	1.56	0.53
2:EC:197:GLU:OE2	5:JH:294:ARG:NH1	2.41	0.53
4:Gd:71:LEU:O	4:Gd:133:ARG:NH1	2.37	0.53
6:JK:151:SER:OG	6:JK:152:ARG:N	2.42	0.53
1:YG:806:THR:O	1:YG:810:GLN:NE2	2.40	0.53
5:BH:194:TYR:HB3	5:BH:228:VAL:HG23	1.90	0.53
9:CN:63:GLY:HA3	4:DD:27:LYS:HB2	1.90	0.53
3:DF:207:ARG:NH1	3:DF:208:ILE:O	2.39	0.53
4:ED:31:ASN:HD22	4:Ed:35:ASP:HA	1.74	0.53
9:EN:63:GLY:HA3	4:FD:27:LYS:HB2	1.89	0.53
1:IG:1003:ASN:HA	1:IG:1006:ILE:HD12	1.90	0.53
1:MG:877:VAL:H	1:MG:1031:VAL:HG22	1.74	0.53
2:AC:217:MET:HB3	2:AC:219:MET:HG2	1.91	0.53
5:GH:238:MET:SD	5:HH:178:SER:OG	2.67	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:GH:313:VAL:HG13	5:GH:337:TYR:HB2	1.91	0.53
7:GL:150:ASN:OD1	7:GL:153:ARG:NH2	2.38	0.53
8:GM:119:GLU:HG3	8:GM:139:ALA:HB3	1.90	0.53
8:GM:209:SER:OG	8:GM:210:ASP:N	2.41	0.53
7:HL:221:HIS:ND1	7:HL:225:GLN:OE1	2.42	0.53
6:KK:65:ILE:HD12	6:KK:78:ILE:HG12	1.90	0.53
5:VH:207:ASP:N	5:VH:207:ASP:OD1	2.40	0.53
2:IC:226:TYR:HB3	2:IC:252:ALA:HB3	1.91	0.53
2:JC:98:LEU:O	2:JC:212:ARG:NH2	2.41	0.53
5:DH:289:PRO:O	5:DH:292:SER:OG	2.27	0.53
9:DN:66:SER:OG	9:DN:67:THR:N	2.37	0.53
1:JG:874:ASP:OD1	1:JG:874:ASP:N	2.42	0.53
2:HC:110:VAL:HB	2:HC:136:ALA:HB3	1.91	0.53
7:FL:200:ALA:O	8:FM:230:ARG:NH2	2.41	0.53
1:Hg:798:THR:HA	1:Hg:801:MET:HE2	1.91	0.53
5:JH:332:ASP:OD1	5:JH:332:ASP:N	2.42	0.53
3:KF:208:ILE:HG13	3:KF:225:SER:H	1.73	0.53
4:CD:29:PRO:HG2	7:CL:225:GLN:HA	1.91	0.53
7:BL:150:ASN:OD1	7:BL:153:ARG:NH2	2.41	0.53
2:JC:218:ASN:ND2	2:JC:260:GLU:O	2.41	0.53
2:MC:173:GLU:HA	2:MC:176:ILE:HG12	1.91	0.53
7:CL:212:ASN:OD1	7:CL:212:ASN:N	2.42	0.53
6:FK:148:GLY:H	4:Fd:30:ILE:HD13	1.74	0.53
1:MG:946:SER:OG	1:MG:1030:GLU:O	2.27	0.53
1:MG:959:LEU:O	1:MG:963:SER:OG	2.26	0.53
1:Bg:820:TYR:OH	1:Bg:822:GLU:OE1	2.27	0.53
7:IL:169:THR:OG1	7:IL:170:ASP:N	2.42	0.53
5:JH:289:PRO:O	5:JH:292:SER:OG	2.25	0.53
4:KD:86:ASP:OD1	2:FC:87:ARG:NH1	2.42	0.53
4:LD:86:ASP:OD1	2:GC:88:ARG:NH1	2.42	0.53
5:MH:171:LEU:HD11	5:MH:241:LEU:HB2	1.90	0.53
5:VH:180:VAL:HG21	5:CH:235:THR:HG22	1.91	0.53
5:YH:170:ARG:HH21	5:YH:245:GLN:HB3	1.74	0.53
8:AM:120:GLY:H	8:AM:140:ASN:HB2	1.74	0.53
3:BF:214:ALA:HB3	3:BF:221:TRP:HB2	1.91	0.53
9:BN:89:GLY:HA3	9:BN:104:ASN:HB2	1.91	0.53
4:AD:60:LYS:NZ	4:AD:60:LYS:O	2.40	0.53
2:FC:118:LEU:HA	2:FC:124:ILE:HG22	1.90	0.53
4:DD:24:LYS:O	7:DL:110:GLN:NE2	2.41	0.53
9:FN:89:GLY:HA3	9:FN:104:ASN:HB2	1.90	0.53
2:LC:152:LEU:HD21	2:LC:203:ILE:HG21	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:GM:210:ASP:N	8:GM:210:ASP:OD1	2.41	0.52
4:Hd:68:ASP:N	4:Hd:68:ASP:OD1	2.41	0.52
1:Ig:797:ARG:NH2	5:JH:121:PRO:O	2.43	0.52
7:IL:130:ASP:OD1	7:IL:130:ASP:N	2.41	0.52
4:Id:72:THR:OG1	4:Id:73:ILE:N	2.42	0.52
3:JF:254:ILE:O	3:JF:261:VAL:HA	2.09	0.52
1:CG:965:LEU:HG	1:CG:1008:LEU:HD22	1.91	0.52
8:KM:165:ILE:HB	8:KM:185:ILE:HG23	1.90	0.52
8:MM:210:ASP:OD1	8:MM:210:ASP:N	2.39	0.52
4:BD:85:VAL:HG23	6:BK:153:ILE:HG13	1.91	0.52
2:IC:246:ARG:HB2	2:JC:126:ILE:HG23	1.92	0.52
7:CL:113:ASP:OD1	7:CL:113:ASP:N	2.32	0.52
7:CL:171:ASN:OD1	7:CL:171:ASN:N	2.41	0.52
1:GG:891:THR:OG1	1:GG:892:GLY:N	2.42	0.52
7:DL:121:ASP:OD1	7:DL:121:ASP:N	2.41	0.52
6:FK:46:ASP:OD1	6:FK:46:ASP:N	2.43	0.52
1:LG:1005:VAL:O	1:LG:1009:ALA:HB2	2.09	0.52
4:HD:55:MET:HE2	2:CC:210:ILE:HD11	1.91	0.52
5:HH:275:SER:HA	2:CC:126:ARG:HD3	1.91	0.52
1:BG:911:LYS:HA	1:BG:943:ALA:HA	1.91	0.52
6:IK:151:SER:OG	6:IK:152:ARG:N	2.41	0.52
4:Ld:110:GLY:HA3	4:Ld:158:TYR:HB2	1.92	0.52
4:Md:36:ASP:N	4:Md:36:ASP:OD1	2.35	0.52
5:VH:179:LEU:O	5:VH:212:THR:HA	2.09	0.52
7:AL:44:HIS:ND1	7:AL:49:ASN:OD1	2.42	0.52
5:ZH:192:ALA:HB2	5:ZH:231:ARG:HA	1.91	0.52
6:CK:107:LYS:NZ	6:CK:148:GLY:O	2.39	0.52
8:CM:211:THR:HA	8:CM:230:ARG:O	2.10	0.52
3:Cf:243:MET:O	3:Cf:245:LYS:NZ	2.42	0.52
7:DL:108:ASP:OD2	7:DL:150:ASN:ND2	2.42	0.52
8:DM:292:MET:N	8:DM:292:MET:SD	2.82	0.52
1:NG:899:LEU:HD13	1:NG:919:MET:HG2	1.91	0.52
1:OG:1003:ASN:HA	1:OG:1006:ILE:HD12	1.90	0.52
1:PG:876:SER:HB2	1:PG:1033:SER:HB3	1.92	0.52
1:AG:1005:VAL:O	1:AG:1009:ALA:HB2	2.09	0.52
5:HH:184:SER:HB2	5:HH:259:TYR:HB3	1.91	0.52
4:JD:158:TYR:O	4:Jd:137:TYR:OH	2.26	0.52
6:JK:121:SER:OG	6:JK:122:LYS:N	2.41	0.52
7:KL:44:HIS:ND1	7:KL:49:ASN:OD1	2.37	0.52
5:LH:280:LEU:HD23	5:LH:328:MET:HB2	1.90	0.52
4:MD:155:GLU:OE2	4:MD:157:ARG:NH2	2.41	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Mg:818:GLN:NE2	5:MH:203:ASN:OD1	2.39	0.52
8:MM:149:ASN:OD1	8:MM:149:ASN:N	2.43	0.52
3:XF:246:LEU:HB2	3:XF:255:LEU:HB2	1.91	0.52
5:XH:198:ASP:OD2	5:XH:201:SER:OG	2.28	0.52
6:CK:114:ILE:HD13	6:CK:184:PHE:HB3	1.91	0.52
6:CK:177:ASN:O	6:CK:179:ARG:NH1	2.43	0.52
9:CN:66:SER:OG	9:CN:67:THR:N	2.41	0.52
4:Cd:35:ASP:OD2	4:Cd:38:THR:N	2.43	0.52
1:GG:871:ALA:HB2	1:GG:889:ILE:HD13	1.92	0.52
1:Eg:818:GLN:NE2	5:EH:203:ASN:OD1	2.42	0.52
1:LG:931:SER:O	1:LG:1042:THR:OG1	2.26	0.52
1:NG:881:GLU:HG3	1:OG:911:LYS:HZ3	1.74	0.52
5:GH:234:ASN:OD1	5:HH:211:ASN:ND2	2.41	0.52
6:HK:115:THR:HG22	6:HK:155:PHE:HB2	1.91	0.52
3:Hf:218:GLY:H	3:Hf:247:ILE:HD11	1.73	0.52
4:ID:162:TYR:O	2:DC:246:ARG:NH1	2.43	0.52
4:LD:26:LYS:O	7:LL:115:GLN:NE2	2.38	0.52
1:Lg:802:LEU:O	1:Lg:806:THR:OG1	2.26	0.52
1:DG:899:LEU:HD13	1:DG:919:MET:HG2	1.91	0.52
5:ZH:206:TRP:HZ3	5:ZH:208:LYS:HZ3	1.56	0.52
8:AM:215:ARG:NH1	8:AM:232:ASP:OD1	2.41	0.52
4:Ad:80:GLN:O	4:Ad:82:ARG:NH1	2.42	0.52
2:IC:111:LEU:HD23	2:IC:213:TYR:HB2	1.90	0.52
8:DM:165:ILE:HB	8:DM:185:ILE:HG23	1.91	0.52
1:IG:899:LEU:HD13	1:IG:919:MET:HG2	1.91	0.52
1:JG:910:ASP:OD1	1:JG:910:ASP:N	2.43	0.52
1:MG:876:SER:OG	1:NG:941:ARG:NH1	2.43	0.52
1:MG:931:SER:O	1:MG:1042:THR:OG1	2.28	0.52
5:HH:188:PRO:O	5:HH:262:ASN:ND2	2.40	0.52
7:HL:169:THR:OG1	7:HL:170:ASP:N	2.42	0.52
3:IF:207:ARG:NH2	3:IF:210:TYR:OH	2.42	0.52
4:LD:140:GLY:O	4:Ld:60:LYS:NZ	2.38	0.52
9:LN:88:HIS:ND1	9:LN:105:ASP:OD2	2.42	0.52
3:MF:207:ARG:HA	3:MF:207:ARG:HH11	1.75	0.52
5:VH:348:SER:HA	5:VH:352:LYS:O	2.09	0.52
5:WH:212:THR:OG1	5:FH:229:ARG:NH1	2.42	0.52
11:XX:21:UNK:N	11:XX:78:UNK:O	2.43	0.52
1:FG:891:THR:OG1	1:FG:892:GLY:N	2.39	0.52
2:KC:263:ARG:NH2	2:KC:264:ALA:O	2.43	0.52
2:MC:169:LYS:H	2:MC:173:GLU:HG3	1.74	0.52
8:EM:308:ASP:OD2	3:Ef:263:LYS:NZ	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AF:269:SER:O	3:ZF:219:ARG:NH1	2.42	0.52
9:GN:78:LEU:O	9:GN:79:GLN:NE2	2.42	0.52
4:HD:23:MET:N	4:HD:23:MET:SD	2.83	0.52
6:HK:78:ILE:HB	6:HK:180:VAL:HG23	1.90	0.52
1:BG:900:ILE:HB	1:BG:918:THR:HB	1.92	0.52
8:IM:181:PRO:O	8:IM:201:THR:OG1	2.27	0.52
4:Dd:35:ASP:O	4:Dd:38:THR:OG1	2.27	0.52
4:Id:60:LYS:NZ	4:Id:61:VAL:O	2.42	0.52
6:JK:90:ARG:NH1	6:JK:91:LEU:O	2.43	0.52
9:JN:104:ASN:OD1	9:JN:104:ASN:N	2.43	0.52
1:CG:958:SER:O	1:CG:962:SER:OG	2.26	0.52
5:AH:173:GLN:NE2	5:AH:219:LYS:O	2.42	0.52
5:AH:277:ASN:OD1	5:AH:277:ASN:N	2.43	0.52
5:LH:170:ARG:HH21	5:LH:245:GLN:HB3	1.75	0.52
5:LH:183:ASP:OD1	5:LH:187:ALA:N	2.43	0.52
6:AK:87:GLN:HB3	6:AK:128:ARG:HH12	1.74	0.52
1:EG:910:ASP:OD1	1:EG:910:ASP:N	2.41	0.52
5:YH:176:VAL:HB	5:YH:216:GLN:HB3	1.91	0.52
5:CH:249:ASP:OD1	5:CH:249:ASP:N	2.42	0.52
8:CM:215:ARG:NH1	8:CM:232:ASP:OD2	2.42	0.52
2:EC:214:LYS:HZ1	4:JD:55:MET:HA	1.75	0.52
7:GL:212:ASN:N	7:GL:212:ASN:OD1	2.40	0.52
7:HL:161:SER:H	7:HL:202:ARG:HH21	1.56	0.52
7:IL:165:VAL:HG12	7:IL:231:ILE:HG12	1.91	0.52
6:JK:50:ASP:OD1	6:JK:50:ASP:N	2.42	0.52
8:KM:186:SER:HA	8:KM:205:TYR:HB2	1.90	0.52
8:KM:271:SER:O	8:KM:290:ASP:HA	2.10	0.52
4:LD:67:LYS:NZ	4:LD:68:ASP:OD1	2.42	0.52
6:LK:115:THR:HB	6:LK:183:THR:HG23	1.92	0.52
6:AK:46:ASP:OD1	6:AK:46:ASP:N	2.39	0.52
3:YF:241:TYR:O	3:YF:258:SER:OG	2.27	0.52
7:AL:192:PHE:O	7:AL:196:ASN:ND2	2.43	0.52
8:BM:119:GLU:HG3	8:BM:139:ALA:HB3	1.92	0.52
11:CX:21:UNK:N	11:CX:78:UNK:O	2.43	0.52
1:AG:963:SER:HB3	1:PG:1011:VAL:HG12	1.92	0.52
2:BC:87:ARG:NH2	4:GD:120:SER:OG	2.42	0.52
2:BC:244:ARG:HB2	2:CC:127:ILE:HG12	1.91	0.52
2:EC:150:TYR:O	2:EC:198:ASN:ND2	2.43	0.52
5:GH:324:TRP:HB3	5:GH:339:MET:HE3	1.90	0.52
5:IH:185:THR:HB	5:IH:265:SER:HB3	1.91	0.52
7:IL:230:GLU:OE2	7:IL:232:GLN:NE2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:KD:150:ASN:N	4:KD:150:ASN:OD1	2.43	0.52
8:KM:308:ASP:OD2	3:Kf:253:ARG:NH2	2.43	0.52
6:AK:92:ASN:OD1	6:AK:92:ASN:N	2.42	0.52
8:MM:153:GLN:NE2	8:MM:172:ASN:OD1	2.43	0.52
3:YF:258:SER:OG	3:YF:260:GLN:NE2	2.40	0.52
9:AN:113:SER:OG	9:AN:114:LEU:N	2.41	0.52
4:Ad:150:ASN:OD1	4:Ad:150:ASN:N	2.39	0.52
2:IC:143:THR:HG22	2:IC:144:THR:HG23	1.92	0.52
1:KG:910:ASP:OD1	1:KG:910:ASP:N	2.40	0.52
4:HD:119:ILE:HG23	4:HD:138:GLN:HG2	1.90	0.52
3:If:256:THR:OG1	3:If:257:SER:N	2.41	0.52
5:LH:203:ASN:HB3	5:LH:216:GLN:HG2	1.92	0.52
1:DG:1024:ASN:OD1	1:DG:1024:ASN:N	2.37	0.52
4:MD:150:ASN:N	4:MD:150:ASN:OD1	2.42	0.52
3:XF:215:VAL:H	5:XH:245:GLN:HE22	1.58	0.52
1:ZG:797:ARG:O	1:ZG:801:MET:HB2	2.10	0.52
6:BK:72:GLN:NE2	7:CL:216:ASP:OD1	2.43	0.52
4:ED:155:GLU:OE1	4:ED:157:ARG:NH2	2.43	0.52
8:EM:189:VAL:HB	8:EM:207:ILE:HG22	1.92	0.52
8:EM:210:ASP:HA	8:EM:229:ASN:H	1.74	0.52
8:GM:257:ASP:N	8:GM:257:ASP:OD1	2.40	0.52
1:BG:928:ILE:HD12	1:BG:1045:VAL:HG11	1.92	0.52
6:IK:46:ASP:OD1	6:IK:46:ASP:N	2.43	0.52
7:IL:173:GLY:O	7:IL:178:LYS:NZ	2.42	0.52
8:IM:123:VAL:HG22	8:IM:143:THR:HB	1.92	0.52
7:LL:171:ASN:HB3	7:LL:217:ASN:HD22	1.75	0.52
7:LL:192:PHE:O	7:LL:196:ASN:ND2	2.43	0.52
8:LM:209:SER:OG	8:LM:210:ASP:N	2.42	0.52
4:MD:132:LEU:HD12	4:MD:145:ILE:HG21	1.92	0.52
5:MH:112:PHE:O	5:MH:116:THR:OG1	2.28	0.52
7:ML:212:ASN:N	7:ML:212:ASN:OD1	2.39	0.52
8:MM:127:ASN:HB3	8:MM:147:ALA:HB3	1.90	0.52
3:VF:266:GLN:O	3:CF:233:ARG:NH1	2.42	0.52
5:XH:186:GLY:HA2	5:XH:255:ARG:HH12	1.74	0.52
7:AL:113:ASP:OD1	7:AL:113:ASP:N	2.39	0.52
8:AM:306:GLN:OE1	3:Af:253:ARG:NH1	2.42	0.52
2:JC:247:ARG:HA	2:KC:123:GLN:HE22	1.75	0.52
1:GG:917:ASN:HA	1:GG:931:SER:HA	1.92	0.52
1:GG:973:GLN:O	1:GG:976:ASN:ND2	2.42	0.52
5:FH:138:GLU:HA	5:FH:141:LYS:HE3	1.92	0.52
1:Gg:806:THR:O	1:Gg:810:GLN:NE2	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:IF:220:ALA:O	3:IF:231:THR:HA	2.10	0.51
5:KH:315:THR:OG1	5:KH:316:ASN:N	2.42	0.51
4:Kd:82:ARG:NH2	4:Kd:125:ASP:OD2	2.43	0.51
6:AK:130:ARG:NH1	4:AD:77:TYR:OH	2.43	0.51
5:ZH:278:ASP:OD1	5:ZH:278:ASP:N	2.43	0.51
8:AM:138:LEU:HD11	8:AM:142:GLY:HA3	1.92	0.51
8:AM:257:ASP:N	8:AM:257:ASP:OD1	2.42	0.51
5:BH:159:ASN:HA	5:BH:257:GLN:HG2	1.92	0.51
2:FC:230:LEU:HB2	2:FC:243:ASP:HB3	1.91	0.51
6:CK:150:ASP:OD1	6:CK:150:ASP:N	2.43	0.51
2:EC:166:LEU:HD13	2:EC:167:PRO:HD2	1.92	0.51
4:HD:39:ILE:HD13	4:Hd:37:ALA:HB2	1.92	0.51
3:HF:241:TYR:HB3	3:HF:256:THR:HG21	1.92	0.51
4:KD:86:ASP:OD2	6:KK:152:ARG:NH2	2.43	0.51
6:KK:109:PHE:O	6:KK:111:LYS:NZ	2.43	0.51
7:KL:163:ILE:O	7:KL:204:LYS:NZ	2.41	0.51
8:KM:192:ARG:HG3	8:KM:193:GLN:HG2	1.92	0.51
3:LF:214:ALA:HB3	3:LF:221:TRP:HB2	1.92	0.51
5:MH:221:TYR:HE2	5:ZH:138:GLU:HB3	1.75	0.51
9:MN:88:HIS:ND1	9:MN:105:ASP:OD2	2.39	0.51
1:ZG:802:LEU:O	1:ZG:806:THR:OG1	2.28	0.51
4:Ad:110:GLY:HA3	4:Ad:158:TYR:HB2	1.92	0.51
4:Ad:136:ASP:HB2	4:Ad:145:ILE:HD11	1.92	0.51
3:Bf:237:LYS:NZ	3:Bf:238:ILE:O	2.44	0.51
5:CH:183:ASP:OD1	5:CH:187:ALA:N	2.42	0.51
6:CK:71:GLY:O	4:DD:27:LYS:NZ	2.43	0.51
1:IG:931:SER:O	1:IG:1042:THR:OG1	2.28	0.51
1:PG:903:PHE:HB3	1:PG:914:ILE:HD13	1.91	0.51
8:GM:180:ASP:O	8:GM:182:LYS:NZ	2.39	0.51
5:HH:176:VAL:HG22	5:HH:216:GLN:HB3	1.91	0.51
4:ID:72:THR:HG23	4:ID:73:ILE:HG22	1.90	0.51
4:ID:77:TYR:OH	6:IK:130:ARG:NH1	2.43	0.51
6:IK:78:ILE:HB	6:IK:180:VAL:HG23	1.92	0.51
1:CG:1017:GLN:NE2	1:CG:1018:GLN:OE1	2.42	0.51
5:AH:316:ASN:N	5:AH:316:ASN:OD1	2.42	0.51
8:KM:288:ARG:NH1	8:KM:290:ASP:OD2	2.44	0.51
8:LM:205:TYR:OH	3:Lf:219:ARG:NH1	2.43	0.51
8:LM:292:MET:N	8:LM:292:MET:SD	2.84	0.51
11:ZX:21:UNK:N	11:ZX:78:UNK:O	2.44	0.51
4:Ad:36:ASP:OD1	4:Ad:36:ASP:N	2.41	0.51
3:Af:243:MET:O	3:Af:257:SER:N	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FG:939:THR:HG22	1:FG:941:ARG:HG3	1.93	0.51
2:KC:89:ASN:N	2:KC:89:ASN:OD1	2.41	0.51
7:CL:170:ASP:OD2	7:CL:227:ARG:NH2	2.43	0.51
8:CM:257:ASP:OD1	8:CM:257:ASP:N	2.43	0.51
5:EH:206:TRP:NE1	5:EH:210:SER:O	2.43	0.51
3:Ef:251:GLN:HB3	3:Ef:253:ARG:HD3	1.92	0.51
6:FK:107:LYS:NZ	6:FK:148:GLY:O	2.42	0.51
11:DX:21:UNK:N	11:DX:78:UNK:O	2.43	0.51
3:JF:268:ASP:OD2	5:JH:170:ARG:NH2	2.41	0.51
5:KH:313:VAL:HG13	5:KH:337:TYR:HB2	1.93	0.51
8:LM:240:GLN:HB3	8:LM:242:LYS:HE3	1.92	0.51
1:Cg:802:LEU:O	1:Cg:806:THR:OG1	2.27	0.51
5:MH:110:LYS:HA	5:MH:113:LYS:HE2	1.92	0.51
8:MM:308:ASP:OD1	8:MM:308:ASP:N	2.44	0.51
5:VH:150:LYS:HE3	3:CF:219:ARG:HH22	1.74	0.51
2:MC:190:ASP:O	2:MC:194:THR:OG1	2.29	0.51
9:DN:103:CYS:N	9:DN:107:TYR:O	2.40	0.51
7:EL:210:ASP:OD1	7:EL:210:ASP:N	2.40	0.51
9:EN:88:HIS:ND1	9:EN:105:ASP:OD2	2.39	0.51
8:FM:141:GLU:OE2	8:FM:143:THR:OG1	2.26	0.51
2:BC:87:ARG:NH1	4:GD:86:ASP:OD1	2.44	0.51
6:GK:46:ASP:OD1	6:GK:46:ASP:N	2.43	0.51
6:IK:71:GLY:O	4:JD:27:LYS:NZ	2.39	0.51
5:LH:176:VAL:HA	5:LH:215:ILE:O	2.11	0.51
1:DG:871:ALA:HB2	1:DG:889:ILE:HD13	1.91	0.51
5:XH:315:THR:OG1	5:XH:316:ASN:N	2.44	0.51
2:DC:57:GLU:OE2	2:DC:61:LYS:NZ	2.42	0.51
7:DL:115:GLN:HB3	7:DL:126:ILE:HB	1.91	0.51
8:DM:257:ASP:N	8:DM:257:ASP:OD1	2.43	0.51
1:PG:966:GLN:O	1:PG:970:ASN:ND2	2.44	0.51
1:AG:1040:LEU:HB2	1:PG:886:LEU:HD21	1.92	0.51
4:Gd:139:ALA:HB1	4:Gd:143:ALA:HB3	1.91	0.51
3:JF:254:ILE:HB	3:JF:262:ILE:HB	1.93	0.51
8:JM:249:GLN:OE1	8:JM:267:ASN:ND2	2.44	0.51
1:CG:886:LEU:HB3	1:CG:900:ILE:HG23	1.92	0.51
5:AH:298:SER:OG	9:MN:72:ARG:NE	2.43	0.51
6:AK:162:ASP:OD1	6:AK:162:ASP:N	2.44	0.51
5:XH:345:LEU:HB2	5:XH:356:LEU:HB2	1.93	0.51
5:BH:316:ASN:HB3	5:BH:334:THR:HG22	1.93	0.51
8:BM:158:VAL:HG13	8:BM:178:LYS:HE2	1.91	0.51
2:FC:227:HIS:HA	2:FC:245:VAL:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GC:263:ARG:NH1	2:GC:264:ALA:O	2.43	0.51
2:IC:152:LEU:HD21	2:IC:203:ILE:HG21	1.91	0.51
2:KC:173:LYS:NZ	2:LC:39:ALA:O	2.44	0.51
2:MC:259:ASN:OD1	2:MC:259:ASN:N	2.43	0.51
8:DM:256:HIS:O	8:DM:259:SER:OG	2.28	0.51
4:ED:132:LEU:HD12	4:ED:145:ILE:HG21	1.93	0.51
1:JG:931:SER:O	1:JG:1042:THR:OG1	2.28	0.51
1:NG:917:ASN:HA	1:NG:931:SER:HA	1.92	0.51
3:Ff:218:GLY:H	3:Ff:247:ILE:HD11	1.76	0.51
1:AG:866:GLY:HA3	1:PG:898:LYS:HD3	1.92	0.51
8:HM:168:VAL:H	8:HM:187:GLY:HA3	1.75	0.51
1:Ig:800:ASP:N	1:Ig:800:ASP:OD1	2.42	0.51
9:JN:76:MET:SD	9:JN:76:MET:N	2.84	0.51
4:Ld:68:ASP:OD1	4:Ld:68:ASP:N	2.35	0.51
7:AL:130:ASP:OD1	7:AL:130:ASP:N	2.39	0.51
6:CK:50:ASP:OD1	6:CK:50:ASP:N	2.42	0.51
2:BC:225:VAL:HG12	2:BC:248:ILE:HG22	1.93	0.51
5:GH:221:TYR:HE2	5:HH:138:GLU:HB3	1.75	0.51
4:Gd:36:ASP:OD1	4:Gd:36:ASP:N	2.41	0.51
1:BG:898:LYS:HD3	1:CG:866:GLY:HA3	1.93	0.51
4:Id:118:LEU:HD22	2:DC:244:ASP:HB2	1.93	0.51
1:Kg:802:LEU:O	1:Kg:806:THR:OG1	2.29	0.51
4:Kd:74:PRO:HG3	4:Kd:147:VAL:HG11	1.93	0.51
4:Ld:148:TYR:HB2	4:Ld:153:VAL:HG12	1.93	0.51
1:EG:911:LYS:HD3	1:EG:942:THR:HB	1.93	0.51
4:BD:36:ASP:OD1	4:BD:36:ASP:N	2.35	0.51
5:BH:198:ASP:OD1	5:BH:200:SER:OG	2.29	0.51
6:CK:121:SER:OG	6:CK:122:LYS:N	2.40	0.51
7:EL:150:ASN:OD1	7:EL:153:ARG:NH2	2.43	0.51
5:FH:226:LEU:HD23	5:FH:241:LEU:HD11	1.92	0.51
1:HG:1017:GLN:NE2	1:IG:1020:GLN:OE1	2.42	0.51
1:LG:1011:VAL:HG12	1:MG:963:SER:HB2	1.93	0.51
2:LC:169:LYS:H	2:LC:173:GLU:HG3	1.75	0.51
6:GK:87:GLN:NE2	6:GK:173:ASP:OD1	2.44	0.51
5:HH:108:ASP:OD2	5:HH:109:LYS:NZ	2.44	0.51
5:IH:324:TRP:HB3	5:IH:339:MET:HE2	1.92	0.51
6:IK:93:TRP:O	4:Id:24:LYS:N	2.43	0.51
4:JD:83:ALA:HA	6:JK:154:ILE:O	2.11	0.51
9:JN:74:ALA:HB3	9:JN:76:MET:HE1	1.92	0.51
4:Ld:36:ASP:OD1	4:Ld:36:ASP:N	2.44	0.51
4:MD:162:TYR:HB3	2:HC:248:LEU:HD21	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:ML:44:HIS:HB2	7:ML:48:ASN:HA	1.93	0.51
9:MN:46:GLY:O	9:MN:61:ASN:ND2	2.44	0.51
1:EG:958:SER:O	1:EG:962:SER:OG	2.27	0.51
5:BH:148:PRO:O	5:BH:246:LYS:NZ	2.44	0.51
1:FG:898:LYS:HD3	1:GG:866:GLY:HA3	1.92	0.51
8:BM:174:GLN:HE22	8:BM:193:GLN:HB3	1.75	0.51
2:GC:110:LEU:HD23	2:GC:212:TYR:HB2	1.92	0.51
5:DH:114:ASP:OD2	5:DH:118:ASN:ND2	2.44	0.51
6:DK:65:ILE:HD12	6:DK:78:ILE:HG12	1.93	0.51
1:HG:876:SER:HB2	1:HG:1033:SER:HB3	1.93	0.51
1:OG:897:SER:HB3	1:OG:919:MET:HE1	1.92	0.51
1:OG:972:PHE:HB3	1:OG:1005:VAL:HG22	1.93	0.51
1:PG:1003:ASN:HA	1:PG:1006:ILE:HD12	1.93	0.51
8:FM:127:ASN:OD1	8:FM:127:ASN:N	2.44	0.51
2:AC:262:ARG:NH2	2:AC:263:ALA:O	2.44	0.51
5:GH:169:ILE:HG12	5:GH:239:LEU:HD11	1.92	0.51
1:BG:1011:VAL:HG12	1:CG:963:SER:HB2	1.93	0.51
3:Hf:213:GLN:HB2	3:Hf:221:TRP:HB3	1.92	0.51
3:IF:251:GLN:OE1	3:IF:253:ARG:NH2	2.43	0.51
3:IF:253:ARG:HG3	3:IF:261:VAL:HG13	1.93	0.51
6:IK:90:ARG:NH1	6:IK:91:LEU:O	2.43	0.51
6:JK:124:VAL:HG12	6:JK:125:SER:HB3	1.93	0.51
3:Jf:219:ARG:HA	3:Jf:232:VAL:O	2.11	0.51
4:Kd:150:ASN:OD1	4:Kd:150:ASN:N	2.44	0.51
1:DG:868:ILE:HA	1:DG:1039:ILE:O	2.11	0.51
3:Cf:243:MET:HB3	3:Cf:257:SER:HB3	1.92	0.51
6:DK:166:THR:HG22	6:DK:168:TYR:H	1.75	0.51
1:MG:1024:ASN:OD1	1:MG:1024:ASN:N	2.34	0.51
2:LC:92:ASP:OD1	2:LC:148:TRP:NE1	2.34	0.51
2:EC:97:ASN:OD1	2:EC:97:ASN:N	2.34	0.50
8:GM:302:ARG:HH11	8:GM:309:LEU:HD11	1.76	0.50
8:HM:221:LYS:NZ	8:HM:240:GLN:OE1	2.44	0.50
9:HN:85:CYS:HB2	9:HN:91:VAL:HG12	1.93	0.50
6:JK:47:GLY:O	6:JK:108:GLN:NE2	2.41	0.50
8:JM:145:ARG:HE	8:JM:164:GLN:HB3	1.77	0.50
1:CG:898:LYS:HE3	1:DG:866:GLY:HA3	1.92	0.50
5:AH:123:ASN:HB3	5:AH:126:GLN:HG3	1.93	0.50
5:LH:229:ARG:HG2	5:LH:236:PRO:HB3	1.92	0.50
3:WF:222:LEU:O	3:WF:229:THR:HA	2.10	0.50
5:XH:282:HIS:HB3	5:XH:287:VAL:HB	1.93	0.50
3:YF:246:LEU:HB2	3:YF:255:LEU:HD21	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:BF:267:GLU:OE2	5:BH:150:LYS:NZ	2.43	0.50
3:CF:250:LEU:HD12	3:CF:251:GLN:HG3	1.93	0.50
8:BM:199:LYS:HA	8:BM:219:ALA:HB3	1.93	0.50
5:DH:194:TYR:HB3	5:DH:228:VAL:HG23	1.93	0.50
9:DN:88:HIS:ND1	9:DN:105:ASP:OD2	2.44	0.50
4:Ed:148:TYR:HB2	4:Ed:153:VAL:HG12	1.93	0.50
2:BC:101:GLU:O	4:GD:142:LYS:NZ	2.42	0.50
3:AF:243:MET:HB3	3:AF:257:SER:HB3	1.92	0.50
3:AF:251:GLN:OE1	11:BX:1:UNK:N	2.45	0.50
4:GD:30:ILE:O	7:GL:131:LYS:NZ	2.44	0.50
6:GK:122:LYS:NZ	6:GK:125:SER:O	2.39	0.50
6:IK:143:TYR:OH	6:IK:147:GLN:NE2	2.42	0.50
6:JK:183:THR:HG21	10:JU:123:UNK:HA	1.93	0.50
8:JM:158:VAL:HA	8:JM:178:LYS:HZ3	1.76	0.50
11:JX:20:UNK:O	11:JX:37:UNK:N	2.44	0.50
4:KD:125:ASP:O	8:KM:317:LYS:NZ	2.44	0.50
5:VH:171:LEU:O	5:VH:244:GLY:N	2.44	0.50
7:AL:225:GLN:HG2	4:AD:29:PRO:HG2	1.93	0.50
3:CF:265:SER:HB3	3:CF:268:ASP:HB3	1.93	0.50
1:FG:917:ASN:OD1	1:FG:917:ASN:N	2.43	0.50
8:BM:233:VAL:HG23	8:BM:253:VAL:HA	1.93	0.50
4:Bd:86:ASP:OD1	2:KC:130:ARG:NH2	2.43	0.50
8:CM:207:ILE:HG13	8:CM:226:GLY:HA3	1.92	0.50
5:DH:207:ASP:OD1	5:DH:207:ASP:N	2.42	0.50
5:DH:343:PRO:HG2	5:DH:344:VAL:HG12	1.93	0.50
8:EM:257:ASP:OD1	8:EM:257:ASP:N	2.44	0.50
1:HG:917:ASN:HA	1:HG:931:SER:HA	1.93	0.50
1:JG:876:SER:OG	1:JG:1031:VAL:O	2.29	0.50
2:BC:239:ILE:HG13	2:CC:132:TYR:HB2	1.92	0.50
4:HD:77:TYR:OH	6:HK:130:ARG:NH1	2.44	0.50
8:IM:303:GLU:HG2	8:IM:305:GLY:H	1.75	0.50
3:Jf:241:TYR:HB3	3:Jf:256:THR:HG21	1.93	0.50
2:CC:221:VAL:HA	2:CC:254:GLU:O	2.11	0.50
5:KH:289:PRO:O	5:KH:292:SER:OG	2.28	0.50
4:Kd:36:ASP:N	4:Kd:36:ASP:OD1	2.43	0.50
9:AN:48:ILE:HD12	9:AN:58:LEU:HD22	1.94	0.50
4:BD:119:ILE:HD12	4:BD:138:GLN:HB3	1.92	0.50
5:BH:171:LEU:O	5:BH:244:GLY:N	2.41	0.50
4:Bd:68:ASP:N	4:Bd:68:ASP:OD1	2.38	0.50
4:AD:123:THR:OG1	4:AD:126:GLU:OE1	2.29	0.50
2:FC:166:PRO:HB2	2:FC:172:LYS:HG3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:CM:163:THR:HB	8:CM:183:VAL:HG12	1.92	0.50
8:CM:308:ASP:N	8:CM:308:ASP:OD1	2.44	0.50
8:DM:210:ASP:O	8:DM:230:ARG:N	2.44	0.50
1:IG:876:SER:OG	1:IG:1031:VAL:O	2.28	0.50
1:IG:1005:VAL:O	1:IG:1009:ALA:CB	2.59	0.50
1:KG:965:LEU:HD12	1:KG:1008:LEU:HD13	1.92	0.50
7:GL:129:THR:O	7:GL:133:PHE:HB2	2.12	0.50
9:IN:66:SER:OG	9:IN:67:THR:N	2.43	0.50
5:AH:107:ILE:HA	5:AH:110:LYS:HE3	1.93	0.50
5:VH:207:ASP:OD2	5:CH:229:ARG:NH1	2.44	0.50
3:WF:211:TYR:N	3:WF:223:ILE:O	2.43	0.50
4:CD:83:ALA:HA	6:CK:154:ILE:O	2.12	0.50
1:EG:931:SER:O	1:EG:1042:THR:OG1	2.29	0.50
5:YH:184:SER:OG	5:YH:257:GLN:O	2.29	0.50
8:CM:282:TYR:HE1	8:CM:301:MET:HG3	1.76	0.50
3:Cf:246:LEU:HB3	3:Cf:255:LEU:HD21	1.92	0.50
4:FD:105:ARG:HB2	4:FD:153:VAL:HG22	1.93	0.50
1:IG:931:SER:H	1:IG:1043:GLN:HE22	1.59	0.50
1:NG:931:SER:O	1:NG:1042:THR:OG1	2.30	0.50
8:FM:275:ASP:HB3	8:FM:294:PHE:HB2	1.93	0.50
1:Hg:811:ASP:O	1:Hg:814:GLN:NE2	2.44	0.50
9:HN:110:GLU:HA	9:HN:113:SER:HB3	1.93	0.50
7:JL:210:ASP:N	7:JL:210:ASP:OD1	2.43	0.50
4:KD:105:ARG:HB2	4:KD:153:VAL:HG22	1.93	0.50
5:LH:250:TYR:HB3	5:YH:238:MET:HG2	1.93	0.50
11:LX:25:UNK:N	11:LX:71:UNK:O	2.44	0.50
7:ML:44:HIS:N	7:ML:48:ASN:OD1	2.43	0.50
4:Cd:150:ASN:OD1	4:Cd:150:ASN:N	2.44	0.50
4:Ed:105:ARG:HB2	4:Ed:153:VAL:HG23	1.94	0.50
1:MG:1005:VAL:O	1:MG:1009:ALA:HB2	2.12	0.50
9:FN:52:ASP:OD2	9:FN:55:ALA:N	2.42	0.50
8:GM:308:ASP:OD1	8:GM:308:ASP:N	2.43	0.50
5:HH:280:LEU:HD23	5:HH:328:MET:HE3	1.92	0.50
5:IH:108:ASP:OD1	5:IH:108:ASP:N	2.43	0.50
5:IH:301:ASP:N	5:IH:301:ASP:OD1	2.43	0.50
6:IK:117:THR:HA	6:IK:157:GLN:O	2.12	0.50
8:IM:158:VAL:HA	8:IM:178:LYS:HZ3	1.76	0.50
8:IM:158:VAL:HG13	8:IM:178:LYS:HE2	1.92	0.50
4:JD:123:THR:OG1	4:JD:124:LYS:N	2.44	0.50
1:CG:891:THR:OG1	1:CG:892:GLY:N	2.43	0.50
3:KF:219:ARG:HG2	5:YH:148:PRO:HB2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:LF:222:LEU:HD21	3:LF:262:ILE:HG21	1.92	0.50
3:LF:237:LYS:NZ	3:LF:243:MET:SD	2.75	0.50
8:LM:165:ILE:HB	8:LM:185:ILE:HG23	1.92	0.50
3:Df:221:TRP:HE1	3:Df:229:THR:HB	1.76	0.50
2:DC:173:GLU:HA	2:DC:176:ILE:HG12	1.93	0.50
4:BD:83:ALA:HA	6:BK:154:ILE:O	2.12	0.50
5:BH:236:PRO:HD2	5:CH:251:ARG:HH12	1.76	0.50
1:FG:917:ASN:HA	1:FG:931:SER:HA	1.94	0.50
2:JC:229:ASP:N	2:JC:229:ASP:OD1	2.45	0.50
8:EM:141:GLU:OE2	8:EM:143:THR:OG1	2.25	0.50
8:EM:210:ASP:OD1	8:EM:210:ASP:N	2.42	0.50
1:Fg:818:GLN:NE2	5:FH:205:GLN:OE1	2.45	0.50
1:JG:867:ASP:O	1:JG:1040:LEU:HA	2.11	0.50
1:LG:947:ARG:HE	1:LG:947:ARG:H	1.59	0.50
1:MG:1044:ASP:OD1	1:MG:1044:ASP:N	2.44	0.50
1:PG:959:LEU:O	1:PG:963:SER:OG	2.28	0.50
7:FL:161:SER:O	7:FL:202:ARG:NH2	2.40	0.50
4:Fd:82:ARG:HH12	4:Fd:127:SER:HA	1.77	0.50
2:AC:141:THR:HG23	2:AC:142:THR:HG22	1.92	0.50
1:AG:941:ARG:NH1	1:PG:1033:SER:OG	2.44	0.50
3:GF:219:ARG:HH22	5:HH:150:LYS:HE2	1.75	0.50
4:Gd:74:PRO:HD2	4:Gd:129:ALA:HB1	1.92	0.50
3:HF:254:ILE:HB	3:HF:262:ILE:HB	1.92	0.50
8:IM:233:VAL:HG13	8:IM:253:VAL:HA	1.94	0.50
4:Id:150:ASN:N	4:Id:150:ASN:OD1	2.45	0.50
4:KD:77:TYR:OH	6:KK:130:ARG:NH1	2.45	0.50
1:DG:958:SER:O	1:DG:962:SER:OG	2.28	0.50
5:VH:138:GLU:HB3	5:CH:221:TYR:HE2	1.75	0.50
4:CD:36:ASP:OD1	4:CD:36:ASP:N	2.43	0.50
3:YF:245:LYS:HB2	3:YF:255:LEU:HD11	1.93	0.50
5:ZH:233:LEU:HD22	5:ZH:235:THR:H	1.77	0.50
1:FG:946:SER:OG	1:FG:1030:GLU:O	2.30	0.50
2:FC:244:ARG:HB3	2:GC:127:ILE:HG22	1.94	0.50
2:KC:146:THR:OG1	2:KC:147:TRP:N	2.45	0.50
2:KC:172:GLU:O	2:KC:176:TRP:HB2	2.12	0.50
1:GG:876:SER:HB2	1:GG:1033:SER:HB3	1.94	0.50
1:KG:958:SER:O	1:KG:962:SER:OG	2.28	0.50
7:FL:150:ASN:OD1	7:FL:153:ARG:NH2	2.43	0.50
3:AF:208:ILE:HG13	3:AF:225:SER:H	1.75	0.50
3:HF:243:MET:O	3:HF:257:SER:N	2.43	0.50
7:HL:210:ASP:OD1	7:HL:210:ASP:N	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Hd:136:ASP:HB2	4:Hd:145:ILE:HD11	1.94	0.50
5:JH:130:LEU:HD23	5:JH:133:ILE:HD11	1.93	0.50
5:JH:178:SER:O	5:JH:251:ARG:HA	2.12	0.50
5:JH:207:ASP:N	5:JH:207:ASP:OD1	2.45	0.50
4:KD:132:LEU:HD12	4:KD:145:ILE:HG21	1.93	0.50
5:KH:342:SER:OG	5:KH:344:VAL:O	2.29	0.50
6:LK:66:LYS:HB3	6:LK:77:SER:HB3	1.94	0.50
1:DG:1017:GLN:OE1	1:DG:1018:GLN:NE2	2.42	0.50
8:MM:303:GLU:OE1	8:MM:306:GLN:N	2.45	0.50
1:Dg:818:GLN:NE2	5:DH:203:ASN:OD1	2.41	0.50
6:CK:173:ASP:OD1	6:CK:173:ASP:N	2.44	0.50
7:DL:201:LYS:O	7:DL:201:LYS:NZ	2.41	0.50
5:FH:150:LYS:H	5:FH:247:ALA:HA	1.75	0.50
1:HG:876:SER:HB3	1:IG:941:ARG:HG2	1.94	0.50
1:HG:1005:VAL:O	1:HG:1009:ALA:HB2	2.11	0.50
1:KG:886:LEU:HA	1:KG:899:LEU:O	2.12	0.50
1:OG:917:ASN:HA	1:OG:931:SER:HA	1.93	0.50
2:HC:226:TYR:HB3	2:HC:252:ALA:HB3	1.94	0.50
2:LC:35:LEU:HA	2:LC:38:MET:HG2	1.94	0.50
6:HK:115:THR:OG1	6:HK:183:THR:OG1	2.29	0.50
3:Hf:238:ILE:HG13	3:Hf:241:TYR:HB2	1.94	0.50
4:ID:71:LEU:HD23	4:Id:64:PRO:HB3	1.94	0.50
8:IM:126:GLY:O	8:IM:146:LEU:HA	2.11	0.50
4:Dd:36:ASP:OD1	4:Dd:36:ASP:N	2.43	0.50
7:JL:124:THR:HG22	7:JL:232:GLN:HG2	1.93	0.50
8:KM:257:ASP:OD1	8:KM:257:ASP:N	2.41	0.50
4:LD:77:TYR:OH	6:LK:130:ARG:NH1	2.45	0.50
8:LM:312:PHE:HA	8:LM:316:ASN:HD21	1.77	0.50
6:AK:115:THR:OG1	6:AK:183:THR:OG1	2.28	0.50
6:MK:125:SER:OG	6:MK:126:VAL:N	2.42	0.50
3:VF:243:MET:HB3	3:VF:257:SER:HB3	1.93	0.50
2:DC:171:LYS:HA	2:DC:174:LYS:HE2	1.93	0.50
5:ZH:126:GLN:HA	5:ZH:129:LYS:HG2	1.93	0.50
6:BK:66:LYS:HB3	6:BK:77:SER:HB3	1.94	0.50
4:Bd:145:ILE:O	4:Bd:146:HIS:ND1	2.45	0.50
7:CL:44:HIS:HB2	7:CL:48:ASN:HA	1.94	0.50
1:GG:874:ASP:OD1	1:GG:874:ASP:N	2.43	0.50
8:DM:136:LEU:HB2	8:DM:155:LEU:HG	1.94	0.50
5:EH:256:VAL:HG12	5:EH:258:GLY:H	1.76	0.50
3:FF:233:ARG:NE	3:FF:235:GLY:O	2.43	0.50
1:IG:897:SER:HB3	1:IG:919:MET:HE1	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:JG:965:LEU:HD12	1:JG:1008:LEU:HD13	1.93	0.50
1:KG:972:PHE:HB3	1:KG:1005:VAL:HG22	1.93	0.50
1:KG:1005:VAL:O	1:KG:1009:ALA:CB	2.59	0.50
1:BG:886:LEU:HA	1:BG:899:LEU:O	2.11	0.49
6:IK:115:THR:HG22	6:IK:155:PHE:HB2	1.93	0.49
4:Jd:76:ALA:O	4:Jd:80:GLN:NE2	2.38	0.49
3:KF:246:LEU:HB3	3:KF:255:LEU:HD12	1.93	0.49
6:KK:87:GLN:N	6:KK:173:ASP:OD2	2.41	0.49
4:LD:91:ILE:O	4:LD:95:THR:OG1	2.30	0.49
4:MD:87:TRP:CD1	4:MD:89:GLY:H	2.30	0.49
8:DM:127:ASN:N	8:DM:127:ASN:OD1	2.44	0.49
5:EH:253:ASP:N	5:EH:253:ASP:OD1	2.45	0.49
1:OG:951:HIS:H	1:OG:1027:THR:HG22	1.77	0.49
3:GF:207:ARG:HA	3:GF:207:ARG:HH11	1.78	0.49
4:HD:36:ASP:OD1	4:HD:36:ASP:N	2.42	0.49
5:HH:201:SER:O	5:HH:218:THR:N	2.43	0.49
7:JL:158:TYR:HD2	7:JL:233:TRP:HE1	1.60	0.49
6:LK:50:ASP:N	6:LK:50:ASP:OD1	2.44	0.49
6:LK:125:SER:HG	6:LK:128:ARG:H	1.58	0.49
4:MD:82:ARG:NE	4:MD:125:ASP:OD1	2.41	0.49
8:MM:125:THR:HG23	8:MM:145:ARG:HB2	1.94	0.49
8:MM:256:HIS:O	8:MM:259:SER:OG	2.29	0.49
5:VH:322:PRO:HG2	5:VH:345:LEU:HA	1.94	0.49
1:EG:872:VAL:HA	1:EG:1036:GLY:HA2	1.93	0.49
1:Dg:800:ASP:OD1	1:Dg:800:ASP:N	2.43	0.49
4:AD:118:LEU:O	2:IC:98:ASN:ND2	2.44	0.49
6:EK:92:ASN:O	6:EK:95:SER:OG	2.30	0.49
2:HC:171:LYS:HA	2:HC:174:LYS:HE2	1.94	0.49
2:AC:103:ASN:OD1	2:AC:103:ASN:N	2.45	0.49
2:EC:109:VAL:HG13	2:EC:136:LYS:H	1.77	0.49
7:HL:145:TYR:HA	7:HL:148:LEU:HD23	1.94	0.49
9:JN:87:TRP:O	9:JN:88:HIS:ND1	2.45	0.49
4:MD:92:GLU:OE2	4:MD:158:TYR:OH	2.31	0.49
5:WH:344:VAL:HG13	5:WH:355:GLN:HE21	1.77	0.49
5:XH:207:ASP:O	5:XH:210:SER:OG	2.28	0.49
1:IG:917:ASN:HA	1:IG:931:SER:HA	1.94	0.49
1:LG:948:THR:HG22	1:LG:1029:VAL:HG12	1.94	0.49
3:Ff:254:ILE:HD11	3:Ff:262:ILE:HB	1.93	0.49
8:HM:177:LEU:HD13	8:HM:181:PRO:HG2	1.94	0.49
5:IH:238:MET:SD	5:JH:178:SER:OG	2.70	0.49
8:IM:269:GLN:NE2	8:IM:290:ASP:OD1	2.35	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:IM:306:GLN:HG3	8:IM:308:ASP:H	1.77	0.49
9:JN:84:CYS:SG	9:JN:85:CYS:N	2.85	0.49
3:Jf:256:THR:OG1	3:Jf:257:SER:N	2.45	0.49
5:KH:259:TYR:HB3	5:KH:263:ALA:HB2	1.94	0.49
4:Kd:93:GLU:OE2	2:GC:263:ARG:NH1	2.44	0.49
1:Cg:794:ILE:O	1:Cg:798:THR:N	2.43	0.49
1:Mg:797:ARG:NH2	5:ZH:121:PRO:O	2.45	0.49
5:MH:280:LEU:HD22	5:MH:328:MET:HE3	1.94	0.49
5:WH:228:VAL:HG12	5:WH:237:VAL:HB	1.94	0.49
5:BH:274:PRO:O	2:JC:117:ASN:ND2	2.43	0.49
1:FG:1011:VAL:HG12	1:GG:963:SER:HB3	1.94	0.49
6:CK:110:ARG:NH1	9:CN:75:VAL:O	2.45	0.49
4:DD:70:THR:HA	4:DD:133:ARG:HH21	1.77	0.49
6:DK:179:ARG:NE	6:DK:181:GLU:OE2	2.45	0.49
1:Eg:816:GLU:O	5:EH:216:GLN:NE2	2.45	0.49
6:FK:49:CYS:O	6:FK:52:THR:OG1	2.27	0.49
1:IG:900:ILE:HG13	1:IG:918:THR:HB	1.94	0.49
1:OG:886:LEU:HD21	1:PG:1040:LEU:HD12	1.94	0.49
1:PG:944:LEU:HD11	1:PG:1031:VAL:HA	1.94	0.49
7:FL:149:ASN:HB3	7:FL:153:ARG:HH12	1.77	0.49
4:Fd:71:LEU:O	4:Fd:133:ARG:NH1	2.44	0.49
3:GF:213:GLN:HA	5:GH:170:ARG:HH21	1.76	0.49
1:BG:1024:ASN:OD1	1:BG:1024:ASN:N	2.46	0.49
4:JD:132:LEU:HD12	4:JD:145:ILE:HG21	1.95	0.49
7:JL:53:ASP:OD1	7:JL:53:ASP:N	2.44	0.49
1:DG:889:ILE:O	1:DG:896:GLY:N	2.42	0.49
4:Ld:72:THR:OG1	4:Ld:73:ILE:N	2.42	0.49
8:MM:275:ASP:HA	8:MM:295:ASN:H	1.77	0.49
5:YH:159:ASN:ND2	5:YH:161:SER:OG	2.45	0.49
4:BD:132:LEU:HD12	4:BD:145:ILE:HG21	1.94	0.49
6:BK:106:LEU:O	6:BK:111:LYS:NZ	2.37	0.49
2:IC:259:ASN:HB2	2:IC:262:GLU:HB2	1.94	0.49
9:CN:92:TYR:HD1	9:CN:94:GLN:H	1.60	0.49
5:DH:193:ALA:HB3	5:DH:229:ARG:HE	1.77	0.49
6:DK:125:SER:OG	6:DK:126:VAL:N	2.43	0.49
4:Gd:64:PRO:HG2	4:Gd:67:LYS:HB2	1.92	0.49
3:HF:213:GLN:O	5:HH:170:ARG:NH1	2.40	0.49
7:HL:178:LYS:O	7:HL:182:SER:OG	2.31	0.49
4:ID:130:GLU:OE2	4:ID:133:ARG:NH1	2.44	0.49
4:JD:77:TYR:OH	6:JK:130:ARG:NH1	2.45	0.49
6:JK:151:SER:O	6:JK:152:ARG:NH1	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CC:231:LEU:HB2	2:CC:244:ASP:HB3	1.94	0.49
5:BH:321:SER:OG	5:BH:346:LEU:N	2.44	0.49
7:BL:170:ASP:OD1	7:BL:170:ASP:N	2.30	0.49
2:KC:196:GLU:HA	2:KC:199:ILE:HG22	1.94	0.49
2:KC:243:ASP:OD2	2:KC:245:ARG:NH2	2.44	0.49
8:EM:209:SER:OG	8:EM:210:ASP:N	2.44	0.49
5:FH:297:VAL:HG11	5:FH:302:ALA:HB3	1.93	0.49
1:OG:870:PHE:HZ	2:LC:56:ARG:HB2	1.78	0.49
7:FL:124:THR:HA	7:FL:231:ILE:O	2.12	0.49
1:AG:891:THR:OG1	1:AG:892:GLY:N	2.41	0.49
5:GH:212:THR:OG1	5:WH:229:ARG:NH1	2.46	0.49
8:HM:157:ALA:O	8:HM:178:LYS:NZ	2.41	0.49
4:ID:31:ASN:OD1	4:ID:31:ASN:N	2.45	0.49
3:IF:233:ARG:NE	3:IF:235:GLY:O	2.40	0.49
5:IH:106:VAL:HA	5:IH:109:LYS:HE2	1.94	0.49
7:IL:212:ASN:OD1	7:IL:212:ASN:N	2.44	0.49
3:If:241:TYR:O	3:If:257:SER:OG	2.31	0.49
3:Jf:209:ILE:HD13	3:Jf:211:TYR:HE1	1.78	0.49
3:LF:243:MET:O	3:LF:257:SER:N	2.46	0.49
9:LN:89:GLY:O	9:LN:104:ASN:ND2	2.46	0.49
1:EG:876:SER:HB3	1:FG:941:ARG:HA	1.94	0.49
5:XH:230:LEU:H	5:XH:233:LEU:HD11	1.77	0.49
8:BM:155:LEU:HB3	8:BM:175:ILE:HD12	1.93	0.49
8:CM:119:GLU:HG3	8:CM:139:ALA:HB3	1.95	0.49
3:GF:269:SER:OG	3:WF:233:ARG:NH1	2.46	0.49
3:IF:248:ASP:OD2	3:IF:253:ARG:NH2	2.44	0.49
7:IL:59:ARG:HH12	7:IL:99:ARG:HH11	1.61	0.49
7:IL:210:ASP:OD1	7:IL:210:ASP:N	2.38	0.49
7:IL:215:SER:HB2	7:IL:226:ASN:HB2	1.94	0.49
1:CG:931:SER:O	1:CG:1042:THR:OG1	2.30	0.49
5:LH:150:LYS:H	5:LH:247:ALA:HA	1.78	0.49
1:DG:1003:ASN:HA	1:DG:1006:ILE:HD12	1.95	0.49
4:MD:86:ASP:OD2	6:MK:152:ARG:NH2	2.37	0.49
1:Cg:810:GLN:HA	1:Cg:813:LYS:HB2	1.93	0.49
6:MK:177:ASN:N	6:MK:177:ASN:OD1	2.45	0.49
4:CD:123:THR:OG1	4:CD:126:GLU:OE2	2.28	0.49
5:YH:171:LEU:HD21	5:YH:241:LEU:HG	1.94	0.49
3:EF:210:TYR:HB3	3:EF:222:LEU:HB3	1.94	0.49
1:JG:917:ASN:OD1	1:JG:917:ASN:N	2.46	0.49
1:LG:1005:VAL:O	1:LG:1009:ALA:CB	2.61	0.49
1:NG:959:LEU:O	1:NG:963:SER:OG	2.30	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Gd:148:TYR:HB2	4:Gd:153:VAL:HG12	1.94	0.49
6:HK:151:SER:OG	6:HK:152:ARG:N	2.46	0.49
7:IL:129:THR:OG1	7:IL:130:ASP:OD1	2.30	0.49
8:IM:205:TYR:OH	3:If:219:ARG:NH2	2.45	0.49
8:IM:306:GLN:HB3	8:IM:309:LEU:HB2	1.94	0.49
8:JM:256:HIS:O	8:JM:259:SER:OG	2.30	0.49
3:Kf:221:TRP:HE1	3:Kf:229:THR:HB	1.77	0.49
7:LL:115:GLN:HB3	7:LL:126:ILE:HB	1.94	0.49
8:LM:277:SER:O	8:LM:297:SER:OG	2.30	0.49
4:Ld:35:ASP:HB3	4:Ld:38:THR:HG22	1.94	0.49
3:Lf:256:THR:OG1	3:Lf:257:SER:N	2.46	0.49
5:VH:190:PRO:HB2	5:VH:231:ARG:HD3	1.94	0.49
8:BM:186:SER:HA	8:BM:205:TYR:HB2	1.95	0.49
4:AD:82:ARG:HH21	4:AD:127:SER:HA	1.76	0.49
2:IC:90:ASN:N	2:IC:90:ASN:OD1	2.44	0.49
2:JC:174:ILE:HA	2:JC:177:ILE:HG12	1.95	0.49
2:MC:91:LEU:O	2:MC:95:TYR:HB2	2.13	0.49
1:GG:1011:VAL:HG12	1:HG:963:SER:HB2	1.94	0.49
5:EH:107:ILE:HA	5:EH:110:LYS:HD2	1.93	0.49
4:Ed:74:PRO:HB3	4:Ed:147:VAL:HG11	1.95	0.49
1:OG:890:VAL:HG23	1:OG:891:THR:HG22	1.95	0.49
9:IN:89:GLY:HA3	9:IN:104:ASN:HB2	1.95	0.49
4:LD:148:TYR:OH	4:Ld:133:ARG:NH2	2.46	0.49
1:DG:1033:SER:OG	1:EG:941:ARG:NH1	2.45	0.49
8:MM:257:ASP:N	8:MM:257:ASP:OD1	2.45	0.49
8:AM:209:SER:OG	8:AM:210:ASP:N	2.45	0.49
9:AN:95:LEU:HA	1:LG:893:LYS:HZ1	1.78	0.49
6:BK:92:ASN:O	6:BK:95:SER:OG	2.31	0.49
6:BK:177:ASN:N	6:BK:177:ASN:OD1	2.40	0.49
7:CL:184:ALA:O	7:CL:188:THR:OG1	2.31	0.49
5:DH:324:TRP:HB3	5:DH:339:MET:HG2	1.95	0.49
1:MG:878:ASN:OD1	1:MG:879:SER:N	2.46	0.49
6:HK:163:LYS:O	6:HK:179:ARG:NH2	2.45	0.48
1:Ig:810:GLN:O	1:Ig:814:GLN:NE2	2.46	0.48
6:JK:117:THR:HA	6:JK:157:GLN:O	2.13	0.48
5:KH:238:MET:SD	5:YH:178:SER:OG	2.70	0.48
4:Kd:84:SER:H	2:GC:267:ALA:HB3	1.78	0.48
1:Lg:807:GLN:NE2	1:Lg:810:GLN:OE1	2.46	0.48
4:Ld:107:ARG:O	4:Ld:155:GLU:HA	2.13	0.48
1:Cg:810:GLN:O	1:Cg:814:GLN:N	2.46	0.48
8:AM:154:LYS:NZ	8:AM:156:GLU:OE2	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:AM:180:ASP:O	8:AM:182:LYS:NZ	2.41	0.48
4:Ad:66:SER:OG	4:Ad:67:LYS:NZ	2.45	0.48
2:GC:249:ILE:HG13	2:HC:124:GLN:HA	1.94	0.48
3:Cf:245:LYS:N	3:Cf:245:LYS:HZ3	2.11	0.48
7:EL:175:ARG:HA	7:EL:178:LYS:HD2	1.95	0.48
1:AG:972:PHE:HB3	1:AG:1005:VAL:HG22	1.95	0.48
3:AF:233:ARG:NE	3:AF:235:GLY:O	2.46	0.48
4:GD:107:ARG:NH1	4:Gd:130:GLU:OE1	2.41	0.48
3:GF:208:ILE:HD11	3:GF:224:GLY:HA3	1.94	0.48
5:GH:183:ASP:OD1	5:GH:187:ALA:N	2.46	0.48
4:ID:150:ASN:OD1	4:ID:150:ASN:N	2.46	0.48
5:IH:207:ASP:OD1	5:IH:207:ASP:N	2.39	0.48
6:IK:50:ASP:OD1	6:IK:50:ASP:N	2.46	0.48
4:Dd:87:TRP:NE1	4:Dd:90:PRO:O	2.47	0.48
5:JH:201:SER:OG	5:JH:219:LYS:NZ	2.43	0.48
4:Jd:149:PRO:O	4:Jd:152:GLN:NE2	2.39	0.48
3:KF:243:MET:O	3:KF:257:SER:N	2.44	0.48
6:KK:121:SER:OG	6:KK:122:LYS:N	2.46	0.48
8:KM:279:ILE:HB	8:KM:298:VAL:HG22	1.95	0.48
9:KN:84:CYS:HA	2:FC:153:ASP:HB3	1.94	0.48
1:DG:966:GLN:O	1:DG:970:ASN:ND2	2.46	0.48
1:Cg:801:MET:HB3	5:DH:115:MET:HE1	1.96	0.48
5:VH:132:GLN:NE2	5:VH:136:THR:OG1	2.46	0.48
3:WF:245:LYS:HE2	3:WF:257:SER:HB3	1.93	0.48
5:WH:150:LYS:HE3	3:FF:231:THR:HG23	1.95	0.48
4:Ad:60:LYS:NZ	4:AD:140:GLY:O	2.46	0.48
1:Dg:802:LEU:O	1:Dg:806:THR:OG1	2.30	0.48
4:AD:132:LEU:HD12	4:AD:145:ILE:HG21	1.95	0.48
2:MC:107:LEU:HD12	2:MC:108:PRO:HD2	1.96	0.48
3:Cf:265:SER:OG	3:Cf:266:GLN:N	2.45	0.48
6:DK:162:ASP:OD1	6:DK:162:ASP:N	2.45	0.48
5:EH:345:LEU:HB2	5:EH:356:LEU:HB2	1.95	0.48
6:FK:66:LYS:NZ	6:FK:67:VAL:O	2.46	0.48
1:JG:877:VAL:H	1:JG:1031:VAL:HG22	1.78	0.48
1:JG:904:ASN:OD1	1:JG:904:ASN:N	2.47	0.48
1:JG:912:MET:HB3	1:JG:944:LEU:HB2	1.94	0.48
1:OG:1011:VAL:HG12	1:PG:963:SER:HB2	1.94	0.48
8:FM:186:SER:HA	8:FM:205:TYR:HB2	1.95	0.48
7:GL:94:VAL:HA	7:GL:97:ILE:HG12	1.95	0.48
8:HM:275:ASP:HB3	8:HM:294:PHE:HB2	1.94	0.48
6:IK:85:ALA:HB3	6:IK:88:SER:HB2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:IM:269:GLN:HE21	8:IM:289:ALA:H	1.61	0.48
5:JH:115:MET:HG2	1:XG:801:MET:HG2	1.95	0.48
5:AH:238:MET:HE3	5:BH:251:ARG:HB2	1.94	0.48
2:CC:121:ASP:OD1	2:CC:122:ALA:N	2.46	0.48
4:Ld:100:LYS:O	4:Ld:100:LYS:NZ	2.41	0.48
6:MK:116:VAL:HG22	6:MK:182:ILE:HG22	1.95	0.48
5:VH:311:MET:HG2	5:VH:341:LYS:HA	1.96	0.48
5:XH:173:GLN:NE2	5:XH:218:THR:O	2.43	0.48
3:YF:267:GLU:O	5:YH:150:LYS:NZ	2.46	0.48
2:DC:142:ILE:HD11	2:DC:145:PRO:HA	1.95	0.48
2:GC:228:HIS:HA	2:GC:246:VAL:O	2.13	0.48
2:IC:216:LEU:HA	2:IC:219:MET:HG2	1.94	0.48
1:GG:951:HIS:H	1:GG:1027:THR:HG22	1.79	0.48
8:DM:181:PRO:O	8:DM:201:THR:OG1	2.31	0.48
1:Eg:797:ARG:HH22	5:FH:117:ARG:HH12	1.61	0.48
1:AG:877:VAL:H	1:AG:1031:VAL:HG22	1.78	0.48
3:GF:251:GLN:OE1	11:HX:2:UNK:N	2.46	0.48
1:Gg:811:ASP:OD1	1:Gg:811:ASP:N	2.46	0.48
5:GH:201:SER:OG	5:GH:219:LYS:NZ	2.45	0.48
4:HD:158:TYR:O	4:Hd:137:TYR:OH	2.31	0.48
1:BG:966:GLN:O	1:BG:970:ASN:ND2	2.46	0.48
4:ID:87:TRP:CD1	4:ID:89:GLY:H	2.31	0.48
3:IF:254:ILE:HB	3:IF:262:ILE:HB	1.95	0.48
1:CG:951:HIS:H	1:CG:1027:THR:HG22	1.78	0.48
1:CG:965:LEU:HD12	1:CG:1008:LEU:HD13	1.94	0.48
3:Jf:218:GLY:H	3:Jf:247:ILE:HD11	1.78	0.48
2:CC:150:TYR:HB3	2:CC:202:ILE:HB	1.95	0.48
5:KH:151:PRO:HA	5:KH:248:VAL:HG23	1.95	0.48
3:Kf:238:ILE:HG13	3:Kf:241:TYR:HB2	1.96	0.48
2:DC:176:ILE:HA	2:DC:179:ILE:HG12	1.95	0.48
5:BH:207:ASP:N	5:BH:207:ASP:OD1	2.45	0.48
5:BH:326:ALA:HB3	5:BH:338:GLU:HB2	1.95	0.48
2:FC:112:GLY:O	2:FC:129:ARG:HA	2.13	0.48
8:DM:170:SER:OG	8:DM:172:ASN:O	2.29	0.48
5:EH:185:THR:HG22	5:EH:266:MET:HG3	1.95	0.48
8:EM:256:HIS:O	8:EM:259:SER:OG	2.28	0.48
9:EN:46:GLY:O	9:EN:61:ASN:ND2	2.46	0.48
1:OG:966:GLN:O	1:OG:970:ASN:ND2	2.46	0.48
7:FL:169:THR:OG1	7:FL:170:ASP:N	2.47	0.48
6:GK:152:ARG:HB2	6:GK:153:ILE:HD12	1.94	0.48
7:GL:170:ASP:N	7:GL:170:ASP:OD1	2.38	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:HL:150:ASN:OD1	7:HL:153:ARG:NH2	2.40	0.48
5:IH:189:TRP:HE1	5:IH:232:GLY:H	1.61	0.48
4:JD:85:VAL:HG23	6:JK:153:ILE:HG23	1.96	0.48
7:JL:170:ASP:N	7:JL:170:ASP:OD1	2.33	0.48
4:KD:87:TRP:CD1	4:KD:89:GLY:H	2.31	0.48
3:Kf:245:LYS:NZ	3:Kf:256:THR:O	2.43	0.48
1:DG:891:THR:OG1	1:DG:892:GLY:N	2.47	0.48
4:MD:78:ASN:H	4:MD:80:GLN:HE22	1.61	0.48
5:MH:173:GLN:NE2	5:MH:218:THR:O	2.44	0.48
3:BF:216:ILE:HD11	3:BF:219:ARG:HB2	1.95	0.48
5:BH:289:PRO:O	5:BH:292:SER:OG	2.28	0.48
2:GC:91:ASP:HB3	2:GC:147:TRP:HE1	1.78	0.48
5:DH:273:PRO:O	2:LC:127:ARG:NH1	2.39	0.48
4:FD:36:ASP:HA	4:FD:39:ILE:HD12	1.95	0.48
1:LG:917:ASN:HA	1:LG:931:SER:HA	1.94	0.48
7:GL:137:SER:HB2	7:GL:139:ARG:HG3	1.95	0.48
1:Hg:791:GLN:N	1:Hg:793:GLU:OE1	2.47	0.48
6:IK:115:THR:OG1	6:IK:183:THR:OG1	2.31	0.48
8:JM:177:LEU:HD11	8:JM:196:MET:HE1	1.94	0.48
9:JN:41:CYS:HB2	9:JN:48:ILE:HD11	1.94	0.48
1:CG:874:ASP:N	1:CG:874:ASP:OD1	2.46	0.48
5:KH:147:THR:O	5:KH:246:LYS:NZ	2.38	0.48
9:KN:46:GLY:HA3	9:KN:61:ASN:HB2	1.94	0.48
9:LN:94:GLN:HE22	9:LN:96:ASN:HB2	1.78	0.48
4:MD:77:TYR:OH	6:MK:130:ARG:NH1	2.46	0.48
6:MK:86:ASP:OD1	6:MK:86:ASP:N	2.46	0.48
7:ML:91:VAL:HA	7:ML:94:VAL:HG22	1.95	0.48
5:ZH:315:THR:OG1	5:ZH:316:ASN:N	2.44	0.48
7:BL:212:ASN:N	7:BL:212:ASN:OD1	2.47	0.48
9:CN:116:LYS:O	9:CN:116:LYS:NZ	2.38	0.48
1:GG:912:MET:HB3	1:GG:944:LEU:HB2	1.96	0.48
1:GG:966:GLN:O	1:GG:970:ASN:ND2	2.47	0.48
6:DK:116:VAL:HG22	6:DK:182:ILE:HG22	1.96	0.48
8:EM:144:THR:O	8:EM:145:ARG:NE	2.42	0.48
5:GH:148:PRO:HD2	3:WF:219:ARG:HG2	1.95	0.48
4:HD:98:ILE:HD11	4:HD:128:LEU:HD22	1.95	0.48
3:HF:208:ILE:HG13	3:HF:225:SER:H	1.77	0.48
7:HL:130:ASP:OD1	7:HL:130:ASP:N	2.46	0.48
4:KD:29:PRO:HG2	7:KL:225:GLN:HG2	1.96	0.48
9:KN:66:SER:OG	9:KN:67:THR:N	2.46	0.48
6:LK:54:ILE:O	6:LK:58:THR:OG1	2.30	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:LM:149:ASN:OD1	8:LM:149:ASN:N	2.44	0.48
6:AK:117:THR:HA	6:AK:157:GLN:O	2.13	0.48
8:MM:141:GLU:OE2	8:MM:143:THR:OG1	2.31	0.48
5:VH:284:LEU:O	5:VH:314:ARG:NH1	2.43	0.48
5:WH:182:LEU:HD13	5:WH:186:GLY:HA2	1.96	0.48
3:Df:256:THR:OG1	3:Df:260:GLN:N	2.41	0.48
6:BK:150:ASP:OD1	6:BK:150:ASP:N	2.43	0.48
8:BM:116:PHE:HE1	8:BM:118:TYR:HB2	1.78	0.48
6:DK:59:ASP:HA	6:DK:62:LYS:HG2	1.96	0.48
4:ED:82:ARG:NH2	4:ED:125:ASP:O	2.46	0.48
4:ED:87:TRP:CD1	4:ED:89:GLY:H	2.31	0.48
3:FF:247:ILE:HG12	3:FF:254:ILE:HG12	1.95	0.48
1:KG:876:SER:OG	1:KG:1031:VAL:O	2.29	0.48
2:LC:173:GLU:HA	2:LC:176:ILE:HG12	1.96	0.48
2:AC:96:ASN:OD1	2:AC:96:ASN:N	2.33	0.48
3:AF:219:ARG:NH2	3:AF:231:THR:OG1	2.46	0.48
7:GL:108:ASP:OD2	7:GL:150:ASN:ND2	2.47	0.48
5:AH:228:VAL:HB	5:AH:237:VAL:HG23	1.96	0.48
1:DG:898:LYS:HE3	1:EG:865:THR:HB	1.96	0.48
6:MK:75:LEU:HD12	6:MK:183:THR:HG22	1.95	0.48
6:MK:123:TYR:HD2	6:MK:124:VAL:HG23	1.79	0.48
3:WF:207:ARG:HD2	3:WF:207:ARG:HA	1.70	0.48
1:EG:965:LEU:HD12	1:EG:1008:LEU:HD13	1.96	0.48
8:AM:201:THR:HG22	8:AM:221:LYS:HB2	1.96	0.48
8:AM:278:ASP:OD1	8:AM:297:SER:OG	2.32	0.48
4:Cd:71:LEU:O	4:Cd:133:ARG:NH1	2.42	0.48
7:DL:173:GLY:O	7:DL:178:LYS:NZ	2.46	0.48
9:DN:46:GLY:HA3	9:DN:61:ASN:HB2	1.96	0.48
8:EM:158:VAL:HA	8:EM:178:LYS:HZ3	1.78	0.48
4:FD:86:ASP:OD2	6:FK:152:ARG:NH2	2.46	0.48
4:FD:150:ASN:OD1	4:FD:150:ASN:N	2.43	0.48
1:MG:1011:VAL:HG12	1:NG:963:SER:HB2	1.95	0.48
2:EC:157:LYS:NZ	2:EC:158:PRO:O	2.38	0.48
3:AF:219:ARG:HG2	5:BH:148:PRO:HD2	1.94	0.48
3:HF:231:THR:O	5:XH:150:LYS:NZ	2.46	0.48
4:ID:55:MET:HE2	2:DC:211:ILE:HD11	1.96	0.48
5:IH:330:SER:HG	5:IH:334:THR:H	1.61	0.48
1:Jg:801:MET:O	1:Jg:805:ALA:N	2.42	0.48
5:JH:253:ASP:OD1	5:JH:253:ASP:N	2.46	0.48
1:Kg:811:ASP:N	1:Kg:811:ASP:OD1	2.45	0.48
5:KH:345:LEU:HB2	5:KH:356:LEU:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:KM:303:GLU:OE2	8:KM:306:GLN:N	2.46	0.48
4:Ld:78:ASN:HD22	4:Ld:104:PHE:HE1	1.61	0.48
3:Lf:243:MET:N	3:Lf:257:SER:OG	2.47	0.48
5:YH:214:MET:HB3	5:YH:214:MET:HE2	1.80	0.48
3:ZF:208:ILE:HD11	3:ZF:224:GLY:HA3	1.96	0.48
1:GG:958:SER:O	1:GG:962:SER:OG	2.32	0.48
7:DL:114:ILE:HD12	7:DL:127:ILE:HG13	1.96	0.48
3:EF:265:SER:OG	3:EF:267:GLU:OE1	2.31	0.48
8:EM:131:THR:HG23	8:EM:151:GLY:H	1.79	0.48
2:EC:231:LEU:HB2	2:EC:244:ASP:HB3	1.96	0.48
1:Gg:797:ARG:NH2	5:HH:121:PRO:O	2.46	0.48
8:HM:201:THR:HG22	8:HM:221:LYS:HB2	1.95	0.48
6:IK:185:ARG:NH2	7:JL:213:ALA:O	2.47	0.48
4:Jd:84:SER:H	2:FC:266:ALA:HB3	1.79	0.48
5:KH:178:SER:OG	5:KH:250:TYR:O	2.31	0.48
8:KM:275:ASP:HB3	8:KM:294:PHE:HB2	1.95	0.48
11:LX:23:UNK:HA	11:LX:33:UNK:HA	1.96	0.48
1:DG:903:PHE:HA	1:DG:915:THR:H	1.78	0.48
5:YH:292:SER:HB2	5:YH:305:TRP:HB3	1.96	0.48
8:BM:203:SER:HA	8:BM:223:GLN:O	2.14	0.48
2:KC:116:THR:HG1	2:KC:128:SER:HG	1.58	0.48
2:MC:127:ARG:HD3	5:EH:275:SER:HA	1.96	0.48
6:CK:53:ILE:HG13	6:CK:108:GLN:HG2	1.96	0.48
8:CM:195:ASP:HB3	8:CM:197:TYR:HE1	1.78	0.48
8:CM:228:VAL:HG11	8:CM:231:LEU:HB3	1.95	0.48
3:DF:210:TYR:HA	3:DF:224:GLY:HA2	1.95	0.48
4:Ed:71:LEU:O	4:Ed:133:ARG:NE	2.47	0.48
9:FN:115:GLN:NE2	2:AC:68:GLN:OE1	2.47	0.48
2:BC:174:ILE:HA	2:BC:177:ILE:HG12	1.96	0.47
2:BC:244:ARG:HD3	2:CC:127:ILE:HD11	1.96	0.47
5:GH:152:THR:OG1	5:GH:248:VAL:O	2.30	0.47
8:HM:209:SER:OG	8:HM:210:ASP:N	2.47	0.47
11:HX:26:UNK:N	11:HX:30:UNK:O	2.47	0.47
6:IK:166:THR:HG22	6:IK:168:TYR:H	1.79	0.47
7:IL:94:VAL:HA	7:IL:97:ILE:HG12	1.95	0.47
6:KK:115:THR:HB	6:KK:183:THR:HG23	1.94	0.47
5:MH:228:VAL:HG13	5:MH:237:VAL:HB	1.96	0.47
6:MK:42:PRO:HD2	9:MN:76:MET:HE3	1.96	0.47
3:XF:214:ALA:HB3	3:XF:221:TRP:HB2	1.96	0.47
5:ZH:324:TRP:O	2:GC:248:ARG:NH1	2.47	0.47
4:BD:31:ASN:N	4:BD:31:ASN:OD1	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FG:928:ILE:HD12	1:FG:1045:VAL:HG11	1.95	0.47
8:BM:196:MET:HE3	8:BM:198:GLY:H	1.78	0.47
4:AD:47:SER:O	4:AD:51:SER:OG	2.32	0.47
2:KC:175:ILE:HA	2:KC:178:ILE:HG12	1.96	0.47
2:MC:110:VAL:HG13	2:MC:209:GLY:HA3	1.96	0.47
4:ED:39:ILE:HG23	7:EL:220:ILE:HG13	1.96	0.47
1:Eg:798:THR:HA	1:Eg:801:MET:HE2	1.96	0.47
6:FK:116:VAL:HG12	6:FK:182:ILE:HG12	1.95	0.47
1:MG:966:GLN:O	1:MG:970:ASN:ND2	2.47	0.47
2:EC:102:GLU:O	4:JD:162:TYR:OH	2.32	0.47
4:Gd:68:ASP:OD1	4:Gd:68:ASP:N	2.37	0.47
6:HK:76:ILE:HB	6:HK:182:ILE:HG13	1.96	0.47
4:Hd:110:GLY:HA3	4:Hd:158:TYR:HB2	1.96	0.47
8:IM:119:GLU:HG3	8:IM:139:ALA:HB3	1.95	0.47
5:JH:183:ASP:OD1	5:JH:187:ALA:N	2.46	0.47
6:JK:65:ILE:HG23	6:JK:78:ILE:HG13	1.96	0.47
4:LD:142:LYS:NZ	2:GC:102:GLU:O	2.42	0.47
3:LF:219:ARG:NH1	3:MF:269:SER:O	2.46	0.47
1:DG:911:LYS:HA	1:DG:943:ALA:HA	1.96	0.47
3:VF:213:GLN:HG3	5:VH:170:ARG:HH11	1.78	0.47
4:CD:136:ASP:O	4:Cd:60:LYS:NZ	2.40	0.47
7:AL:124:THR:HA	7:AL:231:ILE:O	2.14	0.47
8:BM:210:ASP:OD2	8:BM:211:THR:OG1	2.31	0.47
2:FC:100:LEU:HG	2:FC:106:PRO:HG3	1.96	0.47
2:IC:234:VAL:HG12	2:IC:243:ILE:HA	1.95	0.47
2:KC:157:LYS:NZ	2:KC:158:PRO:O	2.48	0.47
1:GG:931:SER:O	1:GG:1042:THR:OG1	2.32	0.47
8:DM:275:ASP:HB3	8:DM:294:PHE:HB2	1.95	0.47
5:EH:130:LEU:HD23	5:EH:133:ILE:HD11	1.96	0.47
7:EL:230:GLU:OE2	7:EL:232:GLN:NE2	2.37	0.47
4:FD:68:ASP:N	4:FD:68:ASP:OD1	2.47	0.47
2:HC:151:TYR:O	2:HC:199:ASN:ND2	2.39	0.47
1:AG:917:ASN:HA	1:AG:931:SER:HA	1.95	0.47
4:GD:77:TYR:OH	6:GK:130:ARG:NH1	2.47	0.47
8:HM:256:HIS:O	8:HM:259:SER:OG	2.32	0.47
1:BG:1005:VAL:O	1:BG:1009:ALA:CB	2.62	0.47
8:JM:311:ASP:OD1	8:JM:312:PHE:N	2.47	0.47
9:KN:63:GLY:HA3	4:LD:27:LYS:HB2	1.96	0.47
7:LL:91:VAL:HA	7:LL:94:VAL:HG12	1.95	0.47
6:MK:127:LYS:HA	6:MK:130:ARG:HB2	1.97	0.47
1:FG:870:PHE:HE1	1:FG:937:PRO:HB3	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:DM:264:SER:O	8:DM:264:SER:OG	2.32	0.47
1:IG:966:GLN:O	1:IG:970:ASN:ND2	2.47	0.47
2:BC:220:VAL:HG13	2:BC:254:LEU:HD13	1.95	0.47
7:GL:232:GLN:NE2	10:FU:127:UNK:O	2.41	0.47
9:HN:82:MET:SD	9:HN:82:MET:N	2.81	0.47
1:BG:917:ASN:HA	1:BG:931:SER:HA	1.96	0.47
4:Hd:76:ALA:HB3	4:Hd:79:LEU:HD23	1.96	0.47
5:JH:342:SER:OG	5:JH:344:VAL:O	2.31	0.47
5:KH:278:ASP:N	5:KH:278:ASP:OD1	2.43	0.47
7:KL:190:MET:HA	7:KL:193:LEU:HD23	1.95	0.47
7:AL:113:ASP:OD2	7:AL:131:LYS:NZ	2.41	0.47
3:ZF:215:VAL:HG13	5:ZH:245:GLN:HE22	1.80	0.47
5:ZH:180:VAL:HG13	5:ZH:253:ASP:HA	1.96	0.47
4:Ad:68:ASP:OD1	4:Ad:68:ASP:N	2.37	0.47
4:Ad:97:ARG:NH1	2:JC:263:ALA:O	2.47	0.47
2:MC:102:LEU:HB2	2:MC:106:ILE:HG23	1.96	0.47
7:CL:210:ASP:OD1	7:CL:210:ASP:N	2.43	0.47
4:DD:87:TRP:CD1	4:DD:89:GLY:H	2.32	0.47
1:GG:911:LYS:HA	1:GG:943:ALA:HA	1.96	0.47
4:ED:150:ASN:O	4:ED:152:GLN:NE2	2.47	0.47
5:EH:324:TRP:HA	5:EH:339:MET:HB3	1.95	0.47
1:HG:910:ASP:OD1	1:HG:910:ASP:N	2.42	0.47
6:GK:177:ASN:N	6:GK:177:ASN:OD1	2.47	0.47
4:HD:30:ILE:O	7:HL:131:LYS:NZ	2.48	0.47
9:HN:56:GLY:HA2	9:HN:71:THR:HG23	1.97	0.47
4:ID:92:GLU:OE1	4:ID:93:GLU:N	2.48	0.47
3:If:221:TRP:HE1	3:If:229:THR:HB	1.79	0.47
8:JM:119:GLU:HG3	8:JM:139:ALA:HB3	1.95	0.47
1:CG:966:GLN:O	1:CG:970:ASN:ND2	2.47	0.47
4:KD:73:ILE:O	4:KD:133:ARG:NH2	2.37	0.47
2:CC:91:ASP:OD1	2:CC:91:ASP:N	2.46	0.47
3:KF:243:MET:N	3:KF:257:SER:OG	2.42	0.47
5:KH:149:PRO:HB2	5:KH:248:VAL:HG22	1.96	0.47
8:KM:275:ASP:HA	8:KM:295:ASN:H	1.79	0.47
3:Kf:216:ILE:HD12	3:Kf:216:ILE:HA	1.82	0.47
7:LL:177:HIS:ND1	8:LM:315:TYR:OH	2.33	0.47
8:LM:183:VAL:O	8:LM:203:SER:OG	2.32	0.47
8:LM:276:ALA:H	8:LM:295:ASN:HB2	1.80	0.47
3:Df:213:GLN:HB2	3:Df:221:TRP:HB3	1.95	0.47
5:ZH:282:HIS:HB3	5:ZH:287:VAL:HB	1.95	0.47
8:BM:308:ASP:OD1	8:BM:308:ASP:N	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CL:129:THR:OG1	7:CL:130:ASP:OD1	2.32	0.47
6:DK:129:GLU:OE1	6:DK:129:GLU:N	2.47	0.47
8:DM:177:LEU:HD23	8:DM:196:MET:HE1	1.96	0.47
8:DM:279:ILE:HB	8:DM:298:VAL:HG22	1.96	0.47
5:FH:126:GLN:HA	5:FH:129:LYS:HG2	1.95	0.47
1:JG:966:GLN:O	1:JG:970:ASN:ND2	2.47	0.47
1:NG:1003:ASN:HA	1:NG:1006:ILE:HD12	1.96	0.47
1:PG:1024:ASN:OD1	1:PG:1024:ASN:N	2.37	0.47
8:FM:275:ASP:N	8:FM:275:ASP:OD1	2.47	0.47
5:GH:320:LEU:HB2	5:GH:346:LEU:HB3	1.96	0.47
5:HH:157:PHE:HA	5:HH:255:ARG:HB3	1.97	0.47
7:JL:221:HIS:ND1	7:JL:225:GLN:OE1	2.46	0.47
5:AH:311:MET:HE3	5:AH:341:LYS:HA	1.95	0.47
4:LD:69:ASN:OD1	4:LD:69:ASN:N	2.47	0.47
1:DG:931:SER:O	1:DG:1042:THR:OG1	2.32	0.47
6:MK:117:THR:HA	6:MK:157:GLN:O	2.15	0.47
3:XF:210:TYR:HB2	3:XF:262:ILE:HD13	1.97	0.47
9:AN:63:GLY:HA3	4:BD:27:LYS:HB2	1.97	0.47
3:BF:220:ALA:O	3:BF:231:THR:HA	2.15	0.47
2:FC:100:LEU:HB2	2:FC:104:ILE:HG13	1.95	0.47
5:CH:179:LEU:O	5:CH:212:THR:HA	2.14	0.47
8:CM:306:GLN:HB2	3:Cf:251:GLN:HE21	1.79	0.47
7:EL:183:GLN:OE1	7:EL:207:GLY:N	2.41	0.47
3:Ef:210:TYR:HB3	3:Ef:222:LEU:HD12	1.97	0.47
4:FD:35:ASP:OD2	4:FD:38:THR:N	2.43	0.47
1:IG:948:THR:HG22	1:IG:1029:VAL:HG12	1.97	0.47
1:LG:966:GLN:O	1:LG:970:ASN:ND2	2.48	0.47
1:OG:1005:VAL:O	1:OG:1009:ALA:CB	2.62	0.47
1:PG:951:HIS:O	1:PG:955:ARG:NE	2.45	0.47
2:EC:110:LEU:HD23	2:EC:212:TYR:HB2	1.97	0.47
4:GD:75:ASN:N	4:GD:75:ASN:OD1	2.46	0.47
5:GH:117:ARG:O	1:WG:797:ARG:NH2	2.48	0.47
8:GM:199:LYS:HA	8:GM:219:ALA:HB3	1.97	0.47
1:Hg:800:ASP:N	1:Hg:800:ASP:OD1	2.45	0.47
1:BG:899:LEU:HD13	1:BG:919:MET:HG2	1.96	0.47
1:BG:915:THR:HG23	1:BG:933:TYR:HE1	1.80	0.47
8:IM:275:ASP:HA	8:IM:295:ASN:H	1.79	0.47
5:JH:301:ASP:OD1	5:JH:301:ASP:N	2.44	0.47
8:JM:200:GLY:O	8:JM:220:ALA:HA	2.15	0.47
1:CG:877:VAL:H	1:CG:1031:VAL:HG22	1.80	0.47
5:AH:251:ARG:NH1	5:ZH:236:PRO:O	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:KK:125:SER:OG	6:KK:126:VAL:N	2.44	0.47
8:LM:163:THR:HB	8:LM:183:VAL:HG12	1.97	0.47
4:Ld:95:THR:HA	4:Ld:98:ILE:HG22	1.97	0.47
5:MH:236:PRO:HD2	5:ZH:251:ARG:HE	1.80	0.47
5:VH:330:SER:OG	5:VH:334:THR:OG1	2.31	0.47
1:EG:919:MET:HB3	1:EG:928:ILE:HG13	1.97	0.47
5:XH:183:ASP:O	5:XH:255:ARG:NH1	2.40	0.47
7:AL:44:HIS:HB3	7:AL:48:ASN:HA	1.95	0.47
5:ZH:249:ASP:N	5:ZH:249:ASP:OD1	2.46	0.47
8:AM:119:GLU:HG3	8:AM:139:ALA:HB3	1.97	0.47
8:AM:302:ARG:HH11	8:AM:309:LEU:HD11	1.78	0.47
4:Bd:150:ASN:OD1	4:Bd:150:ASN:N	2.48	0.47
4:AD:55:MET:HE2	2:IC:211:ILE:HD11	1.96	0.47
6:CK:78:ILE:HB	6:CK:180:VAL:HG13	1.96	0.47
5:DH:114:ASP:O	5:DH:118:ASN:ND2	2.48	0.47
5:DH:253:ASP:OD1	5:DH:253:ASP:N	2.46	0.47
4:ED:125:ASP:OD2	6:EK:138:ARG:NE	2.47	0.47
3:EF:243:MET:HB3	3:EF:257:SER:HB3	1.95	0.47
4:Ed:91:ILE:HB	4:Ed:119:ILE:HD13	1.97	0.47
4:Ed:100:LYS:O	4:Ed:100:LYS:NZ	2.41	0.47
3:Ef:212:ILE:HA	3:Ef:222:LEU:HD22	1.97	0.47
5:FH:198:ASP:OD1	5:FH:200:SER:OG	2.26	0.47
6:FK:151:SER:OG	6:FK:152:ARG:N	2.47	0.47
1:MG:972:PHE:HB3	1:MG:1005:VAL:HG22	1.97	0.47
1:OG:965:LEU:HD12	1:OG:1008:LEU:HD13	1.96	0.47
8:FM:256:HIS:O	8:FM:259:SER:OG	2.32	0.47
4:Fd:105:ARG:HB2	4:Fd:153:VAL:HG23	1.97	0.47
2:AC:100:LEU:HB2	2:AC:104:ILE:HG23	1.96	0.47
2:EC:173:LYS:HE2	2:EC:173:LYS:HB2	1.78	0.47
6:GK:50:ASP:N	6:GK:50:ASP:OD1	2.46	0.47
1:Bg:802:LEU:O	1:Bg:806:THR:OG1	2.27	0.47
8:IM:168:VAL:H	8:IM:187:GLY:HA3	1.79	0.47
5:KH:123:ASN:N	5:KH:123:ASN:OD1	2.46	0.47
1:Lg:806:THR:O	1:Lg:810:GLN:NE2	2.48	0.47
5:LH:238:MET:N	5:LH:238:MET:SD	2.88	0.47
1:DG:1011:VAL:HG12	1:EG:963:SER:HB3	1.97	0.47
3:MF:265:SER:HB3	3:MF:268:ASP:HB3	1.96	0.47
7:ML:121:ASP:O	7:ML:123:ARG:NH1	2.46	0.47
5:VH:168:VAL:HA	5:VH:240:THR:O	2.14	0.47
5:VH:262:ASN:OD1	5:VH:262:ASN:N	2.42	0.47
8:AM:177:LEU:HD13	8:AM:181:PRO:HG2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:AN:87:TRP:O	9:AN:88:HIS:ND1	2.48	0.47
4:Ad:127:SER:HB3	4:Ad:130:GLU:HG3	1.97	0.47
4:Ad:150:ASN:O	4:Ad:152:GLN:NE2	2.48	0.47
7:BL:109:LEU:HD12	7:BL:114:ILE:HG13	1.97	0.47
2:GC:188:ILE:O	2:GC:192:ASN:ND2	2.38	0.47
2:IC:177:TRP:O	2:IC:181:THR:OG1	2.28	0.47
2:MC:41:SER:O	2:MC:44:THR:OG1	2.30	0.47
6:CK:127:LYS:HZ2	6:CK:127:LYS:H	1.62	0.47
7:CL:165:VAL:HG12	7:CL:231:ILE:HG12	1.96	0.47
1:GG:947:ARG:O	1:GG:950:HIS:NE2	2.48	0.47
5:DH:178:SER:OG	5:DH:250:TYR:O	2.32	0.47
9:DN:89:GLY:HA3	9:DN:104:ASN:HB2	1.97	0.47
8:EM:199:LYS:HA	8:EM:219:ALA:HB3	1.96	0.47
5:FH:201:SER:HA	5:FH:219:LYS:HG3	1.97	0.47
1:OG:921:ILE:O	1:OG:926:LYS:NZ	2.47	0.47
2:HC:112:LEU:O	2:HC:133:TYR:HA	2.15	0.47
2:LC:176:ILE:HA	2:LC:179:ILE:HG12	1.95	0.47
2:BC:171:GLU:HA	2:BC:174:ILE:HG12	1.97	0.47
7:GL:115:GLN:HB3	7:GL:126:ILE:HB	1.97	0.47
4:HD:36:ASP:OD1	2:CC:75:ARG:NH2	2.48	0.47
1:BG:889:ILE:HB	1:BG:897:SER:HB2	1.96	0.47
6:IK:92:ASN:O	6:IK:95:SER:OG	2.29	0.47
3:If:212:ILE:HD11	3:If:215:VAL:HB	1.96	0.47
3:If:251:GLN:HG3	3:If:253:ARG:HH11	1.79	0.47
1:CG:955:ARG:NH1	1:CG:1023:PHE:O	2.39	0.47
3:LF:233:ARG:NH1	3:LF:235:GLY:O	2.48	0.47
4:MD:147:VAL:HG22	4:MD:154:VAL:HG22	1.96	0.47
5:VH:203:ASN:OD1	5:VH:203:ASN:N	2.47	0.47
5:WH:105:GLU:O	5:WH:109:LYS:NZ	2.42	0.47
5:WH:294:ARG:HH12	5:WH:303:ARG:HE	1.62	0.47
1:EG:912:MET:HB3	1:EG:944:LEU:HB2	1.95	0.47
8:AM:284:LEU:HD12	8:AM:310:LYS:HG3	1.97	0.47
4:BD:87:TRP:HD1	4:BD:89:GLY:H	1.62	0.47
1:FG:965:LEU:HD12	1:FG:1008:LEU:HD13	1.96	0.47
2:KC:79:ILE:HD13	2:KC:79:ILE:HA	1.79	0.47
2:KC:258:ASN:O	2:KC:262:TRP:NE1	2.34	0.47
5:CH:289:PRO:O	5:CH:292:SER:OG	2.31	0.47
1:LG:965:LEU:HD12	1:LG:1008:LEU:HD13	1.96	0.47
1:MG:897:SER:HA	1:MG:920:SER:O	2.15	0.47
1:NG:958:SER:O	1:NG:962:SER:OG	2.33	0.47
1:PG:946:SER:OG	1:PG:1030:GLU:O	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Hg:797:ARG:NH2	5:XH:121:PRO:O	2.47	0.47
8:HM:303:GLU:OE2	8:HM:306:GLN:N	2.48	0.47
9:HN:87:TRP:HA	2:CC:148:ARG:HH21	1.80	0.47
1:Ig:794:ILE:O	1:Ig:798:THR:OG1	2.31	0.47
7:IL:127:ILE:HB	7:IL:229:ILE:HG23	1.96	0.47
6:JK:57:MET:HE2	6:JK:57:MET:HB2	1.80	0.47
5:KH:115:MET:HE3	5:KH:115:MET:HB3	1.76	0.47
6:KK:124:VAL:HG12	6:KK:125:SER:HB3	1.96	0.47
5:VH:328:MET:HE3	5:CH:267:PRO:HB2	1.97	0.47
3:WF:213:GLN:OE1	3:WF:229:THR:OG1	2.32	0.47
5:ZH:253:ASP:OD1	5:ZH:253:ASP:N	2.48	0.47
9:AN:84:CYS:SG	9:AN:85:CYS:N	2.86	0.47
8:CM:275:ASP:HB3	8:CM:294:PHE:HB2	1.96	0.47
3:DF:226:ASN:ND2	3:DF:228:SER:OG	2.48	0.47
1:GG:1033:SER:OG	1:HG:941:ARG:NH1	2.48	0.47
7:DL:216:ASP:N	7:DL:216:ASP:OD1	2.47	0.47
9:EN:109:SER:OG	9:EN:111:GLU:OE1	2.26	0.47
5:FH:332:ASP:N	5:FH:332:ASP:OD1	2.45	0.47
1:MG:878:ASN:HA	1:MG:1030:GLU:HA	1.96	0.47
1:MG:890:VAL:HG23	1:MG:891:THR:HG22	1.97	0.47
1:NG:1044:ASP:N	1:NG:1044:ASP:OD1	2.48	0.47
3:Ff:211:TYR:N	3:Ff:223:ILE:O	2.43	0.47
2:BC:105:LEU:HD12	2:BC:106:PRO:HD2	1.97	0.46
2:EC:126:ARG:HD3	5:JH:275:SER:HA	1.97	0.46
6:GK:121:SER:OG	6:GK:122:LYS:N	2.47	0.46
1:Ig:801:MET:HB3	5:JH:121:PRO:HB2	1.97	0.46
5:IH:307:SER:OG	5:IH:308:ASN:N	2.48	0.46
8:IM:141:GLU:OE2	8:IM:143:THR:OG1	2.27	0.46
6:JK:129:GLU:OE1	6:JK:129:GLU:N	2.47	0.46
5:AH:205:GLN:HB2	5:AH:214:MET:HE3	1.97	0.46
4:KD:59:GLU:OE2	4:KD:63:THR:OG1	2.30	0.46
8:LM:245:TYR:HB3	3:Lf:215:VAL:HG13	1.97	0.46
4:MD:36:ASP:HA	4:MD:39:ILE:HD12	1.96	0.46
7:ML:102:LYS:NZ	7:ML:158:TYR:OH	2.46	0.46
8:MM:190:ASN:OD1	8:MM:192:ARG:NH2	2.48	0.46
1:VG:823:GLY:HA3	5:CH:206:TRP:HH2	1.80	0.46
5:WH:202:PHE:HB3	5:WH:215:ILE:HD11	1.97	0.46
1:FG:921:ILE:HD12	1:FG:926:LYS:HD2	1.96	0.46
3:Bf:210:TYR:HA	3:Bf:224:GLY:HA2	1.97	0.46
2:GC:109:VAL:HG23	2:GC:136:LYS:H	1.80	0.46
6:CK:39:PRO:HG2	6:CK:40:LYS:HD3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:CL:102:LYS:HE3	7:CL:102:LYS:HB2	1.75	0.46
3:Ef:243:MET:O	3:Ef:257:SER:N	2.48	0.46
1:JG:1024:ASN:OD1	1:JG:1024:ASN:N	2.35	0.46
1:NG:885:ILE:HD11	1:NG:914:ILE:HG23	1.96	0.46
9:FN:39:ASP:N	9:FN:39:ASP:OD1	2.48	0.46
1:AG:868:ILE:HA	1:AG:1039:ILE:O	2.15	0.46
6:GK:76:ILE:HD12	6:GK:102:ILE:HD11	1.97	0.46
1:BG:1003:ASN:HA	1:BG:1006:ILE:HD12	1.95	0.46
5:IH:229:ARG:NH1	5:JH:212:THR:OG1	2.48	0.46
1:Jg:813:LYS:HE2	1:Jg:813:LYS:HB2	1.65	0.46
8:JM:257:ASP:OD1	8:JM:257:ASP:N	2.48	0.46
9:JN:77:ASP:OD1	9:JN:79:GLN:NE2	2.44	0.46
1:DG:910:ASP:OD1	1:DG:910:ASP:N	2.47	0.46
1:DG:946:SER:OG	1:DG:1030:GLU:O	2.29	0.46
1:Cg:818:GLN:NE2	5:CH:205:GLN:OE1	2.48	0.46
8:MM:210:ASP:O	8:MM:230:ARG:N	2.48	0.46
5:WH:189:TRP:HE1	5:WH:232:GLY:H	1.62	0.46
5:XH:183:ASP:HB2	5:XH:259:TYR:HA	1.97	0.46
5:ZH:201:SER:O	5:ZH:218:THR:N	2.46	0.46
8:AM:144:THR:O	8:AM:145:ARG:NE	2.46	0.46
5:BH:275:SER:OG	5:BH:276:ALA:N	2.48	0.46
1:FG:912:MET:HB3	1:FG:944:LEU:HB2	1.96	0.46
1:FG:966:GLN:O	1:FG:970:ASN:ND2	2.48	0.46
3:DF:244:VAL:HG22	3:DF:256:THR:HG22	1.97	0.46
5:DH:262:ASN:OD1	5:DH:262:ASN:N	2.40	0.46
4:Ed:150:ASN:OD1	4:Ed:150:ASN:N	2.44	0.46
1:NG:966:GLN:O	1:NG:970:ASN:ND2	2.49	0.46
1:PG:877:VAL:H	1:PG:1031:VAL:HG22	1.80	0.46
2:EC:121:ASP:N	2:EC:121:ASP:OD1	2.47	0.46
2:EC:169:THR:O	2:EC:173:LYS:HB2	2.14	0.46
8:JM:300:ASP:OD2	8:JM:302:ARG:NH2	2.49	0.46
5:AH:181:PHE:O	5:AH:211:ASN:ND2	2.48	0.46
3:KF:265:SER:HB3	3:KF:268:ASP:HB3	1.96	0.46
6:LK:162:ASP:OD1	6:LK:162:ASP:N	2.46	0.46
6:MK:125:SER:HG	6:MK:128:ARG:H	1.64	0.46
5:XH:106:VAL:HA	5:XH:109:LYS:HE2	1.97	0.46
3:YF:208:ILE:HD11	3:YF:224:GLY:HA3	1.98	0.46
4:Ad:35:ASP:O	4:Ad:38:THR:OG1	2.30	0.46
5:BH:341:LYS:HD2	5:BH:361:LEU:HD11	1.96	0.46
6:BK:104:ALA:HA	6:BK:107:LYS:HZ3	1.81	0.46
1:FG:1033:SER:OG	1:GG:941:ARG:NH1	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:IC:248:LEU:HB2	2:JC:124:ILE:HG13	1.97	0.46
3:DF:207:ARG:NH2	3:DF:239:PRO:O	2.48	0.46
8:EM:288:ARG:O	8:EM:318:GLN:NE2	2.42	0.46
1:HG:966:GLN:O	1:HG:970:ASN:ND2	2.48	0.46
8:HM:292:MET:SD	8:HM:292:MET:N	2.88	0.46
8:IM:165:ILE:HB	8:IM:185:ILE:HG23	1.97	0.46
5:JH:284:LEU:HD11	5:JH:330:SER:HB3	1.98	0.46
1:CG:950:HIS:ND1	1:CG:1028:THR:O	2.48	0.46
5:AH:205:GLN:NE2	1:Ag:818:GLN:O	2.49	0.46
3:KF:218:GLY:HA3	5:YH:148:PRO:HG2	1.97	0.46
5:MH:168:VAL:HG12	5:MH:240:THR:HG23	1.97	0.46
8:MM:228:VAL:HG11	8:MM:231:LEU:HB2	1.98	0.46
1:EG:1003:ASN:HA	1:EG:1006:ILE:HD12	1.97	0.46
5:XH:330:SER:OG	5:XH:332:ASP:OD1	2.28	0.46
7:AL:170:ASP:N	7:AL:170:ASP:OD1	2.40	0.46
2:DC:227:VAL:HA	2:DC:250:ILE:HA	1.97	0.46
1:FG:876:SER:HB3	1:GG:941:ARG:HG2	1.96	0.46
5:CH:343:PRO:HG2	5:CH:344:VAL:HG12	1.97	0.46
1:GG:939:THR:HG22	1:GG:941:ARG:HG3	1.97	0.46
5:DH:191:ILE:HG13	5:DH:211:ASN:HA	1.97	0.46
4:ED:124:LYS:HA	4:ED:124:LYS:HD3	1.83	0.46
5:EH:230:LEU:HD12	5:EH:233:LEU:HD23	1.98	0.46
6:EK:164:PRO:HA	6:EK:177:ASN:HD21	1.80	0.46
7:EL:44:HIS:N	7:EL:48:ASN:OD1	2.45	0.46
6:FK:165:ILE:HG13	6:FK:166:THR:HG22	1.98	0.46
1:JG:999:SER:OG	1:JG:1000:THR:N	2.46	0.46
2:BC:100:LEU:HB2	2:BC:104:ILE:HG23	1.97	0.46
2:EC:172:GLU:HA	2:EC:175:ILE:HG12	1.97	0.46
5:GH:113:LYS:HG3	5:GH:117:ARG:HH12	1.81	0.46
4:Hd:148:TYR:HB2	4:Hd:153:VAL:HG12	1.97	0.46
9:JN:100:LEU:H	9:JN:100:LEU:HG	1.56	0.46
1:Kg:802:LEU:HG	5:LH:115:MET:HB2	1.98	0.46
1:Lg:806:THR:H	1:Lg:806:THR:HG1	1.47	0.46
5:LH:278:ASP:OD1	5:LH:278:ASP:N	2.46	0.46
9:MN:54:SER:OG	9:MN:55:ALA:N	2.48	0.46
5:YH:292:SER:HB3	5:YH:307:SER:HB2	1.97	0.46
3:CF:253:ARG:HG3	3:CF:261:VAL:HG13	1.97	0.46
7:BL:57:VAL:HA	7:BL:60:VAL:HG22	1.98	0.46
1:GG:1006:ILE:O	1:GG:1010:THR:OG1	2.34	0.46
5:FH:189:TRP:HE1	5:FH:232:GLY:HA3	1.81	0.46
1:IG:959:LEU:O	1:IG:963:SER:OG	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:KG:966:GLN:O	1:KG:970:ASN:ND2	2.49	0.46
1:OG:958:SER:O	1:OG:962:SER:OG	2.33	0.46
7:FL:44:HIS:N	7:FL:48:ASN:OD1	2.46	0.46
5:HH:168:VAL:HA	5:HH:240:THR:O	2.15	0.46
1:BG:1042:THR:OG1	1:BG:1043:GLN:OE1	2.28	0.46
4:Dd:148:TYR:HB2	4:Dd:153:VAL:HG12	1.98	0.46
3:JF:263:LYS:NZ	3:JF:266:GLN:OE1	2.48	0.46
6:KK:133:THR:HG21	6:KK:160:GLY:H	1.81	0.46
4:Kd:79:LEU:O	4:Kd:127:SER:OG	2.33	0.46
8:LM:215:ARG:NH1	8:LM:232:ASP:OD2	2.45	0.46
9:LN:85:CYS:N	2:GC:154:ASP:OD2	2.47	0.46
1:DG:917:ASN:HA	1:DG:931:SER:HA	1.98	0.46
1:Cg:794:ILE:HD12	5:DH:110:LYS:HD2	1.97	0.46
5:WH:159:ASN:OD1	5:WH:161:SER:OG	2.26	0.46
5:YH:157:PHE:HA	5:YH:255:ARG:HB2	1.97	0.46
2:DC:92:ASP:OD1	2:DC:148:TRP:NE1	2.40	0.46
11:BX:20:UNK:O	11:BX:37:UNK:N	2.49	0.46
6:CK:109:PHE:O	6:CK:111:LYS:NZ	2.41	0.46
6:CK:117:THR:HA	6:CK:157:GLN:O	2.16	0.46
7:CL:169:THR:OG1	7:CL:170:ASP:N	2.47	0.46
8:CM:271:SER:OG	8:CM:290:ASP:OD1	2.33	0.46
7:DL:91:VAL:HA	7:DL:94:VAL:HG12	1.97	0.46
5:EH:289:PRO:O	5:EH:292:SER:OG	2.34	0.46
4:FD:132:LEU:HD12	4:FD:145:ILE:HG21	1.97	0.46
1:NG:935:ILE:HG23	1:NG:1040:LEU:HD22	1.97	0.46
8:FM:129:LEU:H	8:FM:148:GLY:HA3	1.80	0.46
5:GH:357:LYS:HE2	5:GH:359:GLU:HB3	1.97	0.46
5:HH:230:LEU:HD22	5:HH:233:LEU:HD12	1.98	0.46
5:HH:339:MET:HB2	5:HH:339:MET:HE3	1.81	0.46
8:HM:159:GLY:HA2	8:HM:181:PRO:HG3	1.98	0.46
9:HN:45:MET:HE2	9:HN:45:MET:HB2	1.75	0.46
5:IH:198:ASP:OD1	5:IH:200:SER:OG	2.26	0.46
7:JL:102:LYS:HB2	7:JL:102:LYS:HE3	1.80	0.46
1:CG:867:ASP:OD1	1:CG:867:ASP:N	2.43	0.46
6:KK:125:SER:OG	6:KK:127:LYS:N	2.48	0.46
5:MH:345:LEU:HD12	5:MH:345:LEU:HA	1.80	0.46
5:WH:173:GLN:NE2	5:WH:218:THR:O	2.47	0.46
5:WH:204:ILE:HG12	5:WH:215:ILE:HD13	1.98	0.46
3:XF:220:ALA:HB3	3:XF:232:VAL:HG23	1.97	0.46
7:AL:118:GLU:OE2	7:AL:123:ARG:NH2	2.48	0.46
5:ZH:292:SER:HB3	5:ZH:307:SER:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FG:1003:ASN:HA	1:FG:1006:ILE:HD12	1.98	0.46
2:KC:228:HIS:HB3	2:KC:247:LEU:HD13	1.98	0.46
2:KC:261:GLU:OE1	2:KC:261:GLU:N	2.49	0.46
2:MC:122:ASP:OD1	2:MC:122:ASP:N	2.48	0.46
3:EF:220:ALA:O	3:EF:231:THR:HA	2.15	0.46
6:EK:38:VAL:HA	6:EK:41:LEU:HB2	1.97	0.46
3:FF:258:SER:HG	3:FF:260:GLN:CD	2.23	0.46
8:FM:271:SER:OG	8:FM:290:ASP:OD1	2.32	0.46
8:HM:196:MET:HE3	8:HM:202:LEU:HD11	1.98	0.46
1:BG:939:THR:HB	1:BG:941:ARG:HG3	1.97	0.46
5:IH:313:VAL:HG13	5:IH:337:TYR:HB2	1.98	0.46
3:If:220:ALA:HB3	3:If:232:VAL:HG13	1.97	0.46
1:Jg:794:ILE:H	1:Jg:794:ILE:HG12	1.54	0.46
1:CG:1011:VAL:HG12	1:DG:963:SER:HB3	1.98	0.46
5:KH:267:PRO:HB2	5:YH:328:MET:HE1	1.97	0.46
11:LX:20:UNK:N	11:LX:37:UNK:O	2.47	0.46
6:AK:65:ILE:HD12	6:AK:78:ILE:HG12	1.98	0.46
8:MM:143:THR:HG22	8:MM:145:ARG:HH12	1.81	0.46
3:VF:231:THR:HG23	5:DH:150:LYS:HE3	1.98	0.46
2:MC:58:MET:HA	2:MC:61:LYS:HG2	1.98	0.46
5:CH:123:ASN:OD1	5:CH:123:ASN:N	2.48	0.46
9:CN:88:HIS:ND1	9:CN:105:ASP:OD2	2.45	0.46
5:FH:169:ILE:HG12	5:FH:179:LEU:HD21	1.96	0.46
1:JG:924:ALA:HB3	1:JG:926:LYS:HE3	1.98	0.46
1:JG:969:GLY:HA3	1:JG:1009:ALA:HB2	1.97	0.46
1:PG:899:LEU:HA	1:PG:918:THR:O	2.15	0.46
9:FN:86:LEU:HB3	9:FN:87:TRP:CD1	2.51	0.46
3:GF:243:MET:N	3:GF:257:SER:OG	2.46	0.46
5:JH:173:GLN:HG3	5:JH:220:LEU:HD13	1.98	0.46
6:KK:50:ASP:HB3	9:KN:45:MET:HE3	1.98	0.46
7:KL:190:MET:HE3	7:KL:190:MET:HB3	1.73	0.46
8:MM:155:LEU:HB3	8:MM:175:ILE:HD13	1.97	0.46
5:YH:149:PRO:HA	5:YH:246:LYS:O	2.15	0.46
3:Df:220:ALA:HB3	3:Df:232:VAL:HB	1.98	0.46
5:ZH:280:LEU:HB3	5:ZH:328:MET:HG3	1.97	0.46
5:BH:225:ASN:OD1	5:BH:225:ASN:N	2.49	0.46
8:BM:173:LEU:HD12	8:BM:189:VAL:HG13	1.97	0.46
2:GC:121:ASP:OD1	2:GC:121:ASP:N	2.49	0.46
2:JC:220:VAL:HG22	2:JC:254:LEU:HD23	1.98	0.46
5:DH:115:MET:HB2	5:DH:115:MET:HE3	1.66	0.46
8:EM:284:LEU:HD12	8:EM:310:LYS:HG3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:FD:87:TRP:CD1	4:FD:89:GLY:H	2.33	0.46
1:LG:912:MET:HB3	1:LG:944:LEU:HB2	1.98	0.46
4:GD:87:TRP:CD1	4:GD:89:GLY:H	2.34	0.46
3:Hf:246:LEU:HD21	3:Hf:255:LEU:HD12	1.98	0.46
8:IM:308:ASP:N	8:IM:308:ASP:OD1	2.49	0.46
9:IN:62:ASN:OD1	9:IN:62:ASN:N	2.42	0.46
8:JM:252:PHE:HD1	8:JM:270:SER:HB3	1.81	0.46
4:Kd:88:SER:HA	4:Kd:120:SER:HA	1.98	0.46
7:LL:151:VAL:O	7:LL:155:LEU:HB2	2.16	0.46
7:LL:221:HIS:CE1	7:LL:225:GLN:HE21	2.34	0.46
8:LM:144:THR:O	8:LM:145:ARG:NE	2.46	0.46
8:MM:183:VAL:O	8:MM:202:LEU:HA	2.16	0.46
8:MM:276:ALA:H	8:MM:295:ASN:HB2	1.79	0.46
5:WH:339:MET:N	5:WH:339:MET:SD	2.89	0.46
3:Df:246:LEU:HB3	3:Df:255:LEU:HD21	1.97	0.46
5:ZH:160:LEU:HD13	5:ZH:257:GLN:HB2	1.98	0.46
2:GC:228:HIS:HB3	2:GC:247:LEU:HD13	1.97	0.46
2:JC:120:ASP:OD1	2:JC:123:SER:OG	2.30	0.46
8:CM:117:ARG:HA	8:CM:137:TYR:O	2.16	0.46
5:DH:296:VAL:HB	5:DH:359:GLU:HB2	1.98	0.46
4:ED:158:TYR:O	4:Ed:137:TYR:OH	2.32	0.46
1:HG:869:MET:HB2	1:HG:869:MET:HE3	1.81	0.46
1:LG:898:LYS:HZ1	1:LG:920:SER:HB3	1.80	0.46
7:FL:109:LEU:HD12	7:FL:114:ILE:HG13	1.98	0.46
9:FN:42:CYS:HB2	9:FN:48:ILE:HD13	1.97	0.46
5:GH:307:SER:OG	5:GH:308:ASN:N	2.49	0.45
7:GL:109:LEU:HD13	7:GL:109:LEU:HA	1.83	0.45
3:Gf:216:ILE:HD12	3:Gf:216:ILE:HA	1.84	0.45
5:HH:184:SER:OG	5:HH:257:GLN:O	2.35	0.45
6:HK:116:VAL:HG13	6:HK:182:ILE:HG23	1.98	0.45
8:HM:308:ASP:N	8:HM:308:ASP:OD1	2.49	0.45
5:IH:253:ASP:OD1	5:IH:253:ASP:N	2.49	0.45
6:IK:59:ASP:HA	6:IK:62:LYS:HG2	1.98	0.45
2:CC:136:LYS:NZ	2:CC:205:ASP:OD2	2.41	0.45
2:CC:225:TYR:H	2:CC:251:ALA:HB3	1.80	0.45
5:WH:106:VAL:HA	5:WH:109:LYS:HE2	1.98	0.45
1:EG:876:SER:O	1:FG:942:THR:OG1	2.33	0.45
4:Ad:72:THR:OG1	4:Ad:73:ILE:N	2.49	0.45
4:BD:52:MET:HE2	4:Bd:52:MET:HG2	1.97	0.45
2:JC:169:LYS:HA	2:JC:172:LYS:HE2	1.97	0.45
2:JC:244:ARG:HB2	2:KC:127:ILE:HG23	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:CH:190:PRO:HB2	5:CH:231:ARG:HG3	1.98	0.45
8:CM:209:SER:OG	8:CM:210:ASP:N	2.48	0.45
3:EF:208:ILE:HG13	3:EF:225:SER:H	1.81	0.45
1:HG:898:LYS:HE2	1:HG:898:LYS:HB2	1.81	0.45
1:AG:966:GLN:O	1:AG:970:ASN:ND2	2.49	0.45
5:HH:151:PRO:HA	5:HH:248:VAL:HG13	1.98	0.45
7:HL:97:ILE:HD12	7:HL:97:ILE:HA	1.87	0.45
9:IN:88:HIS:ND1	9:IN:105:ASP:OD2	2.40	0.45
4:Id:68:ASP:OD1	4:Id:68:ASP:N	2.49	0.45
1:CG:939:THR:HG22	1:CG:941:ARG:HG3	1.98	0.45
4:LD:142:LYS:O	4:LD:159:ALA:HB2	2.17	0.45
7:LL:51:GLN:HE21	7:LL:51:GLN:HB2	1.60	0.45
7:LL:133:PHE:HE1	7:LL:138:PRO:HA	1.81	0.45
3:MF:214:ALA:HB3	3:MF:221:TRP:HB2	1.99	0.45
6:MK:87:GLN:N	6:MK:173:ASP:OD2	2.42	0.45
2:DC:260:SER:HA	2:DC:263:TRP:CE2	2.50	0.45
8:AM:275:ASP:HB3	8:AM:294:PHE:HB2	1.99	0.45
8:BM:128:ASN:HB3	8:BM:130:ARG:HH12	1.82	0.45
8:DM:254:LYS:HE2	8:DM:272:LEU:HD23	1.98	0.45
5:EH:297:VAL:HG22	5:EH:358:VAL:HG22	1.98	0.45
5:FH:166:PRO:HA	5:FH:167:PRO:HD3	1.83	0.45
6:FK:90:ARG:HD3	8:FM:292:MET:HB2	1.97	0.45
1:PG:889:ILE:H	1:PG:889:ILE:HG12	1.53	0.45
3:Ff:223:ILE:HD12	3:Ff:223:ILE:HA	1.85	0.45
5:GH:230:LEU:HD12	5:GH:233:LEU:HD21	1.97	0.45
5:GH:304:ALA:HA	5:GH:312:TYR:O	2.16	0.45
7:GL:210:ASP:OD1	7:GL:210:ASP:N	2.44	0.45
6:HK:99:LEU:HD13	6:HK:99:LEU:HA	1.83	0.45
5:IH:168:VAL:HG13	5:IH:242:ILE:HD13	1.98	0.45
6:JK:107:LYS:HB3	6:JK:149:VAL:HG12	1.98	0.45
4:Jd:105:ARG:HB2	4:Jd:153:VAL:HG23	1.98	0.45
5:AH:176:VAL:H	5:ZH:225:ASN:HD21	1.64	0.45
6:KK:49:CYS:O	6:KK:52:THR:OG1	2.31	0.45
5:LH:114:ASP:OD1	5:LH:117:ARG:NH2	2.41	0.45
1:DG:947:ARG:HE	1:DG:947:ARG:H	1.64	0.45
1:Cg:807:GLN:O	1:Cg:810:GLN:NE2	2.39	0.45
5:MH:179:LEU:HD22	5:MH:213:LEU:HD12	1.97	0.45
5:MH:225:ASN:HD21	5:ZH:176:VAL:H	1.65	0.45
5:VH:192:ALA:HB2	5:VH:231:ARG:HA	1.99	0.45
3:XF:210:TYR:HB3	3:XF:222:LEU:HB3	1.98	0.45
5:YH:294:ARG:HE	5:YH:305:TRP:HE1	1.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:ZH:167:PRO:HD2	5:ZH:239:LEU:HD12	1.98	0.45
3:Bf:251:GLN:OE1	3:Bf:253:ARG:NE	2.49	0.45
3:Cf:248:ASP:OD1	3:Cf:248:ASP:N	2.47	0.45
7:DL:102:LYS:HB2	7:DL:102:LYS:HE3	1.76	0.45
1:Eg:801:MET:O	1:Eg:805:ALA:N	2.48	0.45
6:EK:66:LYS:HB3	6:EK:77:SER:HB3	1.98	0.45
6:EK:90:ARG:HG3	8:EM:292:MET:HE2	1.98	0.45
7:EL:201:LYS:HE2	7:EL:201:LYS:HB2	1.88	0.45
4:Ed:86:ASP:OD1	2:AC:129:ARG:NH2	2.50	0.45
6:FK:76:ILE:HG13	6:FK:182:ILE:HB	1.99	0.45
6:FK:179:ARG:NE	6:FK:181:GLU:OE2	2.49	0.45
1:IG:951:HIS:O	1:IG:955:ARG:NE	2.48	0.45
2:AC:111:GLU:HB3	2:AC:210:LEU:HD21	1.99	0.45
8:GM:240:GLN:HB3	8:GM:242:LYS:HE3	1.97	0.45
6:HK:142:GLU:OE2	7:HL:139:ARG:NH1	2.50	0.45
4:Dd:149:PRO:O	4:Dd:152:GLN:NE2	2.44	0.45
3:If:210:TYR:HA	3:If:224:GLY:HA2	1.98	0.45
7:JL:185:GLN:HG2	7:JL:229:ILE:HD11	1.98	0.45
5:AH:207:ASP:OD1	5:AH:207:ASP:N	2.48	0.45
4:LD:67:LYS:HB3	4:Ld:62:ILE:HD11	1.99	0.45
1:Lg:824:THR:H	5:YH:208:LYS:HB3	1.80	0.45
8:LM:200:GLY:O	8:LM:220:ALA:HA	2.17	0.45
5:YH:130:LEU:HA	5:YH:133:ILE:HG22	1.99	0.45
5:YH:189:TRP:HE1	5:YH:232:GLY:H	1.62	0.45
1:ZG:795:GLN:OE1	1:ZG:795:GLN:N	2.49	0.45
8:AM:310:LYS:HB2	8:AM:310:LYS:HE3	1.82	0.45
1:FG:931:SER:O	1:FG:1042:THR:OG1	2.34	0.45
4:Cd:107:ARG:HE	4:Cd:155:GLU:HB2	1.80	0.45
7:EL:173:GLY:O	7:EL:178:LYS:NZ	2.49	0.45
8:EM:203:SER:HA	8:EM:223:GLN:O	2.16	0.45
4:GD:55:MET:HE1	4:Gd:55:MET:HE2	1.99	0.45
7:GL:229:ILE:HD13	7:GL:229:ILE:HA	1.85	0.45
3:HF:241:TYR:O	3:HF:258:SER:OG	2.34	0.45
5:HH:160:LEU:HD13	5:HH:257:GLN:HG3	1.99	0.45
6:IK:89:PRO:HD2	8:IM:297:SER:HB3	1.98	0.45
8:IM:210:ASP:O	8:IM:230:ARG:N	2.45	0.45
4:JD:148:TYR:HB2	4:JD:153:VAL:HB	1.99	0.45
6:JK:66:LYS:HB3	6:JK:77:SER:HB3	1.98	0.45
7:JL:99:ARG:HA	7:JL:104:LYS:HG2	1.98	0.45
1:CG:865:THR:OG1	1:CG:1044:ASP:OD2	2.30	0.45
4:LD:160:LYS:NZ	4:LD:162:TYR:O	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:ML:113:ASP:OD2	7:ML:131:LYS:NZ	2.42	0.45
3:Mf:220:ALA:HB3	3:Mf:232:VAL:HG13	1.98	0.45
1:EG:965:LEU:HG	1:EG:1008:LEU:HD22	1.99	0.45
3:ZF:246:LEU:HB2	3:ZF:255:LEU:HB2	1.99	0.45
5:BH:172:SER:OG	5:BH:173:GLN:N	2.49	0.45
5:BH:306:LEU:HD11	5:BH:309:GLU:HA	1.97	0.45
7:BL:125:LEU:HD13	7:BL:125:LEU:HA	1.86	0.45
7:BL:165:VAL:HG23	7:BL:205:ALA:HA	1.99	0.45
2:FC:110:LEU:HD13	2:FC:110:LEU:HA	1.82	0.45
5:CH:151:PRO:HA	5:CH:248:VAL:HG23	1.99	0.45
3:Ef:216:ILE:HD12	3:Ef:216:ILE:HA	1.83	0.45
2:AC:214:LEU:HD22	2:AC:219:MET:HG3	1.98	0.45
2:EC:91:ASP:OD1	2:EC:91:ASP:N	2.48	0.45
4:GD:160:LYS:HD2	4:GD:160:LYS:HA	1.79	0.45
8:GM:271:SER:OG	8:GM:290:ASP:OD1	2.34	0.45
5:IH:151:PRO:HA	5:IH:248:VAL:HG13	1.98	0.45
5:IH:183:ASP:OD1	5:IH:187:ALA:N	2.46	0.45
6:IK:177:ASN:OD1	6:IK:177:ASN:N	2.49	0.45
1:CG:880:ASP:OD1	1:CG:880:ASP:N	2.48	0.45
7:KL:63:ASP:O	7:KL:88:GLY:N	2.50	0.45
7:KL:178:LYS:O	7:KL:182:SER:OG	2.33	0.45
3:LF:215:VAL:H	5:LH:245:GLN:HE22	1.65	0.45
1:Mg:802:LEU:O	1:Mg:806:THR:OG1	2.28	0.45
5:MH:168:VAL:HA	5:MH:240:THR:O	2.15	0.45
4:Md:148:TYR:HB2	4:Md:153:VAL:HG12	1.97	0.45
5:WH:179:LEU:O	5:WH:212:THR:HA	2.16	0.45
5:ZH:320:LEU:HD11	2:GC:251:ALA:HB2	1.99	0.45
4:BD:161:ILE:HD12	4:BD:161:ILE:HA	1.84	0.45
4:Bd:55:MET:HE2	2:JC:212:ARG:HH11	1.82	0.45
2:KC:243:ASP:O	2:LC:129:SER:OG	2.32	0.45
3:Ef:245:LYS:HE3	3:Ef:257:SER:HA	1.98	0.45
5:FH:251:ARG:NE	5:FH:253:ASP:OD1	2.49	0.45
1:HG:886:LEU:HB3	1:HG:900:ILE:HG23	1.97	0.45
1:HG:1042:THR:OG1	1:HG:1043:GLN:OE1	2.25	0.45
1:IG:947:ARG:O	1:IG:950:HIS:NE2	2.50	0.45
1:NG:944:LEU:HD11	1:NG:1031:VAL:HA	1.97	0.45
8:FM:209:SER:OG	8:FM:210:ASP:N	2.49	0.45
2:LC:107:LEU:HD12	2:LC:108:PRO:HD2	1.97	0.45
1:AG:1019:ALA:HA	1:AG:1022:LEU:HG	1.98	0.45
4:HD:29:PRO:HG2	7:HL:225:GLN:HA	1.97	0.45
8:JM:191:LEU:HB3	8:JM:212:LEU:HD11	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:JM:275:ASP:HA	8:JM:295:ASN:H	1.82	0.45
5:AH:225:ASN:HD21	5:BH:176:VAL:H	1.64	0.45
4:KD:87:TRP:CD1	4:KD:94:LEU:HD22	2.52	0.45
4:Kd:148:TYR:HB2	4:Kd:153:VAL:HG12	1.98	0.45
6:MK:111:LYS:HD3	6:MK:114:ILE:HD11	1.99	0.45
3:VF:215:VAL:O	5:VH:245:GLN:NE2	2.50	0.45
5:WH:238:MET:N	5:WH:238:MET:SD	2.90	0.45
3:Df:209:ILE:HB	3:Df:225:SER:HB3	1.99	0.45
4:Ad:81:ALA:HB3	4:Ad:128:LEU:HD11	1.98	0.45
1:FG:886:LEU:HD21	1:GG:1040:LEU:HB2	1.98	0.45
4:AD:36:ASP:HA	4:AD:39:ILE:HD12	1.98	0.45
3:Cf:220:ALA:HB2	3:Cf:247:ILE:HD12	1.98	0.45
6:DK:76:ILE:HB	6:DK:182:ILE:HG13	1.98	0.45
8:EM:313:ASP:OD1	8:EM:314:ARG:N	2.49	0.45
1:NG:893:LYS:HD2	1:NG:893:LYS:HA	1.81	0.45
8:FM:159:GLY:HA2	8:FM:181:PRO:HG3	1.99	0.45
8:FM:172:ASN:HA	8:FM:192:ARG:HH21	1.82	0.45
8:FM:196:MET:HE1	8:FM:219:ALA:H	1.82	0.45
2:AC:174:ILE:HA	2:AC:177:ILE:HG12	1.98	0.45
2:BC:74:ARG:HB2	2:BC:187:ILE:HD13	1.99	0.45
8:HM:224:LEU:HB2	8:HM:246:LEU:HD22	1.98	0.45
9:JN:96:ASN:OD1	9:JN:98:SER:OG	2.26	0.45
4:Jd:148:TYR:HB2	4:Jd:153:VAL:HG12	1.99	0.45
4:KD:29:PRO:HG2	7:KL:225:GLN:HA	1.99	0.45
6:KK:90:ARG:HD3	8:KM:292:MET:HB2	1.99	0.45
9:KN:94:GLN:NE2	9:KN:95:LEU:O	2.41	0.45
3:LF:209:ILE:O	3:LF:225:SER:N	2.49	0.45
6:LK:91:LEU:HD12	6:LK:91:LEU:HA	1.83	0.45
4:MD:130:GLU:OE2	4:MD:133:ARG:NH1	2.49	0.45
1:EG:969:GLY:HA3	1:EG:1009:ALA:HB2	1.98	0.45
1:EG:1011:VAL:HG12	1:FG:963:SER:HB3	1.98	0.45
4:Ad:141:LYS:HB2	4:Ad:141:LYS:HE3	1.76	0.45
6:BK:76:ILE:HB	6:BK:182:ILE:HG13	1.99	0.45
1:FG:1024:ASN:OD1	1:FG:1024:ASN:N	2.40	0.45
4:Bd:79:LEU:HA	4:Bd:128:LEU:HD11	1.99	0.45
2:FC:208:MET:HE3	2:FC:208:MET:HB3	1.71	0.45
7:CL:109:LEU:HD13	7:CL:109:LEU:HA	1.88	0.45
7:CL:134:MET:SD	7:CL:139:ARG:NH1	2.89	0.45
1:GG:884:PRO:HB2	1:HG:1040:LEU:HD11	1.99	0.45
6:DK:66:LYS:NZ	6:DK:67:VAL:O	2.50	0.45
3:EF:265:SER:HB3	3:EF:268:ASP:HB3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:FD:107:ARG:HE	4:FD:155:GLU:HG3	1.82	0.45
1:HG:1005:VAL:O	1:HG:1009:ALA:CB	2.65	0.45
1:IG:917:ASN:OD1	1:IG:917:ASN:N	2.49	0.45
1:OG:999:SER:OG	1:OG:1000:THR:N	2.48	0.45
8:FM:242:LYS:HA	8:FM:262:GLU:HB3	1.98	0.45
9:FN:111:GLU:HA	2:AC:71:LEU:HD21	1.98	0.45
2:LC:183:ARG:O	2:LC:187:ASN:ND2	2.37	0.45
3:GF:208:ILE:O	3:GF:241:TYR:OH	2.32	0.45
5:GH:170:ARG:N	5:GH:249:ASP:OD2	2.50	0.45
5:GH:183:ASP:OD2	5:GH:260:GLY:N	2.47	0.45
8:GM:256:HIS:O	8:GM:259:SER:OG	2.34	0.45
1:Hg:797:ARG:HA	1:Hg:797:ARG:HD2	1.87	0.45
5:IH:230:LEU:HD12	5:IH:233:LEU:HD21	1.96	0.45
8:JM:292:MET:HE1	8:JM:298:VAL:H	1.82	0.45
5:AH:190:PRO:HA	5:AH:211:ASN:HB3	1.99	0.45
8:KM:133:TYR:HE1	8:KM:154:LYS:H	1.64	0.45
1:DG:951:HIS:H	1:DG:1027:THR:HG22	1.82	0.45
1:DG:969:GLY:HA3	1:DG:1009:ALA:HB2	1.97	0.45
6:AK:125:SER:OG	6:AK:126:VAL:N	2.50	0.45
6:MK:81:SER:OG	6:MK:173:ASP:O	2.35	0.45
8:BM:158:VAL:HA	8:BM:178:LYS:HZ3	1.81	0.45
4:AD:147:VAL:HG22	4:AD:154:VAL:HG12	1.98	0.45
2:GC:263:ARG:HA	2:GC:263:ARG:HD2	1.71	0.45
2:JC:149:TYR:HD2	2:JC:201:ILE:HD13	1.81	0.45
4:Cd:74:PRO:HG3	4:Cd:147:VAL:HG11	1.98	0.45
5:EH:207:ASP:N	5:EH:207:ASP:OD1	2.50	0.45
1:Fg:792:GLN:OE1	1:Fg:795:GLN:NE2	2.50	0.45
1:IG:867:ASP:OD1	1:IG:867:ASP:N	2.33	0.45
2:LC:58:MET:HA	2:LC:61:LYS:HE2	1.99	0.45
2:AC:260:GLU:OE1	2:AC:260:GLU:N	2.50	0.45
1:AG:1011:VAL:HG12	1:BG:963:SER:HB3	1.99	0.45
2:BC:108:VAL:HG13	2:BC:135:LYS:H	1.80	0.45
3:Hf:245:LYS:HE3	3:Hf:257:SER:HA	1.99	0.45
4:Dd:68:ASP:OD2	4:Dd:70:THR:OG1	2.35	0.45
7:JL:226:ASN:O	7:JL:228:ARG:NH1	2.48	0.45
8:JM:161:GLY:H	8:JM:181:PRO:HA	1.82	0.45
9:JN:82:MET:N	9:JN:82:MET:SD	2.90	0.45
2:CC:153:MET:HE2	2:CC:153:MET:HB2	1.68	0.45
7:KL:109:LEU:HD13	7:KL:109:LEU:HA	1.85	0.45
8:KM:177:LEU:HG	8:KM:181:PRO:HG2	1.99	0.45
9:LN:115:GLN:HE21	9:LN:115:GLN:HB3	1.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:VH:315:THR:OG1	5:VH:316:ASN:N	2.48	0.45
5:VH:322:PRO:HG2	5:VH:345:LEU:HD13	1.99	0.45
3:WF:241:TYR:O	3:WF:258:SER:OG	2.29	0.45
7:BL:94:VAL:HA	7:BL:97:ILE:HG12	1.98	0.45
2:GC:170:LYS:HA	2:GC:170:LYS:HD3	1.82	0.45
4:Cd:128:LEU:HA	4:Cd:131:ILE:HB	1.98	0.45
1:GG:910:ASP:N	1:GG:910:ASP:OD1	2.40	0.45
3:FF:243:MET:HE3	3:FF:243:MET:HB3	1.92	0.45
1:LG:886:LEU:HA	1:LG:899:LEU:O	2.16	0.45
1:AG:969:GLY:HA3	1:AG:1009:ALA:HB2	1.99	0.44
2:EC:95:ASP:OD1	2:EC:98:SER:N	2.49	0.44
4:GD:98:ILE:HD12	4:GD:98:ILE:HA	1.90	0.44
4:HD:109:LEU:HD13	4:HD:155:GLU:HG3	1.99	0.44
6:HK:125:SER:OG	6:HK:126:VAL:N	2.47	0.44
7:HL:192:PHE:O	7:HL:196:ASN:ND2	2.50	0.44
8:HM:257:ASP:OD1	8:HM:257:ASP:N	2.50	0.44
4:Hd:150:ASN:OD1	4:Hd:150:ASN:N	2.48	0.44
3:IF:236:SER:OG	3:IF:237:LYS:N	2.49	0.44
8:JM:212:LEU:HD13	8:JM:212:LEU:HA	1.84	0.44
1:CG:898:LYS:HE2	1:CG:898:LYS:HB2	1.68	0.44
5:AH:235:THR:HG23	5:BH:180:VAL:HG21	1.99	0.44
1:Lg:818:GLN:NE2	5:LH:203:ASN:OD1	2.48	0.44
7:ML:121:ASP:OD1	7:ML:121:ASP:N	2.50	0.44
3:VF:254:ILE:HB	3:VF:262:ILE:HB	1.99	0.44
5:YH:279:LEU:HD11	5:YH:289:PRO:HB3	1.98	0.44
5:YH:339:MET:HE3	5:YH:339:MET:HB2	1.88	0.44
2:FC:116:LEU:HB2	2:FC:126:ILE:HG22	1.98	0.44
2:KC:112:GLU:OE2	2:KC:130:ARG:NH1	2.50	0.44
2:KC:150:TYR:O	2:KC:198:ASN:ND2	2.50	0.44
6:DK:163:LYS:HA	6:DK:163:LYS:HD2	1.78	0.44
9:DN:57:ARG:NH2	9:DN:66:SER:O	2.50	0.44
8:EM:149:ASN:OD1	8:EM:149:ASN:N	2.38	0.44
3:FF:210:TYR:HA	3:FF:224:GLY:HA2	1.99	0.44
1:IG:910:ASP:OD1	1:IG:910:ASP:N	2.50	0.44
1:AG:1024:ASN:OD1	1:AG:1024:ASN:N	2.51	0.44
5:GH:158:VAL:HG22	5:GH:167:PRO:HG2	1.99	0.44
5:GH:352:LYS:HE3	5:GH:352:LYS:HB3	1.59	0.44
7:HL:124:THR:HA	7:HL:231:ILE:O	2.17	0.44
5:JH:154:THR:O	5:JH:252:VAL:HA	2.16	0.44
8:JM:278:ASP:OD1	8:JM:297:SER:OG	2.35	0.44
3:LF:246:LEU:HB2	3:LF:255:LEU:HD12	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:LH:346:LEU:HD12	5:LH:346:LEU:HA	1.79	0.44
3:Mf:233:ARG:O	3:Mf:236:SER:OG	2.35	0.44
8:AM:212:LEU:HD13	8:AM:212:LEU:HA	1.85	0.44
9:AN:96:ASN:HD21	9:AN:100:LEU:HD23	1.82	0.44
2:FC:243:ASP:OD2	2:GC:126:ARG:NH2	2.47	0.44
9:CN:89:GLY:HA3	9:CN:104:ASN:HB2	1.99	0.44
4:Cd:92:GLU:OE2	4:Cd:158:TYR:OH	2.35	0.44
3:Cf:220:ALA:HB3	3:Cf:232:VAL:HG13	1.99	0.44
4:DD:55:MET:HA	2:LC:215:LYS:HZ3	1.83	0.44
5:DH:179:LEU:HD23	5:DH:254:LEU:HD21	1.98	0.44
3:EF:207:ARG:NH2	3:EF:239:PRO:O	2.50	0.44
1:NG:889:ILE:H	1:NG:889:ILE:HG12	1.60	0.44
7:FL:139:ARG:H	7:FL:139:ARG:HG3	1.58	0.44
3:IF:247:ILE:HG12	3:IF:254:ILE:HG12	1.99	0.44
1:CG:917:ASN:HA	1:CG:931:SER:HA	1.99	0.44
8:KM:153:GLN:HA	8:KM:173:LEU:HG	1.99	0.44
3:Kf:209:ILE:HD12	3:Kf:209:ILE:HA	1.89	0.44
9:MN:96:ASN:ND2	9:MN:100:LEU:O	2.42	0.44
4:Md:72:THR:OG1	4:Md:73:ILE:N	2.50	0.44
1:EG:1024:ASN:OD1	1:EG:1024:ASN:N	2.36	0.44
5:BH:115:MET:HE3	5:BH:115:MET:HB3	1.85	0.44
2:FC:174:ILE:HA	2:FC:177:ILE:HG12	2.00	0.44
2:IC:128:ILE:HG12	2:HC:246:ARG:HB2	1.99	0.44
5:CH:161:SER:HB2	5:CH:164:SER:HB3	1.98	0.44
8:CM:210:ASP:O	8:CM:230:ARG:N	2.49	0.44
3:FF:243:MET:HB2	3:FF:257:SER:HB3	1.99	0.44
1:HG:947:ARG:HB2	1:HG:950:HIS:HE2	1.81	0.44
1:JG:871:ALA:HB2	1:JG:889:ILE:HD13	1.99	0.44
1:JG:1017:GLN:NE2	1:KG:1020:GLN:OE1	2.43	0.44
2:HC:102:LEU:HB2	2:HC:106:ILE:HB	1.99	0.44
9:GN:46:GLY:HA3	9:GN:61:ASN:HB2	1.99	0.44
6:HK:44:ARG:HA	9:HN:68:CYS:HA	1.99	0.44
1:BG:965:LEU:HD12	1:BG:1008:LEU:HD13	1.99	0.44
8:IM:186:SER:HA	8:IM:205:TYR:HB2	2.00	0.44
5:JH:339:MET:HE3	5:JH:339:MET:HB3	1.86	0.44
7:LL:130:ASP:OD1	7:LL:130:ASP:N	2.49	0.44
1:Ag:801:MET:HE1	5:BH:122:LEU:HA	1.99	0.44
8:BM:257:ASP:OD1	8:BM:257:ASP:N	2.41	0.44
4:AD:36:ASP:OD1	2:IC:76:ARG:NH2	2.50	0.44
2:IC:129:SER:HA	2:HC:244:ASP:O	2.16	0.44
9:CN:84:CYS:SG	9:CN:85:CYS:N	2.91	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:DD:145:ILE:HD13	4:DD:145:ILE:HA	1.83	0.44
6:DK:117:THR:HA	6:DK:157:GLN:O	2.18	0.44
7:DL:226:ASN:O	7:DL:228:ARG:NH1	2.50	0.44
6:EK:179:ARG:NH2	6:EK:181:GLU:OE2	2.50	0.44
9:EN:46:GLY:HA3	9:EN:61:ASN:HB2	2.00	0.44
4:FD:82:ARG:NH2	8:FM:311:ASP:OD1	2.50	0.44
1:LG:899:LEU:HD11	1:LG:916:PHE:HB3	1.98	0.44
1:LG:910:ASP:OD1	1:LG:910:ASP:N	2.43	0.44
2:HC:262:GLU:OE1	2:HC:262:GLU:N	2.51	0.44
1:Gg:813:LYS:HE2	1:Gg:813:LYS:HB2	1.84	0.44
6:HK:44:ARG:NH2	6:HK:48:ALA:O	2.41	0.44
7:HL:169:THR:HG1	7:HL:170:ASP:N	2.15	0.44
5:IH:131:LYS:HD3	5:XH:145:PRO:HD3	2.00	0.44
5:IH:200:SER:OG	1:Jg:816:GLU:OE2	2.35	0.44
4:Dd:97:ARG:HG3	2:MC:265:ALA:HB3	2.00	0.44
8:JM:149:ASN:OD1	8:JM:149:ASN:N	2.43	0.44
5:KH:341:LYS:HE2	5:KH:341:LYS:HB3	1.85	0.44
4:Kd:60:LYS:HD2	4:Kd:60:LYS:HA	1.82	0.44
4:LD:67:LYS:HD2	4:LD:67:LYS:HA	1.73	0.44
5:LH:307:SER:OG	5:LH:308:ASN:N	2.50	0.44
6:LK:70:VAL:HG12	7:ML:214:ILE:HG21	2.00	0.44
3:MF:233:ARG:NH1	3:ZF:269:SER:OG	2.51	0.44
3:Mf:216:ILE:HD12	3:Mf:216:ILE:HA	1.84	0.44
8:AM:233:VAL:HB	8:AM:253:VAL:HG12	2.00	0.44
1:Dg:811:ASP:O	1:Dg:814:GLN:NE2	2.49	0.44
2:JC:225:VAL:HA	2:JC:248:ILE:HA	2.00	0.44
2:KC:91:ASP:HB3	2:KC:147:TRP:HE1	1.82	0.44
2:MC:147:THR:HG23	2:MC:150:GLN:H	1.82	0.44
1:GG:949:ASN:HA	1:GG:952:TYR:HE2	1.82	0.44
5:DH:295:LEU:HD23	5:DH:295:LEU:HA	1.88	0.44
6:DK:92:ASN:O	6:DK:95:SER:OG	2.29	0.44
8:DM:303:GLU:OE2	8:DM:306:GLN:N	2.50	0.44
5:FH:251:ARG:NH2	5:FH:253:ASP:OD2	2.48	0.44
1:KG:862:ILE:HD13	1:KG:1046:THR:HA	1.98	0.44
1:NG:1024:ASN:OD1	1:NG:1024:ASN:N	2.40	0.44
1:PG:867:ASP:H	1:PG:1041:PHE:HB2	1.82	0.44
2:HC:183:ARG:O	2:HC:187:ASN:ND2	2.35	0.44
8:GM:309:LEU:HD12	8:GM:309:LEU:HA	1.84	0.44
7:HL:158:TYR:O	7:HL:161:SER:OG	2.35	0.44
1:Bg:795:GLN:HA	1:Bg:798:THR:HB	1.99	0.44
8:IM:197:TYR:HA	8:IM:217:LYS:HB3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:Dd:150:ASN:OD1	4:Dd:150:ASN:N	2.50	0.44
4:JD:55:MET:HE3	4:JD:55:MET:HB3	1.86	0.44
5:JH:184:SER:OG	5:JH:258:GLY:O	2.34	0.44
7:JL:121:ASP:N	7:JL:121:ASP:OD1	2.50	0.44
7:JL:202:ARG:HE	7:JL:202:ARG:HB3	1.64	0.44
5:AH:251:ARG:HH22	5:ZH:236:PRO:HD2	1.83	0.44
5:MH:342:SER:OG	5:MH:344:VAL:O	2.31	0.44
8:MM:145:ARG:HE	8:MM:164:GLN:HB3	1.83	0.44
4:BD:141:LYS:HG2	2:JC:101:GLU:HG2	2.00	0.44
8:BM:288:ARG:NH1	8:BM:318:GLN:O	2.44	0.44
2:IC:241:ILE:HG13	2:JC:131:TYR:HB2	1.99	0.44
2:JC:243:ASP:OD2	2:KC:126:ARG:NH2	2.50	0.44
2:MC:214:ARG:NH1	4:Ed:59:GLU:OE2	2.50	0.44
7:CL:169:THR:HG21	7:CL:178:LYS:HB3	2.00	0.44
8:CM:303:GLU:OE1	8:CM:305:GLY:N	2.43	0.44
6:EK:186:ARG:NH2	9:EN:65:TYR:O	2.50	0.44
5:FH:302:ALA:O	5:FH:303:ARG:NH1	2.40	0.44
2:LC:226:TYR:HB3	2:LC:252:ALA:HB3	2.00	0.44
1:BG:972:PHE:HB3	1:BG:1005:VAL:HG22	1.98	0.44
3:JF:243:MET:O	3:JF:257:SER:N	2.47	0.44
6:JK:78:ILE:HB	6:JK:180:VAL:HG13	1.98	0.44
3:Jf:221:TRP:HE1	3:Jf:229:THR:HB	1.82	0.44
1:Kg:808:LEU:H	1:Kg:808:LEU:HG	1.67	0.44
8:KM:168:VAL:H	8:KM:187:GLY:HA3	1.83	0.44
7:LL:129:THR:OG1	7:LL:130:ASP:OD1	2.35	0.44
8:LM:181:PRO:O	8:LM:201:THR:OG1	2.29	0.44
1:Mg:804:ALA:HB1	5:ZH:122:LEU:HD11	2.00	0.44
9:MN:63:GLY:HA3	4:AD:27:LYS:HB2	1.99	0.44
5:BH:167:PRO:HB2	5:BH:239:LEU:HD23	2.00	0.44
5:BH:339:MET:HE2	5:BH:339:MET:HB3	1.80	0.44
6:BK:115:THR:OG1	6:BK:183:THR:OG1	2.26	0.44
9:BN:79:GLN:O	5:CH:355:GLN:NE2	2.51	0.44
6:CK:53:ILE:HD11	6:CK:108:GLN:HE21	1.82	0.44
4:Cd:76:ALA:O	4:Cd:80:GLN:NE2	2.41	0.44
7:DL:141:ASN:HD21	7:DL:143:ILE:HB	1.82	0.44
2:HC:171:LYS:H	2:HC:171:LYS:HG3	1.61	0.44
8:FM:292:MET:HE1	8:FM:298:VAL:H	1.83	0.44
9:FN:81:LEU:HD13	9:FN:81:LEU:HA	1.85	0.44
5:GH:132:GLN:O	5:GH:136:THR:OG1	2.35	0.44
8:HM:271:SER:OG	8:HM:290:ASP:OD1	2.35	0.44
3:JF:212:ILE:HB	3:JF:264:PHE:HA	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:JH:198:ASP:OD2	5:JH:201:SER:OG	2.29	0.44
5:JH:221:TYR:HE2	5:KH:138:GLU:HG3	1.83	0.44
5:JH:282:HIS:HB3	5:JH:287:VAL:HB	2.00	0.44
9:KN:78:LEU:HD13	9:KN:78:LEU:HA	1.85	0.44
9:KN:114:LEU:HD22	9:KN:114:LEU:HA	1.87	0.44
5:LH:198:ASP:OD1	5:LH:200:SER:OG	2.34	0.44
5:LH:275:SER:HA	2:GC:126:ARG:HD3	1.99	0.44
9:LN:89:GLY:HA3	9:LN:104:ASN:HB2	1.99	0.44
3:MF:216:ILE:HD11	3:MF:219:ARG:HB2	1.98	0.44
3:VF:236:SER:OG	3:VF:237:LYS:N	2.51	0.44
4:CD:55:MET:SD	2:KC:214:LYS:NZ	2.74	0.44
3:Df:256:THR:HG1	3:Df:260:GLN:H	1.65	0.44
1:FG:931:SER:H	1:FG:1043:GLN:HE22	1.65	0.44
8:BM:126:GLY:O	8:BM:146:LEU:HA	2.18	0.44
2:JC:164:LEU:HD12	2:JC:164:LEU:HA	1.88	0.44
8:CM:219:ALA:HB1	8:CM:221:LYS:HZ1	1.83	0.44
4:ED:131:ILE:HD13	4:ED:131:ILE:HA	1.88	0.44
1:IG:912:MET:HB3	1:IG:944:LEU:HB2	1.99	0.44
1:OG:931:SER:O	1:OG:1042:THR:OG1	2.29	0.44
2:HC:212:LEU:HA	2:HC:212:LEU:HD12	1.84	0.44
8:FM:199:LYS:HA	8:FM:219:ALA:HB3	1.99	0.44
9:FN:49:ASN:ND2	9:FN:61:ASN:OD1	2.43	0.44
4:Fd:148:TYR:HB2	4:Fd:153:VAL:HG12	1.98	0.44
5:GH:266:MET:HE3	5:GH:267:PRO:HD2	1.99	0.44
6:GK:66:LYS:HD2	6:GK:66:LYS:HA	1.83	0.44
6:GK:150:ASP:OD1	6:GK:150:ASP:N	2.48	0.44
4:Gd:142:LYS:NZ	4:Gd:142:LYS:H	2.16	0.44
7:HL:44:HIS:N	7:HL:48:ASN:OD1	2.44	0.44
9:HN:88:HIS:ND1	9:HN:105:ASP:OD2	2.46	0.44
4:KD:130:GLU:OE2	4:KD:133:ARG:NH1	2.43	0.44
6:AK:87:GLN:N	6:AK:173:ASP:OD2	2.50	0.44
4:Md:105:ARG:HB2	4:Md:153:VAL:HG23	2.00	0.44
3:WF:209:ILE:O	3:WF:225:SER:N	2.50	0.44
11:WX:24:UNK:N	11:WX:32:UNK:O	2.50	0.44
11:XX:3:UNK:O	11:XX:7:UNK:CB	2.66	0.44
5:ZH:198:ASP:OD1	5:ZH:201:SER:OG	2.29	0.44
3:BF:213:GLN:HG3	5:BH:170:ARG:HH12	1.83	0.44
4:AD:35:ASP:O	4:AD:38:THR:OG1	2.29	0.44
2:FC:113:ARG:HG2	2:FC:129:ARG:HG2	2.00	0.44
2:MC:98:ASN:ND2	4:ED:118:LEU:O	2.51	0.44
7:CL:54:ARG:HH22	7:CL:56:ALA:HB3	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:DH:228:VAL:HG12	5:DH:237:VAL:HB	2.00	0.44
8:DM:201:THR:HG22	8:DM:221:LYS:HB2	1.99	0.44
6:EK:114:ILE:HB	6:EK:154:ILE:HG12	2.00	0.44
5:FH:345:LEU:HB2	5:FH:356:LEU:HB2	1.99	0.44
1:OG:865:THR:OG1	1:OG:1044:ASP:OD2	2.35	0.44
1:PG:969:GLY:HA3	1:PG:1009:ALA:HB2	2.00	0.44
1:AG:871:ALA:HA	1:AG:890:VAL:HG22	1.99	0.43
3:IF:263:LYS:NZ	3:IF:264:PHE:O	2.41	0.43
4:JD:88:SER:O	4:JD:88:SER:OG	2.34	0.43
5:JH:229:ARG:NH2	5:KH:212:THR:OG1	2.51	0.43
7:LL:109:LEU:HD13	7:LL:109:LEU:HA	1.88	0.43
4:Md:84:SER:H	2:IC:268:ALA:HB3	1.82	0.43
3:VF:208:ILE:HD11	3:VF:224:GLY:HA3	1.99	0.43
5:WH:354:MET:HE2	5:WH:354:MET:HB2	1.85	0.43
5:YH:120:TYR:HA	5:YH:121:PRO:HD3	1.89	0.43
5:YH:159:ASN:HA	5:YH:257:GLN:HB2	2.00	0.43
1:FG:972:PHE:HB3	1:FG:1005:VAL:HG22	2.00	0.43
2:GC:111:LEU:HD13	2:GC:111:LEU:HA	1.77	0.43
6:CK:87:GLN:N	6:CK:173:ASP:OD2	2.50	0.43
6:CK:133:THR:HG21	6:CK:160:GLY:H	1.82	0.43
7:DL:94:VAL:HA	7:DL:97:ILE:HG12	2.00	0.43
3:EF:233:ARG:HD2	3:EF:235:GLY:H	1.82	0.43
6:FK:92:ASN:O	6:FK:95:SER:OG	2.30	0.43
4:Fd:93:GLU:H	4:Fd:93:GLU:HG3	1.63	0.43
5:GH:131:LYS:HG2	5:WH:145:PRO:HG3	2.00	0.43
5:GH:339:MET:HE3	5:GH:339:MET:HB3	1.93	0.43
4:HD:131:ILE:HD13	4:HD:131:ILE:HA	1.91	0.43
6:HK:65:ILE:HD12	6:HK:78:ILE:HG23	1.99	0.43
6:HK:177:ASN:OD1	6:HK:177:ASN:N	2.49	0.43
4:ID:70:THR:HA	4:ID:133:ARG:HH21	1.83	0.43
5:IH:196:LEU:HD21	5:IH:199:PRO:HG3	1.99	0.43
6:IK:107:LYS:NZ	6:IK:148:GLY:O	2.50	0.43
6:IK:109:PHE:O	6:IK:111:LYS:NZ	2.45	0.43
4:JD:87:TRP:CD1	4:JD:89:GLY:H	2.36	0.43
8:JM:186:SER:HA	8:JM:205:TYR:HB2	1.99	0.43
1:CG:972:PHE:O	1:CG:976:ASN:ND2	2.48	0.43
2:CC:81:GLU:O	2:CC:84:ASN:ND2	2.50	0.43
1:DG:912:MET:HB3	1:DG:944:LEU:HB2	1.99	0.43
5:MH:161:SER:O	5:MH:164:SER:OG	2.32	0.43
8:MM:286:LYS:HA	8:MM:316:ASN:HD21	1.83	0.43
5:VH:189:TRP:HZ3	5:VH:260:GLY:HA2	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:VH:313:VAL:HG13	5:VH:337:TYR:HB2	2.00	0.43
5:XH:189:TRP:O	5:XH:211:ASN:ND2	2.36	0.43
7:AL:177:HIS:HA	7:AL:180:LYS:HD2	1.99	0.43
2:DC:163:ASN:OD1	2:DC:163:ASN:N	2.50	0.43
7:BL:163:ILE:HB	7:BL:203:LEU:HD13	2.00	0.43
11:BX:13:UNK:O	11:BX:17:UNK:CB	2.66	0.43
2:GC:119:LEU:HA	2:GC:125:ILE:HG22	1.99	0.43
2:IC:246:ARG:HE	2:IC:246:ARG:HB3	1.61	0.43
6:DK:87:GLN:NE2	6:DK:173:ASP:OD1	2.52	0.43
5:EH:301:ASP:OD1	5:EH:301:ASP:N	2.37	0.43
4:Ed:29:PRO:HB2	4:Ed:32:ASN:HB2	1.99	0.43
1:Fg:793:GLU:O	1:Fg:796:GLN:NE2	2.51	0.43
1:OG:910:ASP:OD1	1:OG:910:ASP:N	2.44	0.43
1:PG:999:SER:OG	1:PG:1000:THR:N	2.50	0.43
1:PG:1005:VAL:O	1:PG:1009:ALA:CB	2.65	0.43
2:BC:208:MET:HE2	2:BC:208:MET:HB3	1.86	0.43
2:EC:101:LEU:HB2	2:EC:105:ILE:HG23	2.01	0.43
4:HD:82:ARG:HD2	6:HK:138:ARG:HD2	2.00	0.43
1:Ig:791:GLN:N	1:Ig:793:GLU:OE1	2.52	0.43
5:IH:347:VAL:HG23	5:IH:354:MET:HG2	1.98	0.43
8:JM:275:ASP:HB3	8:JM:294:PHE:HB2	1.99	0.43
4:KD:73:ILE:HD12	4:KD:147:VAL:HG23	2.01	0.43
8:KM:306:GLN:NE2	8:KM:308:ASP:OD1	2.46	0.43
1:DG:862:ILE:HD13	1:DG:1046:THR:HA	1.99	0.43
4:Ld:86:ASP:OD1	2:HC:131:ARG:NH2	2.49	0.43
6:MK:49:CYS:O	6:MK:52:THR:OG1	2.29	0.43
11:VX:27:UNK:O	5:EH:132:GLN:NE2	2.51	0.43
8:AM:250:ARG:HD2	8:AM:268:HIS:HB2	1.98	0.43
6:BK:130:ARG:O	6:BK:133:THR:OG1	2.30	0.43
4:AD:31:ASN:OD1	4:AD:31:ASN:N	2.51	0.43
2:FC:146:TRP:HB2	2:FC:150:LEU:HD23	2.01	0.43
2:MC:220:ASN:ND2	2:MC:262:GLU:O	2.51	0.43
4:Cd:95:THR:HA	4:Cd:98:ILE:HG22	1.99	0.43
4:DD:29:PRO:HG2	7:DL:225:GLN:HA	2.01	0.43
8:DM:134:LEU:HD13	8:DM:136:LEU:HD21	2.01	0.43
4:ED:87:TRP:CD2	4:ED:94:LEU:HD13	2.53	0.43
8:EM:191:LEU:HD21	8:EM:194:LEU:HD13	1.99	0.43
8:EM:235:LEU:HG	8:EM:239:ALA:HB3	2.00	0.43
8:FM:165:ILE:HB	8:FM:185:ILE:HG23	2.00	0.43
2:BC:103:ASN:OD1	2:BC:103:ASN:N	2.51	0.43
5:GH:149:PRO:HB2	5:GH:248:VAL:HG12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:HH:270:GLU:OE2	5:XH:327:SER:N	2.48	0.43
6:IK:111:LYS:HE3	6:IK:111:LYS:HB3	1.88	0.43
8:JM:163:THR:HB	8:JM:183:VAL:HG12	1.99	0.43
4:KD:158:TYR:O	4:Kd:137:TYR:OH	2.28	0.43
2:CC:175:ILE:HA	2:CC:178:ILE:HG12	1.99	0.43
6:KK:92:ASN:O	6:KK:95:SER:OG	2.35	0.43
7:KL:114:ILE:HG23	7:KL:127:ILE:HG13	1.99	0.43
9:KN:39:ASP:N	9:KN:39:ASP:OD1	2.49	0.43
3:ZF:220:ALA:O	3:ZF:231:THR:HA	2.17	0.43
5:BH:341:LYS:HB3	5:BH:361:LEU:HD21	1.99	0.43
3:Bf:209:ILE:HD12	3:Bf:209:ILE:HA	1.80	0.43
2:KC:129:ASP:OD1	2:KC:129:ASP:N	2.37	0.43
2:MC:176:ILE:HA	2:MC:179:ILE:HG12	2.00	0.43
6:CK:120:SER:N	6:CK:160:GLY:O	2.40	0.43
8:CM:218:LYS:HE2	8:CM:218:LYS:HB2	1.86	0.43
8:DM:180:ASP:O	8:DM:182:LYS:NZ	2.40	0.43
2:HC:176:ILE:HA	2:HC:179:ILE:HG12	2.00	0.43
7:FL:125:LEU:HD13	7:FL:125:LEU:HA	1.87	0.43
4:Fd:135:ILE:HD13	4:Fd:135:ILE:HA	1.90	0.43
5:GH:278:ASP:HA	5:GH:281:LEU:HD12	2.00	0.43
4:Gd:82:ARG:HH22	4:Gd:127:SER:HA	1.82	0.43
3:HF:245:LYS:HD3	3:HF:257:SER:HA	2.01	0.43
1:Hg:797:ARG:HH12	5:XH:121:PRO:HB3	1.83	0.43
7:HL:116:TYR:OH	7:HL:118:GLU:OE1	2.36	0.43
7:IL:44:HIS:HB2	7:IL:48:ASN:HA	2.01	0.43
1:Jg:791:GLN:N	1:Jg:793:GLU:OE1	2.52	0.43
2:CC:111:LEU:HD13	2:CC:111:LEU:HA	1.87	0.43
3:LF:229:THR:OG1	3:LF:230:LEU:N	2.52	0.43
1:Lg:808:LEU:H	1:Lg:808:LEU:HG	1.50	0.43
4:Ld:149:PRO:O	4:Ld:152:GLN:NE2	2.49	0.43
6:AK:81:SER:OG	6:AK:173:ASP:O	2.36	0.43
8:MM:278:ASP:OD1	8:MM:297:SER:OG	2.36	0.43
4:CD:41:LEU:HD22	2:KC:199:ILE:HD12	1.99	0.43
5:YH:178:SER:OG	5:YH:250:TYR:O	2.37	0.43
3:Df:211:TYR:O	3:Df:223:ILE:N	2.43	0.43
4:AD:136:ASP:OD1	4:AD:145:ILE:N	2.50	0.43
2:IC:45:ARG:HE	2:IC:45:ARG:HB3	1.54	0.43
5:CH:106:VAL:HA	5:CH:109:LYS:HE2	2.00	0.43
5:CH:311:MET:HG3	5:CH:341:LYS:HA	2.00	0.43
8:CM:174:GLN:NE2	8:CM:193:GLN:O	2.51	0.43
4:Cd:141:LYS:HD3	4:Cd:141:LYS:HA	1.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:DD:55:MET:HE2	2:LC:211:ILE:HD11	2.00	0.43
4:DD:132:LEU:HD12	4:DD:145:ILE:HG21	2.00	0.43
4:DD:161:ILE:HD12	4:DD:161:ILE:HA	1.84	0.43
3:DF:269:SER:HA	5:DH:247:ALA:HB2	2.01	0.43
5:DH:190:PRO:HB2	5:DH:231:ARG:HG3	2.01	0.43
6:FK:144:LEU:HD22	6:FK:144:LEU:HA	1.86	0.43
2:BC:109:LEU:HD13	2:BC:109:LEU:HA	1.89	0.43
2:EC:262:TRP:HH2	2:DC:234:VAL:HG11	1.83	0.43
5:GH:272:ILE:HD13	5:GH:272:ILE:HA	1.92	0.43
6:HK:50:ASP:OD1	6:HK:50:ASP:N	2.39	0.43
8:HM:207:ILE:HG12	8:HM:226:GLY:HA3	2.01	0.43
8:HM:230:ARG:HA	8:HM:250:ARG:HB2	2.00	0.43
3:Hf:256:THR:HG23	3:Hf:258:SER:H	1.84	0.43
5:IH:121:PRO:O	1:XG:797:ARG:NH2	2.51	0.43
8:IM:155:LEU:HB3	8:IM:175:ILE:HD13	2.00	0.43
8:IM:274:THR:OG1	8:IM:275:ASP:N	2.52	0.43
1:CG:969:GLY:HA3	1:CG:1009:ALA:HB2	2.01	0.43
4:Jd:72:THR:OG1	4:Jd:73:ILE:N	2.51	0.43
6:KK:72:GLN:NE2	7:LL:215:SER:OG	2.39	0.43
6:KK:111:LYS:HE3	6:KK:111:LYS:HB3	1.86	0.43
6:KK:129:GLU:OE1	6:KK:129:GLU:N	2.48	0.43
1:Lg:808:LEU:O	1:Lg:812:TRP:N	2.47	0.43
8:LM:263:ILE:O	8:LM:281:TYR:HA	2.18	0.43
3:MF:210:TYR:HB3	3:MF:222:LEU:HB3	2.00	0.43
6:MK:92:ASN:O	6:MK:95:SER:OG	2.37	0.43
7:ML:116:TYR:OH	7:ML:118:GLU:OE1	2.36	0.43
5:VH:151:PRO:HA	5:VH:248:VAL:HG13	2.00	0.43
3:WF:258:SER:OG	3:WF:260:GLN:NE2	2.40	0.43
9:AN:49:ASN:HD21	9:AN:61:ASN:HA	1.84	0.43
4:Ad:135:ILE:HD13	4:Ad:135:ILE:HA	1.90	0.43
6:BK:90:ARG:HG3	8:BM:292:MET:HG2	2.01	0.43
2:JC:165:LEU:HD22	2:JC:166:PRO:HD2	2.00	0.43
2:MC:61:LYS:HB2	2:MC:61:LYS:HE3	1.73	0.43
7:CL:175:ARG:H	7:CL:175:ARG:HG2	1.52	0.43
8:CM:131:THR:OG1	8:CM:132:SER:N	2.51	0.43
3:Cf:211:TYR:HD1	3:Cf:211:TYR:HA	1.73	0.43
7:DL:190:MET:HE2	7:DL:190:MET:HB2	1.87	0.43
5:EH:144:THR:HA	5:FH:131:LYS:HD3	1.99	0.43
5:EH:307:SER:OG	5:EH:308:ASN:N	2.51	0.43
1:HG:944:LEU:HD22	1:HG:944:LEU:HA	1.92	0.43
1:AG:963:SER:OG	1:PG:1010:THR:O	2.31	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:GH:189:TRP:CD2	5:GH:261:PRO:HD3	2.54	0.43
7:GL:141:ASN:HD21	7:GL:143:ILE:HD12	1.82	0.43
5:HH:341:LYS:HE2	5:HH:341:LYS:HB3	1.85	0.43
6:HK:117:THR:HG22	6:HK:157:GLN:HG3	2.00	0.43
4:ID:39:ILE:HD12	7:IL:220:ILE:HG21	2.01	0.43
4:Id:34:SER:O	4:Id:34:SER:OG	2.36	0.43
3:JF:226:ASN:ND2	3:JF:228:SER:OG	2.49	0.43
6:JK:66:LYS:HD2	6:JK:66:LYS:HA	1.82	0.43
2:CC:240:ILE:O	2:DC:132:THR:HA	2.19	0.43
6:LK:53:ILE:HA	6:LK:53:ILE:HD13	1.82	0.43
8:LM:275:ASP:HB3	8:LM:294:PHE:HB2	2.00	0.43
4:MD:160:LYS:HA	4:MD:160:LYS:HD2	1.88	0.43
3:MF:208:ILE:O	3:MF:241:TYR:OH	2.31	0.43
5:MH:106:VAL:HA	5:MH:109:LYS:HB2	2.01	0.43
8:MM:121:ALA:HA	8:MM:141:GLU:HB3	2.01	0.43
8:MM:209:SER:OG	8:MM:210:ASP:N	2.51	0.43
1:EG:966:GLN:O	1:EG:970:ASN:ND2	2.51	0.43
1:EG:1005:VAL:O	1:EG:1009:ALA:HB2	2.19	0.43
5:YH:136:THR:H	5:YH:136:THR:HG1	1.55	0.43
5:YH:166:PRO:HA	5:YH:167:PRO:HD3	1.89	0.43
2:DC:148:TRP:HB2	2:DC:152:LEU:HD23	2.01	0.43
8:AM:253:VAL:HG23	8:AM:271:SER:HA	2.00	0.43
5:BH:319:ILE:HD11	5:BH:345:LEU:HD12	2.01	0.43
1:FG:1005:VAL:O	1:FG:1009:ALA:CB	2.66	0.43
9:BN:85:CYS:N	2:JC:153:ASP:OD2	2.46	0.43
2:FC:227:HIS:HB3	2:FC:246:LEU:HD13	2.00	0.43
2:MC:122:ASP:OD1	2:MC:125:SER:OG	2.34	0.43
9:EN:109:SER:OG	9:EN:110:GLU:N	2.52	0.43
1:AG:931:SER:H	1:AG:1043:GLN:NE2	2.17	0.43
4:GD:87:TRP:CD2	4:GD:94:LEU:HD13	2.54	0.43
5:GH:169:ILE:HD12	5:GH:252:VAL:HG21	2.01	0.43
3:HF:237:LYS:HD3	3:HF:243:MET:HB2	2.01	0.43
4:Dd:105:ARG:HB2	4:Dd:153:VAL:HG23	2.01	0.43
6:JK:92:ASN:O	6:JK:95:SER:OG	2.37	0.43
7:JL:190:MET:HE1	7:JL:203:LEU:HB3	1.99	0.43
1:CG:870:PHE:HB2	1:CG:891:THR:HG22	2.00	0.43
2:CC:211:LEU:HD23	2:CC:211:LEU:HA	1.90	0.43
5:KH:246:LYS:HD3	5:KH:246:LYS:HA	1.78	0.43
7:KL:179:ARG:HE	7:KL:179:ARG:HB2	1.60	0.43
8:KM:292:MET:HE1	8:KM:298:VAL:HB	2.00	0.43
5:LH:129:LYS:HB3	5:LH:129:LYS:HE3	1.72	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:LH:166:PRO:HA	5:LH:167:PRO:HD3	1.88	0.43
4:Ld:150:ASN:O	4:Ld:152:GLN:NE2	2.51	0.43
7:ML:134:MET:HB2	7:ML:139:ARG:HB2	2.00	0.43
3:VF:214:ALA:HB3	3:VF:221:TRP:HB2	2.00	0.43
4:BD:160:LYS:HA	4:BD:160:LYS:HD2	1.86	0.43
9:BN:46:GLY:HA3	9:BN:61:ASN:HB2	2.01	0.43
4:Bd:84:SER:H	2:KC:267:ALA:HB3	1.83	0.43
4:AD:36:ASP:OD1	4:AD:36:ASP:N	2.52	0.43
4:AD:161:ILE:HD12	4:AD:161:ILE:HA	1.86	0.43
2:IC:154:MET:H	2:IC:154:MET:HG3	1.66	0.43
6:CK:151:SER:OG	6:CK:152:ARG:N	2.52	0.43
3:DF:251:GLN:OE1	3:DF:253:ARG:NH1	2.42	0.43
6:FK:129:GLU:N	6:FK:129:GLU:OE1	2.50	0.43
1:NG:1033:SER:HB2	1:OG:940:ALA:HB3	2.01	0.43
1:OG:1001:LEU:H	1:OG:1001:LEU:HG	1.52	0.43
7:FL:168:PHE:HB2	7:FL:228:ARG:HG2	1.99	0.43
2:BC:136:GLN:HG2	2:BC:251:LEU:HD22	1.99	0.43
6:GK:127:LYS:HB3	8:GM:301:MET:HG3	2.01	0.43
4:Gd:132:LEU:HD13	4:Gd:132:LEU:HA	1.83	0.43
5:HH:230:LEU:HB2	5:HH:233:LEU:HB2	2.01	0.43
7:HL:91:VAL:HA	7:HL:94:VAL:HG12	2.01	0.43
4:Hd:160:LYS:HB2	4:Hd:160:LYS:HE2	1.85	0.43
8:IM:269:GLN:HG3	8:IM:288:ARG:HA	2.00	0.43
5:AH:126:GLN:HA	5:AH:129:LYS:HG2	2.01	0.43
2:CC:110:LEU:HD23	2:CC:110:LEU:HA	1.88	0.43
7:KL:129:THR:OG1	7:KL:130:ASP:OD1	2.36	0.43
6:LK:183:THR:HG21	10:LU:123:UNK:HA	2.01	0.43
1:DG:999:SER:OG	1:DG:1000:THR:N	2.50	0.43
4:MD:36:ASP:OD1	2:HC:76:ARG:NH2	2.52	0.43
5:MH:152:THR:O	5:MH:250:TYR:N	2.47	0.43
8:MM:131:THR:HG23	8:MM:151:GLY:H	1.82	0.43
8:MM:158:VAL:HG13	8:MM:178:LYS:HE2	2.00	0.43
4:Md:29:PRO:HB2	4:Md:32:ASN:HB2	2.00	0.43
5:YH:126:GLN:HA	5:YH:129:LYS:HG2	2.00	0.43
5:ZH:203:ASN:HB3	5:ZH:216:GLN:HB3	1.99	0.43
3:CF:216:ILE:HD11	3:CF:219:ARG:HB2	2.00	0.43
3:CF:243:MET:O	3:CF:257:SER:N	2.50	0.43
4:Bd:47:SER:O	4:Bd:51:SER:OG	2.30	0.43
2:FC:260:GLU:OE1	2:FC:260:GLU:N	2.52	0.43
2:GC:175:ILE:HA	2:GC:178:ILE:HG12	2.01	0.43
2:IC:112:LEU:HD23	2:IC:112:LEU:HA	1.75	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:IC:210:MET:HB3	2:IC:210:MET:HE3	1.75	0.43
6:DK:78:ILE:HB	6:DK:180:VAL:HG23	2.01	0.43
4:FD:87:TRP:CD2	4:FD:94:LEU:HD13	2.53	0.43
2:HC:60:LEU:HG	2:HC:166:LEU:HD13	2.00	0.43
2:HC:107:LEU:HD12	2:HC:108:PRO:HD2	2.01	0.43
8:FM:261:ALA:HB1	8:FM:263:ILE:HD11	2.00	0.43
11:FX:21:UNK:O	11:FX:78:UNK:N	2.52	0.43
1:AG:1017:GLN:HE21	1:AG:1017:GLN:HB2	1.64	0.43
7:GL:136:SER:OG	7:GL:136:SER:O	2.29	0.43
4:HD:105:ARG:HB3	4:HD:153:VAL:HG12	2.00	0.43
6:HK:40:LYS:HA	6:HK:40:LYS:HD3	1.88	0.43
4:ID:62:ILE:HD13	4:ID:62:ILE:HA	1.81	0.43
5:IH:180:VAL:HG13	5:IH:253:ASP:HA	2.01	0.43
6:IK:99:LEU:HA	6:IK:102:ILE:HD12	2.00	0.43
4:Jd:141:LYS:HD3	4:Jd:141:LYS:HA	1.88	0.43
4:KD:68:ASP:OD2	4:KD:70:THR:OG1	2.30	0.43
2:CC:83:LEU:HD22	2:CC:83:LEU:HA	1.87	0.43
4:Kd:76:ALA:O	4:Kd:80:GLN:NE2	2.45	0.43
1:DG:1006:ILE:HG21	1:EG:968:PHE:HD2	1.84	0.43
1:Mg:794:ILE:O	1:Mg:798:THR:N	2.52	0.43
6:MK:65:ILE:HD12	6:MK:78:ILE:HG12	2.01	0.43
7:ML:113:ASP:OD1	7:ML:113:ASP:N	2.43	0.43
5:VH:326:ALA:HB3	5:VH:338:GLU:HB3	2.01	0.43
4:CD:59:GLU:HB2	2:KC:214:LYS:NZ	2.34	0.43
11:WX:22:UNK:HA	11:WX:77:UNK:HA	2.01	0.43
8:AM:308:ASP:OD1	8:AM:308:ASP:N	2.52	0.43
4:Ad:64:PRO:HG2	4:Ad:67:LYS:HG2	2.01	0.43
6:BK:73:ASN:ND2	7:CL:214:ILE:O	2.52	0.43
7:BL:194:TRP:HE1	7:BL:200:ALA:HB2	1.84	0.43
8:BM:212:LEU:HD12	8:BM:214:ILE:HD11	2.00	0.43
2:FC:224:TYR:HB2	2:FC:250:ALA:HB3	2.00	0.43
5:CH:111:ALA:O	5:CH:115:MET:HB2	2.18	0.43
4:ED:31:ASN:N	4:ED:31:ASN:OD1	2.51	0.43
3:EF:216:ILE:HD11	3:EF:219:ARG:HB2	2.00	0.43
4:Ed:65:PRO:HA	4:Ed:68:ASP:HB2	2.00	0.43
5:FH:356:LEU:HD23	5:FH:356:LEU:HA	1.91	0.43
1:JG:1005:VAL:O	1:JG:1009:ALA:CB	2.67	0.43
1:LG:946:SER:OG	1:LG:1030:GLU:O	2.25	0.43
8:FM:280:TYR:HA	8:FM:299:LEU:O	2.19	0.43
2:BC:156:LYS:NZ	2:BC:157:PRO:O	2.44	0.42
8:GM:303:GLU:OE1	8:GM:306:GLN:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:IH:354:MET:HB3	5:IH:354:MET:HE3	1.75	0.42
7:IL:91:VAL:HA	7:IL:94:VAL:HG22	1.99	0.42
5:LH:132:GLN:O	5:LH:136:THR:OG1	2.31	0.42
9:LN:86:LEU:HB3	9:LN:87:TRP:CD1	2.54	0.42
4:MD:158:TYR:O	4:Md:137:TYR:OH	2.35	0.42
1:Cg:800:ASP:N	1:Cg:800:ASP:OD1	2.50	0.42
5:MH:316:ASN:N	5:MH:316:ASN:OD1	2.52	0.42
8:MM:120:GLY:H	8:MM:140:ASN:HB2	1.84	0.42
7:AL:91:VAL:HA	7:AL:94:VAL:HG22	2.01	0.42
9:AN:104:ASN:N	9:AN:104:ASN:OD1	2.52	0.42
1:FG:1019:ALA:O	1:FG:1023:PHE:HB2	2.19	0.42
5:CH:223:TYR:HB2	5:CH:242:ILE:HG13	2.01	0.42
1:GG:931:SER:H	1:GG:1043:GLN:NE2	2.17	0.42
6:DK:66:LYS:HD2	6:DK:66:LYS:HA	1.85	0.42
8:EM:218:LYS:HE2	8:EM:218:LYS:HB2	1.85	0.42
4:Ed:149:PRO:O	4:Ed:152:GLN:NE2	2.46	0.42
5:FH:149:PRO:HB2	5:FH:248:VAL:HG22	2.01	0.42
1:PG:917:ASN:HA	1:PG:931:SER:HA	2.00	0.42
2:EC:240:ILE:HG12	2:FC:254:LEU:HD13	2.01	0.42
2:EC:268:LYS:HD2	2:EC:268:LYS:HA	1.91	0.42
3:GF:219:ARG:HG2	5:HH:148:PRO:HD2	2.01	0.42
5:GH:160:LEU:HD12	5:GH:160:LEU:HA	1.91	0.42
6:GK:62:LYS:HD3	6:GK:62:LYS:HA	1.85	0.42
6:GK:92:ASN:O	6:GK:95:SER:OG	2.37	0.42
7:GL:184:ALA:O	7:GL:188:THR:OG1	2.35	0.42
9:GN:56:GLY:HA3	9:GN:74:ALA:HB2	2.01	0.42
7:HL:59:ARG:HH12	7:HL:99:ARG:HH11	1.67	0.42
8:HM:141:GLU:OE2	8:HM:143:THR:OG1	2.35	0.42
1:BG:946:SER:OG	1:BG:1030:GLU:O	2.35	0.42
4:Id:105:ARG:HG3	4:Id:153:VAL:HG23	2.00	0.42
5:KH:307:SER:OG	5:KH:308:ASN:N	2.53	0.42
7:KL:44:HIS:HB3	7:KL:48:ASN:HA	2.00	0.42
8:KM:127:ASN:OD1	8:KM:127:ASN:N	2.53	0.42
4:Ld:73:ILE:HG22	4:Ld:75:ASN:H	1.84	0.42
8:MM:275:ASP:OD1	8:MM:275:ASP:N	2.53	0.42
8:MM:310:LYS:H	8:MM:310:LYS:HG3	1.62	0.42
3:VF:219:ARG:NH2	3:VF:231:THR:OG1	2.47	0.42
5:VH:166:PRO:HA	5:VH:167:PRO:HD3	1.94	0.42
3:WF:210:TYR:HA	3:WF:224:GLY:HA2	2.02	0.42
3:XF:243:MET:O	3:XF:257:SER:N	2.52	0.42
4:AD:121:ILE:HD13	4:AD:121:ILE:HA	1.89	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:IC:58:MET:HA	2:IC:61:LYS:HG2	2.01	0.42
2:KC:268:LYS:HD2	2:KC:268:LYS:HA	1.79	0.42
3:Cf:256:THR:HG1	3:Cf:259:GLY:H	1.67	0.42
3:DF:245:LYS:HB2	3:DF:257:SER:HB3	2.00	0.42
5:EH:288:PRO:HB3	5:EH:305:TRP:CE2	2.54	0.42
8:EM:174:GLN:NE2	8:EM:193:GLN:O	2.53	0.42
5:FH:307:SER:OG	5:FH:308:ASN:N	2.52	0.42
6:FK:54:ILE:O	6:FK:58:THR:OG1	2.31	0.42
1:HG:931:SER:H	1:HG:1043:GLN:NE2	2.16	0.42
1:KG:898:LYS:HE3	1:KG:900:ILE:HG13	2.01	0.42
7:FL:98:TYR:O	7:FL:101:SER:OG	2.33	0.42
4:GD:69:ASN:OD1	4:GD:69:ASN:N	2.39	0.42
9:GN:96:ASN:HD22	9:GN:97:SER:H	1.66	0.42
4:ID:28:PRO:HG3	7:IL:115:GLN:HB2	2.01	0.42
5:IH:242:ILE:HG22	5:IH:245:GLN:HE22	1.83	0.42
7:IL:102:LYS:HB2	7:IL:102:LYS:HE3	1.77	0.42
4:Dd:43:GLU:HB3	7:DL:172:VAL:HG11	2.01	0.42
4:Id:141:LYS:HD3	4:Id:141:LYS:HA	1.82	0.42
4:JD:140:GLY:O	4:Jd:60:LYS:NZ	2.40	0.42
5:JH:214:MET:SD	5:JH:214:MET:N	2.93	0.42
5:KH:328:MET:HE3	2:FC:115:THR:HB	2.00	0.42
6:KK:188:VAL:O	9:KN:57:ARG:NH1	2.53	0.42
6:AK:50:ASP:HA	6:AK:53:ILE:HD12	2.01	0.42
3:MF:241:TYR:HB3	3:MF:256:THR:HG21	2.02	0.42
8:MM:271:SER:O	8:MM:290:ASP:HA	2.19	0.42
4:Md:48:VAL:HG11	2:HC:94:ILE:HA	2.01	0.42
5:VH:180:VAL:HG13	5:VH:253:ASP:HA	2.01	0.42
3:Af:241:TYR:O	3:Af:258:SER:OG	2.36	0.42
1:Dg:808:LEU:H	1:Dg:808:LEU:HG	1.68	0.42
2:FC:77:ILE:HD13	2:FC:77:ILE:HA	1.89	0.42
2:FC:251:LEU:HD23	2:FC:251:LEU:HA	1.91	0.42
5:CH:189:TRP:CD2	5:CH:230:LEU:HD13	2.54	0.42
8:EM:154:LYS:HE2	8:EM:174:GLN:HB3	2.01	0.42
5:FH:154:THR:HB	5:FH:156:GLN:HE22	1.83	0.42
5:FH:180:VAL:HB	5:FH:212:THR:HG22	2.00	0.42
1:HG:911:LYS:HA	1:HG:943:ALA:HA	2.01	0.42
8:FM:172:ASN:OD1	8:FM:173:LEU:N	2.52	0.42
1:AG:1005:VAL:O	1:AG:1009:ALA:CB	2.68	0.42
9:GN:111:GLU:OE1	9:GN:112:CYS:N	2.53	0.42
5:HH:189:TRP:NE1	5:HH:231:ARG:H	2.14	0.42
5:IH:187:ALA:HB1	5:IH:262:ASN:HB2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:JH:296:VAL:HB	5:JH:359:GLU:HB3	2.01	0.42
1:CG:903:PHE:HA	1:CG:915:THR:H	1.85	0.42
6:MK:66:LYS:HA	6:MK:66:LYS:HD2	1.87	0.42
8:MM:208:LYS:HD3	8:MM:208:LYS:HA	1.86	0.42
3:XF:243:MET:HB3	3:XF:257:SER:HB3	2.01	0.42
4:BD:130:GLU:OE2	4:BD:133:ARG:NH1	2.53	0.42
9:BN:66:SER:OG	9:BN:67:THR:N	2.52	0.42
4:Bd:36:ASP:OD1	4:Bd:36:ASP:N	2.50	0.42
2:IC:148:TRP:HB2	2:IC:152:LEU:HD23	2.00	0.42
2:MC:119:ASN:ND2	5:EH:274:PRO:O	2.52	0.42
3:DF:213:GLN:HB3	3:DF:221:TRP:HB3	2.00	0.42
5:DH:210:SER:OG	5:DH:211:ASN:N	2.52	0.42
6:DK:75:LEU:HD11	6:DK:181:GLU:HB3	2.01	0.42
7:DL:168:PHE:HB2	7:DL:228:ARG:HG2	2.02	0.42
9:DN:110:GLU:HA	9:DN:113:SER:HB2	2.01	0.42
1:Eg:813:LYS:HB2	1:Eg:813:LYS:HE2	1.79	0.42
6:EK:51:ALA:HB1	9:EN:44:LYS:HE2	2.01	0.42
11:EX:70:UNK:H2	5:FH:146:GLY:H	1.67	0.42
5:FH:170:ARG:HG2	5:FH:245:GLN:HG3	2.02	0.42
1:MG:1005:VAL:O	1:MG:1009:ALA:CB	2.67	0.42
1:OG:959:LEU:O	1:OG:963:SER:OG	2.33	0.42
7:FL:170:ASP:N	7:FL:170:ASP:OD1	2.51	0.42
1:AG:965:LEU:HG	1:AG:1008:LEU:HD22	2.00	0.42
8:GM:158:VAL:HA	8:GM:178:LYS:HE2	2.02	0.42
7:HL:115:GLN:HB3	7:HL:126:ILE:HB	2.00	0.42
4:Hd:76:ALA:O	4:Hd:80:GLN:NE2	2.42	0.42
1:Bg:821:THR:OG1	5:AH:194:TYR:O	2.36	0.42
1:Ig:824:THR:HG23	5:XH:231:ARG:HH22	1.83	0.42
6:IK:111:LYS:N	6:IK:111:LYS:HZ2	2.17	0.42
5:JH:320:LEU:N	5:JH:346:LEU:O	2.48	0.42
6:JK:56:MET:HE2	6:JK:56:MET:HB3	1.88	0.42
8:JM:240:GLN:HA	8:JM:260:VAL:HG23	2.02	0.42
5:AH:141:LYS:HE2	5:AH:141:LYS:HB3	1.91	0.42
6:KK:47:GLY:O	6:KK:108:GLN:NE2	2.52	0.42
1:Lg:811:ASP:OD1	1:Lg:811:ASP:N	2.52	0.42
5:LH:180:VAL:HG13	5:LH:253:ASP:HA	2.01	0.42
9:LN:110:GLU:HA	9:LN:113:SER:HB3	2.01	0.42
1:Ag:798:THR:O	1:Ag:802:LEU:N	2.51	0.42
6:MK:107:LYS:NZ	6:MK:148:GLY:O	2.39	0.42
6:MK:166:THR:HG22	6:MK:168:TYR:H	1.83	0.42
5:VH:352:LYS:HE3	5:VH:352:LYS:HB3	1.90	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:WF:216:ILE:HD11	3:WF:219:ARG:HB2	2.01	0.42
5:YH:332:ASP:OD1	5:YH:332:ASP:N	2.42	0.42
8:AM:254:LYS:HB2	8:AM:254:LYS:HE3	1.77	0.42
3:Af:238:ILE:HD12	3:Af:239:PRO:HD2	2.00	0.42
5:BH:246:LYS:HD2	5:BH:246:LYS:HA	1.81	0.42
2:FC:108:VAL:HG13	2:FC:207:GLY:HA3	2.02	0.42
2:FC:109:LEU:HD13	2:FC:109:LEU:HA	1.87	0.42
2:KC:141:ILE:HD12	2:KC:141:ILE:HA	1.90	0.42
4:DD:130:GLU:OE2	4:DD:133:ARG:NH1	2.52	0.42
5:DH:354:MET:HE3	5:DH:354:MET:HB2	1.72	0.42
7:EL:59:ARG:HD2	7:EL:59:ARG:HA	1.88	0.42
8:EM:275:ASP:OD1	8:EM:275:ASP:N	2.50	0.42
4:FD:124:LYS:HD2	6:FK:145:TRP:CD1	2.55	0.42
1:LG:876:SER:OG	1:LG:1031:VAL:O	2.31	0.42
1:MG:917:ASN:HA	1:MG:931:SER:HA	2.01	0.42
1:NG:1011:VAL:HG12	1:OG:963:SER:HB2	2.02	0.42
4:Fd:73:ILE:HD12	4:Fd:129:ALA:HB1	2.01	0.42
4:Fd:82:ARG:NH2	4:Fd:126:GLU:O	2.40	0.42
1:AG:898:LYS:HE3	1:BG:865:THR:HB	2.02	0.42
2:BC:94:ASP:OD1	2:BC:97:SER:N	2.42	0.42
2:BC:98:LEU:HD13	2:BC:98:LEU:HA	1.90	0.42
3:GF:230:LEU:HD12	3:GF:230:LEU:HA	1.87	0.42
5:GH:171:LEU:HD11	5:GH:241:LEU:HB3	2.01	0.42
9:GN:39:ASP:OD1	9:GN:39:ASP:N	2.51	0.42
3:Gf:244:VAL:HA	3:Gf:256:THR:HA	2.02	0.42
7:IL:103:ARG:H	7:IL:103:ARG:HG3	1.66	0.42
4:Dd:92:GLU:OE2	4:Dd:158:TYR:OH	2.32	0.42
3:If:247:ILE:HD13	3:If:247:ILE:HA	1.94	0.42
7:JL:118:GLU:OE2	7:JL:123:ARG:NH2	2.52	0.42
5:AH:182:LEU:O	5:AH:255:ARG:HA	2.19	0.42
6:KK:144:LEU:HD22	6:KK:144:LEU:HA	1.89	0.42
5:MH:170:ARG:NE	5:MH:249:ASP:OD1	2.42	0.42
3:WF:208:ILE:O	3:WF:241:TYR:OH	2.32	0.42
8:AM:163:THR:O	8:AM:183:VAL:HA	2.20	0.42
9:BN:39:ASP:OD1	9:BN:39:ASP:N	2.53	0.42
2:GC:106:LEU:HD12	2:GC:107:PRO:HD2	2.01	0.42
2:KC:220:MET:HA	2:KC:256:ASN:HD21	1.83	0.42
2:MC:145:PRO:HA	2:MC:146:PRO:HD3	1.85	0.42
2:MC:227:VAL:HA	2:MC:250:ILE:HA	2.01	0.42
5:CH:200:SER:O	5:CH:218:THR:OG1	2.33	0.42
6:CK:92:ASN:O	6:CK:95:SER:OG	2.29	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:CM:274:THR:OG1	8:CM:275:ASP:OD1	2.30	0.42
1:Eg:800:ASP:O	1:Eg:803:THR:OG1	2.32	0.42
5:EH:228:VAL:HB	5:EH:237:VAL:HG23	2.01	0.42
9:EN:86:LEU:HD12	9:EN:86:LEU:HA	1.84	0.42
3:FF:246:LEU:HB2	3:FF:255:LEU:HB2	2.01	0.42
1:KG:1017:GLN:NE2	1:LG:1020:GLN:OE1	2.51	0.42
1:OG:951:HIS:O	1:OG:955:ARG:NE	2.44	0.42
1:PG:958:SER:O	1:PG:962:SER:OG	2.34	0.42
1:AG:916:PHE:HD1	1:AG:916:PHE:HA	1.70	0.42
2:EC:261:GLU:OE1	2:EC:261:GLU:N	2.53	0.42
5:HH:253:ASP:N	5:HH:253:ASP:OD1	2.52	0.42
5:HH:277:ASN:HB3	5:HH:279:LEU:HD12	2.02	0.42
3:IF:216:ILE:HG12	3:IF:221:TRP:HZ3	1.83	0.42
4:JD:93:GLU:H	4:JD:93:GLU:HG3	1.58	0.42
5:LH:146:GLY:HA2	11:YX:70:UNK:H2	1.84	0.42
1:DG:893:LYS:HB3	1:DG:893:LYS:HE3	1.91	0.42
5:MH:238:MET:SD	5:MH:238:MET:N	2.92	0.42
5:MH:273:PRO:O	2:HC:127:ARG:NH1	2.45	0.42
8:MM:204:LEU:HD13	8:MM:204:LEU:HA	1.93	0.42
4:CD:87:TRP:CD1	4:CD:89:GLY:H	2.38	0.42
5:XH:151:PRO:HA	5:XH:248:VAL:HG13	2.01	0.42
1:YG:796:GLN:O	1:YG:799:SER:OG	2.33	0.42
2:DC:169:LYS:H	2:DC:173:GLU:HG3	1.85	0.42
8:AM:145:ARG:HH21	8:AM:163:THR:HA	1.85	0.42
4:AD:131:ILE:HD13	4:AD:131:ILE:HA	1.88	0.42
4:AD:150:ASN:OD1	4:AD:150:ASN:N	2.53	0.42
2:MC:55:ILE:HD12	1:PG:938:ASN:H	1.84	0.42
5:CH:130:LEU:HD22	5:CH:130:LEU:HA	1.92	0.42
8:CM:303:GLU:OE1	8:CM:306:GLN:N	2.46	0.42
8:DM:153:GLN:HA	8:DM:173:LEU:HD12	2.02	0.42
5:EH:284:LEU:HD23	5:EH:284:LEU:HA	1.91	0.42
5:EH:346:LEU:HD12	5:EH:346:LEU:HA	1.88	0.42
4:FD:87:TRP:CD1	4:FD:94:LEU:HD22	2.54	0.42
1:KG:947:ARG:O	1:KG:950:HIS:NE2	2.52	0.42
5:GH:130:LEU:HD23	5:GH:133:ILE:HB	2.02	0.42
6:GK:96:TYR:CG	4:Gd:26:LYS:HD3	2.55	0.42
6:GK:111:LYS:HD3	6:GK:151:SER:HB2	2.01	0.42
1:BG:925:GLU:H	1:BG:925:GLU:HG2	1.60	0.42
3:IF:219:ARG:HG2	5:JH:148:PRO:HG2	2.01	0.42
8:JM:273:ALA:HB1	8:JM:277:SER:HB2	2.01	0.42
2:CC:113:GLY:O	2:CC:130:ARG:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:KH:191:ILE:HG13	5:KH:211:ASN:HA	2.02	0.42
8:KM:307:SER:OG	8:KM:308:ASP:OD2	2.34	0.42
4:Kd:86:ASP:OD1	4:Kd:122:SER:OG	2.36	0.42
7:LL:229:ILE:HD13	7:LL:229:ILE:HA	1.82	0.42
1:DG:888:THR:HA	1:DG:897:SER:O	2.19	0.42
1:DG:1005:VAL:O	1:DG:1009:ALA:CB	2.67	0.42
1:DG:1019:ALA:O	1:DG:1023:PHE:HB2	2.19	0.42
5:MH:104:ALA:N	5:MH:105:GLU:OE1	2.53	0.42
6:MK:50:ASP:HA	6:MK:53:ILE:HD12	2.02	0.42
6:MK:87:GLN:NE2	6:MK:173:ASP:OD1	2.49	0.42
4:CD:162:TYR:OH	2:KC:102:GLU:OE1	2.36	0.42
8:AM:149:ASN:OD1	8:AM:149:ASN:N	2.43	0.42
3:BF:238:ILE:HD12	3:BF:239:PRO:HD2	2.01	0.42
2:KC:225:TYR:HB2	2:KC:251:ALA:HB3	2.00	0.42
6:CK:57:MET:HG3	6:CK:67:VAL:HG11	2.01	0.42
6:CK:65:ILE:HG23	6:CK:78:ILE:HG13	2.02	0.42
3:DF:247:ILE:HG23	3:DF:254:ILE:HG12	2.01	0.42
1:GG:1001:LEU:H	1:GG:1001:LEU:HG	1.61	0.42
8:DM:212:LEU:HD13	8:DM:212:LEU:HA	1.84	0.42
8:DM:228:VAL:HG11	8:DM:231:LEU:HB2	2.01	0.42
3:EF:207:ARG:HA	3:EF:207:ARG:HH11	1.83	0.42
7:EL:124:THR:HG22	7:EL:232:GLN:HG2	2.01	0.42
5:FH:201:SER:O	5:FH:218:THR:N	2.38	0.42
1:KG:924:ALA:HB3	1:KG:926:LYS:HE3	2.01	0.42
1:PG:972:PHE:HB3	1:PG:1005:VAL:HG22	2.01	0.42
9:FN:101:VAL:HG11	9:FN:112:CYS:HB3	2.02	0.42
8:HM:191:LEU:HD21	8:HM:194:LEU:HD12	2.02	0.42
4:KD:121:ILE:HD13	4:KD:121:ILE:HA	1.90	0.42
2:CC:169:THR:HG23	2:CC:172:GLU:H	1.83	0.42
6:KK:40:LYS:HE2	6:KK:40:LYS:HB2	1.93	0.42
7:KL:53:ASP:OD2	7:KL:153:ARG:NH1	2.53	0.42
8:KM:160:ASN:OD1	8:KM:160:ASN:N	2.53	0.42
6:LK:66:LYS:NZ	6:LK:67:VAL:O	2.53	0.42
8:LM:300:ASP:OD1	8:LM:302:ARG:NE	2.37	0.42
5:MH:166:PRO:HA	5:MH:167:PRO:HD3	1.93	0.42
8:MM:212:LEU:HD13	8:MM:212:LEU:HA	1.93	0.42
5:WH:210:SER:HB2	5:FH:229:ARG:HH12	1.85	0.42
5:BH:207:ASP:O	5:BH:210:SER:OG	2.34	0.42
6:BK:129:GLU:OE1	6:BK:129:GLU:N	2.49	0.42
2:JC:227:HIS:HB3	2:JC:246:LEU:HD13	2.01	0.42
2:KC:83:LEU:HD11	2:KC:151:LEU:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:KC:213:ARG:HG3	2:KC:214:LYS:HE3	2.02	0.42
9:CN:39:ASP:N	9:CN:39:ASP:OD1	2.53	0.42
1:GG:969:GLY:HA2	1:GG:1005:VAL:HA	2.01	0.42
7:DL:230:GLU:OE2	7:DL:232:GLN:NE2	2.53	0.42
1:IG:916:PHE:HD1	1:IG:916:PHE:HA	1.67	0.42
1:LG:873:LEU:HB2	1:LG:1037:LEU:HD22	2.02	0.42
1:LG:969:GLY:HA3	1:LG:1009:ALA:HB2	2.02	0.42
2:LC:122:ASP:OD1	2:LC:122:ASP:N	2.53	0.42
2:BC:115:THR:HG22	5:GH:328:MET:HG2	2.02	0.42
5:GH:143:ALA:O	5:HH:131:LYS:NZ	2.45	0.42
8:GM:292:MET:HE2	8:GM:292:MET:HB3	1.74	0.42
9:GN:89:GLY:HA3	9:GN:104:ASN:HB2	2.01	0.42
9:GN:94:GLN:HE22	9:GN:96:ASN:HB2	1.84	0.42
4:Gd:78:ASN:OD1	4:Gd:78:ASN:N	2.53	0.42
5:HH:221:TYR:OH	5:XH:135:GLU:OE2	2.33	0.42
9:HN:58:LEU:HG	9:HN:70:CYS:HB3	2.01	0.42
2:CC:79:ILE:HD11	2:CC:195:LEU:HD13	2.02	0.42
4:LD:87:TRP:CG	4:LD:94:LEU:HD22	2.55	0.42
7:LL:199:ALA:HB3	7:LL:202:ARG:HD3	2.02	0.42
8:MM:150:ILE:O	8:MM:168:VAL:HA	2.20	0.42
5:VH:281:LEU:HD13	5:VH:281:LEU:HA	1.94	0.42
1:EG:1025:THR:HA	1:EG:1026:PRO:HD3	1.93	0.42
4:Bd:82:ARG:NH2	4:Bd:125:ASP:OD2	2.53	0.42
2:FC:98:LEU:HD13	2:FC:98:LEU:HA	1.92	0.42
2:GC:165:LEU:HD12	2:GC:165:LEU:HA	1.91	0.42
2:IC:214:ARG:HA	2:IC:214:ARG:HD3	1.85	0.42
2:MC:169:LYS:HA	2:MC:169:LYS:HD3	1.86	0.42
6:CK:76:ILE:HB	6:CK:182:ILE:HG13	2.02	0.42
6:CK:83:LEU:HD22	6:CK:83:LEU:HA	1.83	0.42
6:CK:122:LYS:HD2	6:CK:122:LYS:HA	1.89	0.42
4:DD:148:TYR:O	4:DD:152:GLN:N	2.53	0.42
7:DL:113:ASP:OD1	7:DL:113:ASP:N	2.38	0.42
7:DL:165:VAL:HG12	7:DL:231:ILE:HG12	2.00	0.42
9:EN:81:LEU:HD11	5:FH:357:LYS:HG3	2.02	0.42
6:FK:151:SER:O	6:FK:152:ARG:NH1	2.53	0.42
1:JG:1005:VAL:O	1:JG:1009:ALA:HB2	2.20	0.42
1:NG:924:ALA:HB3	1:NG:926:LYS:HE3	2.00	0.42
1:NG:951:HIS:H	1:NG:1027:THR:HG22	1.85	0.42
1:PG:871:ALA:HA	1:PG:890:VAL:HG22	2.02	0.42
2:LC:110:VAL:HB	2:LC:137:LYS:H	1.85	0.42
2:LC:122:ASP:OD1	2:LC:125:SER:OG	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:GD:137:TYR:CZ	4:Gd:57:LYS:HG3	2.55	0.41
5:GH:325:LEU:N	5:GH:338:GLU:O	2.42	0.41
4:HD:79:LEU:HA	4:HD:128:LEU:HD12	2.02	0.41
1:BG:870:PHE:HA	1:BG:1038:GLY:HA2	2.00	0.41
5:IH:330:SER:OG	5:IH:333:GLY:N	2.44	0.41
8:JM:271:SER:O	8:JM:290:ASP:HA	2.20	0.41
9:JN:89:GLY:HA3	9:JN:104:ASN:HB2	2.00	0.41
5:AH:157:PHE:HA	5:AH:255:ARG:HB3	2.01	0.41
5:AH:160:LEU:HB2	5:BH:251:ARG:HH12	1.85	0.41
5:AH:238:MET:HB3	5:BH:250:TYR:HD2	1.84	0.41
2:CC:215:LEU:HD22	2:CC:220:MET:HG3	2.02	0.41
5:KH:207:ASP:OD1	5:KH:207:ASP:N	2.53	0.41
6:KK:142:GLU:OE1	7:KL:139:ARG:NH1	2.52	0.41
4:MD:80:GLN:N	4:MD:80:GLN:OE1	2.53	0.41
1:Ag:805:ALA:HB1	5:CH:119:LEU:HD11	2.01	0.41
5:VH:117:ARG:HA	5:VH:117:ARG:HD2	1.91	0.41
5:XH:189:TRP:HE1	5:XH:232:GLY:H	1.68	0.41
5:ZH:106:VAL:HA	5:ZH:109:LYS:HE2	2.01	0.41
5:ZH:205:GLN:HB2	5:ZH:214:MET:HE3	2.02	0.41
8:AM:171:ARG:HH21	8:AM:172:ASN:HB2	1.85	0.41
9:AN:42:CYS:HA	9:AN:45:MET:HE3	2.01	0.41
4:Ad:128:LEU:HA	4:Ad:131:ILE:HD12	2.02	0.41
3:CF:222:LEU:O	3:CF:229:THR:OG1	2.31	0.41
8:BM:190:ASN:OD1	8:BM:192:ARG:NH2	2.38	0.41
8:BM:275:ASP:OD1	8:BM:275:ASP:N	2.52	0.41
4:AD:93:GLU:OE2	4:AD:94:LEU:N	2.52	0.41
2:GC:110:LEU:HD13	2:GC:110:LEU:HA	1.87	0.41
2:GC:130:ARG:NH1	2:GC:132:TYR:OH	2.49	0.41
2:MC:151:TYR:CG	2:MC:203:ILE:HD13	2.55	0.41
6:CK:81:SER:OG	6:CK:173:ASP:O	2.36	0.41
8:CM:131:THR:HG21	8:CM:134:LEU:HG	2.01	0.41
6:EK:111:LYS:HE3	6:EK:111:LYS:HB3	1.91	0.41
8:EM:117:ARG:HE	8:EM:117:ARG:HB3	1.57	0.41
8:EM:242:LYS:HA	8:EM:262:GLU:HG2	2.02	0.41
1:KG:946:SER:OG	1:KG:1030:GLU:O	2.27	0.41
1:AG:925:GLU:H	1:AG:925:GLU:HG2	1.58	0.41
2:BC:262:ARG:NH2	2:BC:263:ALA:O	2.50	0.41
3:GF:215:VAL:H	5:GH:245:GLN:HE22	1.68	0.41
9:HN:86:LEU:HB3	9:HN:87:TRP:HD1	1.84	0.41
8:IM:279:ILE:HB	8:IM:298:VAL:HG22	2.02	0.41
3:JF:207:ARG:HA	3:JF:207:ARG:HD2	1.81	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:JN:86:LEU:HB3	9:JN:87:TRP:CD1	2.55	0.41
4:KD:61:VAL:HG21	2:FC:266:ALA:HA	2.03	0.41
4:KD:83:ALA:HA	6:KK:154:ILE:O	2.20	0.41
2:CC:168:LYS:NZ	2:CC:172:GLU:OE2	2.43	0.41
3:KF:267:GLU:O	5:KH:150:LYS:NZ	2.39	0.41
5:KH:225:ASN:HD21	5:YH:176:VAL:HG13	1.85	0.41
6:LK:163:LYS:HD2	6:LK:163:LYS:HA	1.82	0.41
11:LX:20:UNK:HA	11:LX:79:UNK:HA	2.02	0.41
8:MM:171:ARG:H	8:MM:171:ARG:HG2	1.57	0.41
4:Md:40:LYS:HE2	4:Md:40:LYS:HB2	1.89	0.41
3:ZF:238:ILE:HD12	3:ZF:239:PRO:HD2	2.02	0.41
5:BH:166:PRO:HA	5:BH:167:PRO:HD3	1.91	0.41
5:BH:275:SER:HA	2:JC:125:ARG:HD3	2.02	0.41
2:GC:213:ARG:HA	2:GC:213:ARG:HD3	1.90	0.41
2:JC:239:ILE:HG12	2:KC:255:LEU:HD13	2.02	0.41
2:KC:110:LEU:HD13	2:KC:110:LEU:HA	1.89	0.41
7:CL:174:SER:HG	7:CL:176:SER:HG	1.66	0.41
1:GG:880:ASP:OD1	1:GG:880:ASP:N	2.52	0.41
1:Eg:800:ASP:OD1	1:Eg:800:ASP:N	2.50	0.41
5:EH:168:VAL:HA	5:EH:240:THR:HG23	2.02	0.41
1:MG:933:TYR:HD1	1:MG:933:TYR:HA	1.65	0.41
1:OG:869:MET:HE3	1:OG:869:MET:HB2	1.86	0.41
7:FL:102:LYS:HE3	7:FL:102:LYS:HB2	1.96	0.41
11:FX:21:UNK:N	11:FX:78:UNK:O	2.53	0.41
2:AC:249:THR:OG1	2:AC:250:ALA:N	2.51	0.41
4:GD:67:LYS:HB2	4:GD:67:LYS:HE3	1.82	0.41
3:GF:254:ILE:O	3:GF:261:VAL:HA	2.20	0.41
8:GM:163:THR:O	8:GM:183:VAL:HA	2.20	0.41
3:Gf:256:THR:OG1	3:Gf:257:SER:N	2.52	0.41
4:Hd:79:LEU:HD13	4:Hd:79:LEU:HA	1.92	0.41
4:ID:27:LYS:HA	4:ID:27:LYS:HD3	1.75	0.41
3:JF:215:VAL:O	5:JH:245:GLN:NE2	2.50	0.41
5:JH:229:ARG:HG2	5:JH:236:PRO:HB3	2.02	0.41
7:JL:129:THR:O	7:JL:133:PHE:HB2	2.19	0.41
5:AH:216:GLN:OE1	1:Ag:818:GLN:N	2.53	0.41
4:KD:57:LYS:HE3	4:KD:57:LYS:HB2	1.92	0.41
5:KH:249:ASP:OD1	5:KH:249:ASP:N	2.53	0.41
5:KH:325:LEU:HA	5:KH:325:LEU:HD23	1.85	0.41
7:LL:94:VAL:HA	7:LL:97:ILE:HG12	2.02	0.41
3:MF:214:ALA:O	3:MF:221:TRP:N	2.49	0.41
5:MH:122:LEU:HD13	5:MH:122:LEU:HA	1.96	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:VH:131:LYS:NZ	5:CH:141:LYS:O	2.39	0.41
3:WF:243:MET:O	3:WF:257:SER:N	2.53	0.41
4:CD:79:LEU:HD23	4:CD:129:ALA:HB2	2.02	0.41
4:CD:158:TYR:O	4:CD:137:TYR:OH	2.36	0.41
3:XF:226:ASN:OD1	3:XF:226:ASN:N	2.54	0.41
8:BM:114:ASN:O	8:BM:134:LEU:HA	2.20	0.41
8:BM:171:ARG:HE	8:BM:171:ARG:HB3	1.61	0.41
1:Dg:801:MET:HG3	5:FH:115:MET:HG3	2.01	0.41
4:AD:67:LYS:HE3	4:AD:67:LYS:HB3	1.91	0.41
2:FC:140:ILE:HD12	2:FC:140:ILE:HA	1.85	0.41
2:IC:145:PRO:HA	2:IC:146:PRO:HD3	1.95	0.41
9:CN:72:ARG:HH21	5:DH:296:VAL:HG13	1.86	0.41
4:Ed:141:LYS:HD3	4:Ed:141:LYS:HA	1.78	0.41
3:Ef:230:LEU:HD12	3:Ef:230:LEU:HA	1.94	0.41
4:FD:55:MET:HA	4:FD:58:VAL:HG12	2.02	0.41
5:FH:161:SER:O	5:FH:164:SER:OG	2.38	0.41
5:FH:277:ASN:HD21	5:FH:279:LEU:HD13	1.84	0.41
1:NG:925:GLU:H	1:NG:925:GLU:HG2	1.53	0.41
1:NG:1005:VAL:O	1:NG:1009:ALA:CB	2.68	0.41
2:HC:41:SER:O	2:HC:44:THR:OG1	2.30	0.41
7:FL:193:LEU:HA	7:FL:193:LEU:HD13	1.86	0.41
8:FM:149:ASN:OD1	8:FM:149:ASN:N	2.50	0.41
2:AC:165:LEU:HD13	2:AC:165:LEU:HA	1.90	0.41
1:AG:951:HIS:H	1:AG:1027:THR:HG22	1.85	0.41
2:EC:210:ILE:HD11	4:JD:55:MET:HE2	2.01	0.41
5:GH:169:ILE:HD13	5:GH:169:ILE:HA	1.97	0.41
6:GK:87:GLN:N	6:GK:173:ASP:OD2	2.53	0.41
4:Gd:123:THR:OG1	4:Gd:124:LYS:N	2.54	0.41
7:HL:44:HIS:HB2	7:HL:48:ASN:HA	2.01	0.41
1:BG:879:SER:HG	1:BG:1029:VAL:H	1.69	0.41
5:IH:273:PRO:HA	5:IH:274:PRO:HD3	1.88	0.41
5:AH:166:PRO:HA	5:AH:167:PRO:HD3	1.89	0.41
2:CC:157:LYS:NZ	2:CC:158:PRO:O	2.53	0.41
5:KH:319:ILE:HD11	5:KH:337:TYR:CG	2.55	0.41
7:KL:54:ARG:HH21	7:KL:57:VAL:HG13	1.86	0.41
7:KL:165:VAL:HG12	7:KL:231:ILE:HG12	2.01	0.41
8:KM:224:LEU:HB2	8:KM:246:LEU:HD22	2.01	0.41
3:Lf:254:ILE:HB	3:Lf:262:ILE:HG23	2.02	0.41
7:ML:53:ASP:OD1	7:ML:53:ASP:N	2.53	0.41
4:Md:112:SER:HA	4:Md:113:PRO:HD3	1.96	0.41
5:VH:109:LYS:HE2	5:VH:109:LYS:HB2	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:VH:189:TRP:CZ2	5:VH:230:LEU:HB3	2.55	0.41
5:XH:159:ASN:ND2	5:XH:257:GLN:OE1	2.40	0.41
7:AL:193:LEU:HD13	7:AL:193:LEU:HA	1.92	0.41
3:Df:216:ILE:HD12	3:Df:216:ILE:HA	1.84	0.41
5:ZH:357:LYS:HE3	5:ZH:357:LYS:HB3	1.87	0.41
8:AM:199:LYS:HG3	8:AM:219:ALA:HB3	2.03	0.41
2:FC:87:ARG:HD2	2:FC:87:ARG:HA	1.91	0.41
2:KC:97:ASN:OD1	2:KC:97:ASN:N	2.34	0.41
8:CM:299:LEU:HD13	8:CM:299:LEU:HA	1.85	0.41
3:Ef:222:LEU:HD11	3:Ef:262:ILE:HD12	2.02	0.41
4:FD:41:LEU:HD13	4:FD:41:LEU:HA	1.92	0.41
4:FD:54:GLU:OE2	2:AC:213:LYS:NZ	2.46	0.41
5:FH:151:PRO:HA	5:FH:248:VAL:HG23	2.02	0.41
5:FH:158:VAL:HB	5:FH:256:VAL:HA	2.01	0.41
1:JG:917:ASN:HA	1:JG:931:SER:HA	2.03	0.41
1:LG:871:ALA:HB2	1:LG:889:ILE:HD13	2.02	0.41
3:AF:269:SER:HA	5:AH:246:LYS:HE2	2.02	0.41
4:Gd:72:THR:OG1	4:Gd:73:ILE:N	2.53	0.41
1:BG:965:LEU:HG	1:BG:1008:LEU:HD22	2.02	0.41
1:Ig:820:TYR:OH	1:Ig:822:GLU:OE1	2.31	0.41
5:IH:115:MET:HE3	5:IH:115:MET:HB3	1.87	0.41
11:IX:23:UNK:HA	11:IX:33:UNK:HA	2.02	0.41
5:JH:249:ASP:OD1	5:JH:249:ASP:N	2.53	0.41
4:Jd:97:ARG:HA	4:Jd:97:ARG:HD3	1.79	0.41
3:Jf:237:LYS:HB3	3:Jf:237:LYS:HE3	1.65	0.41
5:KH:280:LEU:HD11	5:KH:338:GLU:HB2	2.01	0.41
8:KM:137:TYR:HA	8:KM:156:GLU:O	2.21	0.41
3:MF:237:LYS:HD3	3:MF:237:LYS:HA	1.89	0.41
3:MF:245:LYS:HA	3:MF:245:LYS:HD2	1.79	0.41
5:VH:178:SER:OG	5:CH:238:MET:SD	2.69	0.41
1:EG:893:LYS:HE3	1:EG:893:LYS:HB3	1.91	0.41
4:BD:55:MET:HB2	2:JC:209:ILE:HD11	2.03	0.41
5:BH:229:ARG:NH2	5:CH:212:THR:OG1	2.48	0.41
5:BH:279:LEU:HD12	5:BH:279:LEU:HA	1.95	0.41
7:BL:134:MET:HE2	7:BL:141:ASN:HA	2.03	0.41
2:KC:109:VAL:HG23	2:KC:136:LYS:H	1.85	0.41
2:MC:147:THR:OG1	2:MC:148:TRP:N	2.53	0.41
5:EH:171:LEU:HD23	5:EH:171:LEU:HA	1.93	0.41
5:EH:294:ARG:HG3	5:EH:305:TRP:HE1	1.85	0.41
5:FH:342:SER:OG	5:FH:344:VAL:O	2.39	0.41
2:HC:151:TYR:CG	2:HC:203:ILE:HD13	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AC:105:LEU:HD12	2:AC:106:PRO:HD2	2.03	0.41
1:AG:1003:ASN:HA	1:AG:1006:ILE:HD12	2.01	0.41
2:EC:110:LEU:HD13	2:EC:110:LEU:HA	1.89	0.41
4:Gd:84:SER:H	2:CC:267:ALA:HB3	1.85	0.41
5:JH:266:MET:HE3	5:JH:266:MET:HB2	1.91	0.41
4:KD:67:LYS:HB2	4:Kd:62:ILE:HD11	2.02	0.41
11:KX:23:UNK:N	11:KX:76:UNK:O	2.53	0.41
5:WH:130:LEU:HD12	5:WH:130:LEU:HA	1.92	0.41
4:CD:69:ASN:OD1	4:CD:69:ASN:N	2.49	0.41
5:YH:151:PRO:HA	5:YH:248:VAL:HG23	2.03	0.41
8:AM:123:VAL:HG22	8:AM:143:THR:HB	2.02	0.41
9:AN:89:GLY:HA3	9:AN:104:ASN:HB2	2.02	0.41
5:BH:110:LYS:HA	5:BH:113:LYS:HG2	2.02	0.41
6:BK:50:ASP:OD1	6:BK:50:ASP:N	2.48	0.41
6:BK:124:VAL:N	6:BK:129:GLU:OE2	2.41	0.41
1:Dg:809:VAL:HA	1:Dg:812:TRP:HB2	2.02	0.41
5:CH:313:VAL:HG13	5:CH:337:TYR:HB2	2.02	0.41
4:Cd:31:ASN:OD1	4:Cd:31:ASN:N	2.43	0.41
6:DK:144:LEU:HD13	6:DK:144:LEU:HA	1.82	0.41
9:DN:85:CYS:N	2:LC:155:ASP:OD2	2.54	0.41
1:Eg:801:MET:HB3	5:FH:121:PRO:HB2	2.03	0.41
6:EK:55:LYS:HE2	6:EK:55:LYS:HB2	1.89	0.41
6:EK:91:LEU:HD13	6:EK:91:LEU:HA	1.90	0.41
1:KG:999:SER:OG	1:KG:1000:THR:N	2.53	0.41
1:LG:885:ILE:HG13	1:LG:916:PHE:HE1	1.85	0.41
1:LG:965:LEU:HG	1:LG:1008:LEU:HD22	2.02	0.41
1:PG:862:ILE:HD13	1:PG:1046:THR:HA	2.03	0.41
2:AC:108:VAL:HG13	2:AC:135:LYS:H	1.84	0.41
1:AG:951:HIS:O	1:AG:955:ARG:NE	2.44	0.41
2:EC:111:LEU:HD13	2:EC:111:LEU:HA	1.80	0.41
2:EC:133:LYS:NZ	5:JH:278:ASP:OD2	2.44	0.41
3:GF:233:ARG:NH1	3:GF:235:GLY:O	2.54	0.41
1:Gg:791:GLN:N	1:Gg:793:GLU:OE1	2.53	0.41
1:Gg:794:ILE:O	1:Gg:798:THR:N	2.47	0.41
5:GH:324:TRP:H	2:AC:141:THR:HG21	1.85	0.41
5:GH:346:LEU:HD21	5:GH:353:VAL:HG13	2.01	0.41
4:HD:87:TRP:CD1	4:HD:89:GLY:H	2.39	0.41
4:ID:36:ASP:N	4:ID:36:ASP:OD1	2.53	0.41
4:ID:46:VAL:O	4:ID:49:SER:OG	2.37	0.41
7:IL:129:THR:HB	7:IL:133:PHE:HD2	1.85	0.41
5:JH:357:LYS:HE2	5:JH:357:LYS:HB2	1.91	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CG:937:PRO:HD3	1:CG:1037:LEU:HA	2.02	0.41
2:CC:114:ARG:HG2	2:CC:130:ARG:HG2	2.01	0.41
5:KH:332:ASP:OD1	5:KH:332:ASP:N	2.35	0.41
9:KN:110:GLU:H	9:KN:110:GLU:HG3	1.61	0.41
8:LM:154:LYS:HD3	8:LM:154:LYS:HA	1.85	0.41
1:DG:879:SER:HB3	1:DG:912:MET:HE2	2.02	0.41
3:Lf:243:MET:O	3:Lf:257:SER:N	2.51	0.41
5:MH:295:LEU:HD23	5:MH:295:LEU:HA	1.94	0.41
7:ML:174:SER:OG	7:ML:176:SER:OG	2.35	0.41
5:ZH:328:MET:HE3	5:ZH:328:MET:HB3	1.99	0.41
2:FC:239:ILE:HG12	2:GC:255:LEU:HD13	2.03	0.41
6:CK:119:TYR:HE2	6:CK:163:LYS:HB2	1.85	0.41
7:DL:111:LYS:HE2	7:DL:111:LYS:HB2	1.94	0.41
5:EH:356:LEU:HD13	5:EH:356:LEU:HA	1.88	0.41
7:EL:58:LYS:HA	7:EL:58:LYS:HD3	1.84	0.41
2:EC:199:ILE:HD13	2:EC:199:ILE:HA	1.89	0.41
3:AF:269:SER:OG	3:ZF:233:ARG:NH1	2.54	0.41
8:GM:300:ASP:CG	8:GM:302:ARG:HE	2.29	0.41
7:HL:139:ARG:CZ	8:HM:319:PHE:HB2	2.51	0.41
9:HN:62:ASN:OD1	9:HN:62:ASN:N	2.51	0.41
7:IL:138:PRO:HB3	7:IL:184:ALA:HB1	2.02	0.41
9:IN:95:LEU:HD13	1:FG:893:LYS:HE2	2.01	0.41
6:JK:49:CYS:O	6:JK:52:THR:OG1	2.32	0.41
2:CC:268:LYS:HD2	2:CC:268:LYS:HA	1.86	0.41
7:KL:124:THR:HG22	7:KL:232:GLN:HG2	2.02	0.41
8:KM:212:LEU:HD13	8:KM:212:LEU:HA	1.85	0.41
8:LM:281:TYR:CZ	8:LM:300:ASP:HA	2.55	0.41
5:MH:357:LYS:HE2	5:MH:359:GLU:HB3	2.01	0.41
9:MN:58:LEU:HG	9:MN:70:CYS:HB3	2.01	0.41
3:VF:207:ARG:HH11	3:VF:207:ARG:HA	1.85	0.41
5:WH:194:TYR:HB3	5:WH:228:VAL:HG23	2.03	0.41
5:YH:228:VAL:HG13	5:YH:237:VAL:HB	2.03	0.41
2:DC:107:LEU:HD12	2:DC:108:PRO:HD2	2.03	0.41
8:AM:117:ARG:HE	8:AM:117:ARG:HB3	1.76	0.41
8:AM:271:SER:OG	8:AM:290:ASP:OD1	2.39	0.41
4:Bd:107:ARG:O	4:Bd:155:GLU:HA	2.20	0.41
5:CH:213:LEU:HD23	5:CH:213:LEU:HA	1.91	0.41
5:CH:214:MET:N	5:CH:214:MET:SD	2.93	0.41
6:CK:151:SER:OG	6:CK:153:ILE:N	2.54	0.41
5:DH:126:GLN:HA	5:DH:129:LYS:HG2	2.02	0.41
9:DN:86:LEU:HD12	9:DN:86:LEU:HA	1.94	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:EK:49:CYS:O	6:EK:52:THR:OG1	2.25	0.41
7:EL:104:LYS:HD2	7:EL:104:LYS:HA	1.92	0.41
1:MG:876:SER:HB3	1:NG:941:ARG:HG2	2.03	0.41
1:OG:867:ASP:O	1:OG:1040:LEU:HA	2.19	0.41
7:FL:94:VAL:HA	7:FL:97:ILE:HG12	2.02	0.41
8:FM:275:ASP:HA	8:FM:295:ASN:H	1.86	0.41
2:AC:78:ILE:HA	2:AC:78:ILE:HD12	1.74	0.41
1:AG:886:LEU:HA	1:AG:899:LEU:O	2.21	0.41
2:EC:88:ARG:HD2	2:EC:88:ARG:HA	1.93	0.41
2:EC:175:ILE:HA	2:EC:178:ILE:HG12	2.02	0.41
5:GH:254:LEU:HD12	5:GH:254:LEU:HA	1.82	0.41
7:GL:109:LEU:HD12	7:GL:114:ILE:HB	2.02	0.41
7:GL:177:HIS:CE1	8:GM:314:ARG:HH12	2.38	0.41
7:HL:129:THR:OG1	7:HL:130:ASP:OD1	2.39	0.41
4:Hd:119:ILE:HD12	4:Hd:121:ILE:HD11	2.03	0.41
5:IH:288:PRO:HB3	5:IH:305:TRP:CE2	2.56	0.41
7:IL:109:LEU:HD13	7:IL:109:LEU:HA	1.91	0.41
4:Dd:29:PRO:HB2	4:Dd:32:ASN:HB2	2.02	0.41
4:Id:135:ILE:HD13	4:Id:135:ILE:HA	1.92	0.41
1:Jg:802:LEU:O	1:Jg:806:THR:OG1	2.33	0.41
5:JH:151:PRO:HA	5:JH:248:VAL:HG13	2.02	0.41
6:JK:72:GLN:HB2	7:KL:215:SER:HA	2.03	0.41
4:Jd:98:ILE:HD13	4:Jd:98:ILE:HA	1.89	0.41
4:Jd:135:ILE:HD13	4:Jd:135:ILE:HA	1.89	0.41
5:AH:295:LEU:HD11	5:AH:306:LEU:HB2	2.01	0.41
3:KF:207:ARG:HH11	3:KF:207:ARG:HA	1.86	0.41
3:KF:237:LYS:HB3	3:KF:237:LYS:HE3	1.85	0.41
5:KH:213:LEU:HB3	5:KH:215:ILE:HD11	2.02	0.41
8:KM:123:VAL:HG22	8:KM:143:THR:HB	2.03	0.41
9:KN:62:ASN:OD1	9:KN:62:ASN:N	2.33	0.41
4:Kd:57:LYS:HE2	4:Kd:57:LYS:HB3	1.75	0.41
4:Kd:141:LYS:HA	4:Kd:141:LYS:HD3	1.83	0.41
6:LK:122:LYS:NZ	6:LK:125:SER:O	2.43	0.41
4:MD:161:ILE:HD12	4:MD:161:ILE:HA	1.94	0.41
7:ML:155:LEU:HD12	7:ML:155:LEU:HA	1.85	0.41
8:MM:199:LYS:HA	8:MM:219:ALA:HB3	2.03	0.41
4:Md:150:ASN:OD1	4:Md:150:ASN:N	2.53	0.41
5:VH:144:THR:HA	5:VH:145:PRO:HD3	1.95	0.41
5:XH:311:MET:HG2	5:XH:341:LYS:HA	2.03	0.41
7:AL:168:PHE:HB2	7:AL:228:ARG:HG2	2.03	0.41
5:YH:278:ASP:N	5:YH:278:ASP:OD1	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Df:263:LYS:HE3	3:Df:263:LYS:HB2	1.84	0.41
5:ZH:110:LYS:HB2	5:ZH:110:LYS:HE2	1.76	0.41
8:AM:145:ARG:NH2	8:AM:162:VAL:O	2.54	0.41
4:Ad:32:ASN:HD22	4:Ad:32:ASN:HA	1.73	0.41
4:BD:86:ASP:HA	4:BD:121:ILE:O	2.21	0.41
6:BK:106:LEU:HD23	6:BK:149:VAL:HG11	2.01	0.41
1:FG:868:ILE:HA	1:FG:1039:ILE:O	2.20	0.41
9:BN:88:HIS:ND1	9:BN:105:ASP:OD2	2.53	0.41
4:AD:87:TRP:CD1	4:AD:89:GLY:H	2.39	0.41
2:GC:226:VAL:HG23	2:GC:249:ILE:HG23	2.03	0.41
2:IC:39:ALA:HB1	2:HC:174:LYS:HG2	2.03	0.41
2:IC:80:ILE:HD12	2:IC:196:LEU:HD22	2.03	0.41
2:JC:100:LEU:HB2	2:JC:104:ILE:HG13	2.01	0.41
2:KC:101:LEU:HD23	2:KC:101:LEU:HA	1.83	0.41
2:KC:103:HIS:CD2	2:KC:226:VAL:HG21	2.56	0.41
2:KC:117:LEU:HD23	5:CH:324:TRP:HH2	1.86	0.41
5:CH:166:PRO:HA	5:CH:167:PRO:HD3	1.90	0.41
7:CL:102:LYS:HA	7:CL:105:ILE:HD12	2.03	0.41
9:CN:81:LEU:HD13	9:CN:81:LEU:HA	1.94	0.41
3:DF:219:ARG:HG2	5:EH:148:PRO:HD2	2.03	0.41
1:GG:885:ILE:O	1:GG:900:ILE:HA	2.20	0.41
1:GG:1002:GLU:H	1:GG:1002:GLU:HG3	1.64	0.41
6:DK:73:ASN:OD1	6:DK:73:ASN:N	2.52	0.41
6:DK:102:ILE:HD13	6:DK:102:ILE:HA	1.89	0.41
8:DM:276:ALA:H	8:DM:295:ASN:HB2	1.86	0.41
8:EM:269:GLN:HE21	8:EM:269:GLN:HB3	1.54	0.41
3:Ef:209:ILE:HG23	3:Ef:225:SER:HB3	2.02	0.41
5:FH:250:TYR:HD1	5:FH:250:TYR:HA	1.78	0.41
1:IG:893:LYS:HE3	1:IG:893:LYS:HB3	1.80	0.41
1:KG:944:LEU:HD11	1:KG:1031:VAL:HA	2.03	0.41
1:MG:1030:GLU:OE2	1:NG:941:ARG:NH2	2.41	0.41
1:PG:936:ASP:HB2	1:PG:941:ARG:H	1.85	0.41
7:FL:93:LEU:HD13	7:FL:93:LEU:HA	1.94	0.41
5:GH:317:LEU:HD13	5:GH:347:VAL:HG11	2.03	0.41
6:GK:98:LEU:HD12	6:GK:98:LEU:HA	1.95	0.41
6:GK:122:LYS:NZ	6:GK:129:GLU:OE2	2.42	0.41
3:If:212:ILE:HA	3:If:222:LEU:HD12	2.03	0.41
4:JD:34:SER:OG	4:Jd:36:ASP:OD1	2.34	0.41
8:JM:120:GLY:H	8:JM:140:ASN:HB2	1.85	0.41
1:CG:924:ALA:HB3	1:CG:926:LYS:HG2	2.02	0.41
3:Kf:210:TYR:HA	3:Kf:224:GLY:HA2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:LK:110:ARG:NH2	9:LN:77:ASP:OD2	2.53	0.41
1:DG:944:LEU:HD11	1:DG:1031:VAL:HA	2.03	0.41
1:DG:1025:THR:HA	1:DG:1026:PRO:HD3	1.89	0.41
3:Lf:244:VAL:HA	3:Lf:256:THR:HA	2.01	0.41
5:MH:120:TYR:HD1	5:MH:120:TYR:HA	1.77	0.41
5:MH:131:LYS:HD3	5:MH:131:LYS:HA	1.76	0.41
1:EG:880:ASP:OD1	1:EG:880:ASP:N	2.51	0.41
8:AM:235:LEU:HD23	8:AM:259:SER:HB2	2.03	0.41
2:GC:240:ILE:HG12	2:HC:256:LEU:HD13	2.02	0.41
2:IC:110:VAL:HB	2:IC:137:LYS:H	1.85	0.41
2:JC:110:LEU:HD13	2:JC:110:LEU:HA	1.89	0.41
2:JC:145:THR:H	2:JC:148:GLN:HE22	1.68	0.41
2:MC:226:TYR:HB3	2:MC:252:ALA:HB3	2.03	0.41
4:DD:46:VAL:O	4:DD:49:SER:OG	2.36	0.41
6:EK:166:THR:HG22	6:EK:168:TYR:H	1.86	0.41
4:Ed:72:THR:OG1	4:Ed:73:ILE:N	2.54	0.41
5:FH:159:ASN:HD22	5:FH:159:ASN:HA	1.61	0.41
5:FH:170:ARG:NH1	5:FH:247:ALA:O	2.50	0.41
1:IG:880:ASP:OD1	1:IG:880:ASP:N	2.53	0.41
1:NG:884:PRO:HA	1:NG:901:GLY:O	2.21	0.41
1:NG:898:LYS:NZ	1:OG:865:THR:O	2.46	0.41
7:FL:59:ARG:HD2	7:FL:59:ARG:HA	1.92	0.41
8:FM:136:LEU:HD23	8:FM:152:LEU:HD13	2.03	0.41
9:FN:116:LYS:HE3	9:FN:116:LYS:HB3	1.88	0.41
4:GD:85:VAL:HG23	6:GK:153:ILE:HG13	2.02	0.40
5:GH:250:TYR:OH	5:WH:239:LEU:O	2.38	0.40
7:GL:216:ASP:CG	7:GL:218:ALA:H	2.30	0.40
8:GM:233:VAL:HB	8:GM:253:VAL:HG22	2.04	0.40
4:HD:148:TYR:HA	4:HD:149:PRO:HD3	1.91	0.40
3:HF:208:ILE:HD11	3:HF:224:GLY:HA3	2.02	0.40
7:HL:59:ARG:HA	7:HL:59:ARG:HD2	1.89	0.40
1:BG:916:PHE:HD1	1:BG:916:PHE:HA	1.82	0.40
5:IH:141:LYS:HG2	5:JH:127:VAL:HG11	2.04	0.40
8:JM:158:VAL:HG13	8:JM:178:LYS:HE2	2.02	0.40
3:Jf:216:ILE:HA	3:Jf:216:ILE:HD12	1.82	0.40
6:KK:89:PRO:HG2	8:KM:292:MET:HE3	2.03	0.40
7:KL:124:THR:HA	7:KL:231:ILE:O	2.21	0.40
8:KM:173:LEU:HD23	8:KM:175:ILE:HD11	2.03	0.40
4:LD:55:MET:HE2	2:GC:210:ILE:HD11	2.02	0.40
6:LK:60:LEU:HA	6:LK:63:LYS:HE2	2.03	0.40
7:ML:109:LEU:HD13	7:ML:109:LEU:HA	1.84	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:WF:212:ILE:HB	3:WF:264:PHE:HA	2.03	0.40
5:WH:109:LYS:HE2	5:WH:109:LYS:HB2	1.90	0.40
5:XH:167:PRO:HB2	5:XH:239:LEU:HD12	2.02	0.40
2:DC:204:LYS:HE3	2:DC:204:LYS:HB3	1.88	0.40
7:BL:169:THR:OG1	7:BL:170:ASP:N	2.53	0.40
4:Bd:97:ARG:HD3	4:Bd:97:ARG:HA	1.80	0.40
4:AD:132:LEU:HA	4:AD:132:LEU:HD13	1.89	0.40
2:FC:150:LEU:HD21	2:FC:201:ILE:HG21	2.03	0.40
2:MC:89:ARG:O	2:MC:93:ALA:HB2	2.21	0.40
5:CH:214:MET:HE2	5:CH:214:MET:HB2	1.94	0.40
9:CN:78:LEU:HD13	9:CN:78:LEU:HA	1.86	0.40
4:DD:93:GLU:H	4:DD:93:GLU:HG3	1.55	0.40
3:DF:245:LYS:HD3	3:DF:246:LEU:HB2	2.02	0.40
3:EF:226:ASN:OD1	3:EF:226:ASN:N	2.54	0.40
5:EH:341:LYS:HD3	5:EH:361:LEU:HD22	2.03	0.40
8:EM:286:LYS:HA	8:EM:316:ASN:HD21	1.86	0.40
4:FD:161:ILE:HD12	4:FD:161:ILE:HA	1.87	0.40
1:JG:893:LYS:HB3	1:JG:893:LYS:HE3	1.86	0.40
9:FN:47:GLY:O	9:FN:61:ASN:N	2.52	0.40
2:EC:123:GLN:HA	2:DC:250:ILE:HG23	2.03	0.40
4:GD:131:ILE:HD13	4:GD:131:ILE:HA	1.90	0.40
5:HH:316:ASN:N	5:HH:316:ASN:OD1	2.53	0.40
7:HL:216:ASP:OD1	7:HL:218:ALA:N	2.48	0.40
5:IH:304:ALA:HA	5:IH:312:TYR:O	2.22	0.40
6:IK:129:GLU:OE1	6:IK:129:GLU:N	2.48	0.40
4:Id:111:LYS:HE2	4:Id:111:LYS:HB2	1.95	0.40
8:JM:275:ASP:N	8:JM:275:ASP:OD1	2.54	0.40
1:CG:916:PHE:HD1	1:CG:916:PHE:HA	1.74	0.40
3:KF:213:GLN:HE22	5:KH:168:VAL:HB	1.86	0.40
5:KH:171:LEU:HD13	5:KH:217:ALA:HB2	2.03	0.40
5:KH:214:MET:HE2	5:KH:214:MET:HB2	1.98	0.40
6:LK:119:TYR:HE1	6:LK:159:LEU:HD13	1.85	0.40
7:LL:44:HIS:N	7:LL:48:ASN:OD1	2.50	0.40
1:Ag:797:ARG:HA	1:Ag:797:ARG:HD2	1.86	0.40
7:ML:216:ASP:OD1	7:ML:217:ASN:N	2.54	0.40
3:Mf:260:GLN:HE21	3:Mf:260:GLN:HB3	1.61	0.40
5:XH:236:PRO:HG2	5:XH:238:MET:HE1	2.03	0.40
5:YH:324:TRP:HA	5:YH:339:MET:HG3	2.03	0.40
1:FG:965:LEU:HG	1:FG:1008:LEU:HD22	2.02	0.40
8:BM:172:ASN:OD1	8:BM:173:LEU:N	2.54	0.40
8:BM:212:LEU:HD13	8:BM:212:LEU:HA	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:IC:43:TYR:HD1	2:IC:43:TYR:HA	1.76	0.40
3:Cf:216:ILE:HA	3:Cf:216:ILE:HD12	1.81	0.40
4:DD:77:TYR:OH	6:DK:130:ARG:NH1	2.54	0.40
5:DH:316:ASN:N	5:DH:316:ASN:OD1	2.54	0.40
4:ED:135:ILE:HD13	4:ED:135:ILE:HA	1.92	0.40
4:FD:160:LYS:HD2	4:FD:160:LYS:HA	1.80	0.40
6:FK:119:TYR:HE1	6:FK:159:LEU:HB2	1.86	0.40
1:LG:944:LEU:HD22	1:LG:944:LEU:HA	1.88	0.40
1:MG:969:GLY:HA3	1:MG:1009:ALA:HB2	2.03	0.40
1:OG:893:LYS:HB3	1:OG:893:LYS:HE3	1.89	0.40
2:AC:143:PRO:HA	2:AC:144:PRO:HD3	1.97	0.40
1:AG:880:ASP:OD1	1:AG:880:ASP:N	2.54	0.40
2:BC:265:VAL:HA	4:Fd:85:VAL:HG23	2.02	0.40
5:GH:126:GLN:HA	5:GH:129:LYS:HB2	2.03	0.40
4:HD:27:LYS:HA	4:HD:28:PRO:HD3	1.94	0.40
5:HH:297:VAL:HG13	5:HH:358:VAL:HG22	2.03	0.40
3:Hf:216:ILE:HA	3:Hf:216:ILE:HD12	1.85	0.40
3:IF:219:ARG:HH22	3:JF:269:SER:HG	1.69	0.40
5:IH:275:SER:O	2:DC:119:ASN:ND2	2.54	0.40
4:Dd:88:SER:HA	4:Dd:120:SER:HA	2.03	0.40
9:JN:47:GLY:O	9:JN:61:ASN:N	2.49	0.40
3:Jf:245:LYS:HE3	3:Jf:245:LYS:HB3	1.99	0.40
2:CC:255:LEU:HD13	2:CC:255:LEU:HA	1.96	0.40
1:Lg:810:GLN:H	1:Lg:810:GLN:HG3	1.46	0.40
8:LM:218:LYS:HB2	8:LM:218:LYS:HE2	1.82	0.40
9:LN:78:LEU:HD13	9:LN:78:LEU:HA	1.96	0.40
3:MF:248:ASP:HB3	3:MF:253:ARG:HG3	2.04	0.40
1:Mg:813:LYS:HA	1:Mg:813:LYS:HD3	1.88	0.40
1:Ag:794:ILE:O	1:Ag:798:THR:N	2.54	0.40
6:MK:102:ILE:HD13	6:MK:102:ILE:HA	1.96	0.40
4:Md:127:SER:OG	4:Md:128:LEU:N	2.54	0.40
5:WH:166:PRO:HA	5:WH:167:PRO:HD3	1.85	0.40
5:WH:341:LYS:HE2	5:WH:341:LYS:HB3	1.93	0.40
1:YG:813:LYS:HE2	1:YG:813:LYS:HB2	1.93	0.40
5:YH:316:ASN:N	5:YH:316:ASN:OD1	2.55	0.40
3:Df:230:LEU:HD12	3:Df:230:LEU:HA	1.93	0.40
8:AM:197:TYR:HA	8:AM:217:LYS:HB3	2.03	0.40
2:GC:184:TRP:CZ3	2:HC:31:SER:HB3	2.57	0.40
6:CK:66:LYS:HB3	6:CK:77:SER:HB3	2.03	0.40
9:CN:105:ASP:OD1	9:CN:105:ASP:N	2.50	0.40
3:Cf:245:LYS:HE2	3:Cf:255:LEU:HD12	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:FK:81:SER:OG	6:FK:173:ASP:O	2.33	0.40
1:HG:1024:ASN:OD1	1:HG:1024:ASN:N	2.37	0.40
1:JG:965:LEU:HG	1:JG:1008:LEU:HD22	2.04	0.40
1:NG:1013:LYS:HE3	1:NG:1013:LYS:HB2	1.85	0.40
2:HC:264:ARG:HA	2:HC:264:ARG:HD2	1.79	0.40
7:FL:113:ASP:OD1	7:FL:113:ASP:N	2.41	0.40
8:FM:177:LEU:HD22	8:FM:181:PRO:HG2	2.04	0.40
2:AC:74:ARG:HB2	2:AC:187:ILE:HD13	2.03	0.40
2:AC:227:HIS:HA	2:AC:245:VAL:O	2.20	0.40
4:GD:87:TRP:CD1	4:GD:94:LEU:HD22	2.57	0.40
5:GH:345:LEU:HD13	5:GH:345:LEU:HA	1.91	0.40
8:GM:290:ASP:HB3	8:GM:298:VAL:HG21	2.03	0.40
3:HF:245:LYS:HD2	3:HF:245:LYS:HA	1.95	0.40
5:HH:356:LEU:HD23	5:HH:356:LEU:HA	1.89	0.40
7:HL:104:LYS:HE3	7:HL:104:LYS:HB3	1.90	0.40
5:JH:109:LYS:HE2	5:JH:109:LYS:HB2	1.90	0.40
6:JK:102:ILE:O	6:JK:106:LEU:HB2	2.21	0.40
6:JK:106:LEU:HD22	6:JK:106:LEU:HA	1.92	0.40
5:AH:282:HIS:O	5:AH:285:GLU:HG2	2.22	0.40
2:CC:116:THR:OG1	2:CC:128:SER:OG	2.28	0.40
5:KH:141:LYS:O	5:YH:131:LYS:NZ	2.42	0.40
6:KK:48:ALA:HA	6:KK:108:GLN:HE22	1.87	0.40
4:LD:161:ILE:HG13	4:LD:162:TYR:H	1.86	0.40
6:MK:99:LEU:HD13	6:MK:99:LEU:HA	1.89	0.40
7:ML:124:THR:HA	7:ML:231:ILE:O	2.22	0.40
1:EG:935:ILE:HG23	1:EG:1040:LEU:HD22	2.04	0.40
8:AM:162:VAL:HG12	8:AM:182:LYS:HB2	2.03	0.40
5:BH:239:LEU:HD21	5:BH:254:LEU:HD21	2.04	0.40
7:BL:124:THR:HG22	7:BL:232:GLN:HG2	2.03	0.40
7:BL:193:LEU:HD13	7:BL:193:LEU:HA	1.89	0.40
9:BN:62:ASN:OD1	9:BN:62:ASN:N	2.43	0.40
2:JC:208:MET:HE3	2:JC:208:MET:HB3	1.93	0.40
5:CH:329:THR:HG23	5:CH:335:HIS:CD2	2.57	0.40
8:CM:205:TYR:HD1	8:CM:205:TYR:HA	1.79	0.40
1:GG:898:LYS:HE3	1:HG:866:GLY:HA3	2.03	0.40
5:DH:238:MET:HE2	5:DH:238:MET:HB2	1.93	0.40
6:DK:110:ARG:HE	6:DK:110:ARG:HB2	1.74	0.40
6:DK:168:TYR:CZ	6:DK:170:LEU:HB2	2.57	0.40
8:DM:158:VAL:HA	8:DM:178:LYS:HE2	2.04	0.40
8:DM:275:ASP:OD1	8:DM:275:ASP:N	2.55	0.40
5:EH:170:ARG:HB3	5:EH:245:GLN:HG3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:EK:92:ASN:OD1	6:EK:92:ASN:N	2.54	0.40
4:Ed:98:ILE:HD13	4:Ed:98:ILE:HA	1.85	0.40
3:FF:215:VAL:H	5:FH:245:GLN:HE22	1.69	0.40
6:FK:53:ILE:HD11	6:FK:108:GLN:HG2	2.03	0.40
1:IG:904:ASN:OD1	1:IG:904:ASN:N	2.55	0.40
1:NG:878:ASN:OD1	1:NG:879:SER:N	2.55	0.40
1:NG:904:ASN:ND2	1:NG:905:LEU:O	2.54	0.40
1:OG:862:ILE:HD13	1:OG:1046:THR:HA	2.02	0.40
7:FL:187:GLU:HA	7:FL:190:MET:HB3	2.03	0.40
8:FM:302:ARG:HE	8:FM:302:ARG:HB2	1.63	0.40
5:GH:130:LEU:HA	5:GH:133:ILE:HD12	2.03	0.40
4:Gd:56:ALA:O	4:Gd:60:LYS:HB2	2.22	0.40
8:HM:217:LYS:HE2	8:HM:217:LYS:HB2	1.92	0.40
1:BG:898:LYS:HZ3	1:BG:920:SER:HB2	1.86	0.40
5:IH:130:LEU:HA	5:IH:133:ILE:HG22	2.04	0.40
5:JH:340:GLN:OE1	5:JH:341:LYS:N	2.54	0.40
8:JM:191:LEU:HD22	8:JM:212:LEU:HD11	2.03	0.40
5:AH:189:TRP:CD1	5:AH:256:VAL:HG21	2.56	0.40
4:KD:27:LYS:HA	4:KD:27:LYS:HD3	1.86	0.40
1:Kg:813:LYS:NZ	5:YH:134:TYR:OH	2.42	0.40
7:KL:54:ARG:HD2	7:KL:54:ARG:HA	1.78	0.40
8:KM:126:GLY:O	8:KM:146:LEU:HA	2.21	0.40
8:KM:256:HIS:O	8:KM:259:SER:OG	2.39	0.40
9:KN:58:LEU:HD13	9:KN:58:LEU:HA	1.89	0.40
5:LH:153:ALA:HB1	5:LH:251:ARG:HD2	2.03	0.40
5:LH:236:PRO:HG2	5:LH:238:MET:HE1	2.04	0.40
4:MD:87:TRP:CD2	4:MD:94:LEU:HD13	2.57	0.40
5:MH:184:SER:O	5:MH:255:ARG:NH2	2.55	0.40
8:MM:244:LYS:HE3	8:MM:245:TYR:CZ	2.56	0.40
9:MN:46:GLY:HA3	9:MN:61:ASN:HB2	2.03	0.40
1:VG:792:GLN:HA	1:VG:795:GLN:HG2	2.03	0.40
1:EG:1001:LEU:H	1:EG:1001:LEU:HG	1.67	0.40
3:XF:223:ILE:HA	3:XF:229:THR:HA	2.03	0.40
3:XF:234:GLU:HA	3:XF:247:ILE:HD12	2.04	0.40
2:DC:80:ILE:HD11	2:DC:196:LEU:HD13	2.03	0.40
5:ZH:315:THR:O	5:ZH:334:THR:OG1	2.37	0.40
6:BK:76:ILE:HG21	6:BK:102:ILE:HD11	2.02	0.40
6:BK:106:LEU:HG	6:BK:111:LYS:HE2	2.03	0.40
7:CL:54:ARG:HD2	7:CL:54:ARG:HA	1.94	0.40
8:CM:142:GLY:O	8:CM:144:THR:OG1	2.40	0.40
4:ED:105:ARG:NH2	4:Ed:130:GLU:OE2	2.47	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:EF:246:LEU:HD12	3:EF:255:LEU:HD12	2.03	0.40
7:EL:118:GLU:OE2	7:EL:123:ARG:NH2	2.55	0.40
1:OG:948:THR:HG22	1:OG:1029:VAL:HG12	2.04	0.40
7:FL:58:LYS:HB3	7:FL:58:LYS:HE3	1.88	0.40
7:FL:91:VAL:HA	7:FL:94:VAL:HG22	2.02	0.40
8:FM:278:ASP:N	8:FM:278:ASP:OD1	2.54	0.40
2:LC:262:GLU:OE1	2:LC:262:GLU:N	2.55	0.40
2:AC:220:VAL:HG13	2:AC:254:LEU:HD13	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AG	161/1048 (15%)	147 (91%)	14 (9%)	0	100	100
1	Ag	32/1048 (3%)	32 (100%)	0	0	100	100
1	BG	161/1048 (15%)	143 (89%)	18 (11%)	0	100	100
1	Bg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	CG	161/1048 (15%)	146 (91%)	15 (9%)	0	100	100
1	Cg	32/1048 (3%)	32 (100%)	0	0	100	100
1	DG	161/1048 (15%)	152 (94%)	9 (6%)	0	100	100
1	Dg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	EG	161/1048 (15%)	150 (93%)	11 (7%)	0	100	100
1	Eg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	FG	161/1048 (15%)	149 (92%)	12 (8%)	0	100	100
1	Fg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	GG	161/1048 (15%)	147 (91%)	14 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Gg	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	HG	161/1048 (15%)	152 (94%)	9 (6%)	0	100	100
1	Hg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	IG	161/1048 (15%)	154 (96%)	7 (4%)	0	100	100
1	Ig	32/1048 (3%)	32 (100%)	0	0	100	100
1	JG	161/1048 (15%)	153 (95%)	8 (5%)	0	100	100
1	Jg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	KG	161/1048 (15%)	153 (95%)	8 (5%)	0	100	100
1	Kg	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	LG	161/1048 (15%)	150 (93%)	11 (7%)	0	100	100
1	Lg	32/1048 (3%)	32 (100%)	0	0	100	100
1	MG	161/1048 (15%)	147 (91%)	14 (9%)	0	100	100
1	Mg	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	NG	161/1048 (15%)	151 (94%)	10 (6%)	0	100	100
1	OG	161/1048 (15%)	148 (92%)	13 (8%)	0	100	100
1	PG	161/1048 (15%)	149 (92%)	12 (8%)	0	100	100
1	VG	32/1048 (3%)	31 (97%)	1 (3%)	0	100	100
1	WG	32/1048 (3%)	32 (100%)	0	0	100	100
1	XG	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	YG	32/1048 (3%)	30 (94%)	2 (6%)	0	100	100
1	ZG	32/1048 (3%)	32 (100%)	0	0	100	100
2	AC	207/303 (68%)	191 (92%)	16 (8%)	0	100	100
2	BC	207/303 (68%)	195 (94%)	12 (6%)	0	100	100
2	CC	207/303 (68%)	188 (91%)	19 (9%)	0	100	100
2	DC	241/303 (80%)	229 (95%)	12 (5%)	0	100	100
2	EC	207/303 (68%)	192 (93%)	15 (7%)	0	100	100
2	FC	207/303 (68%)	189 (91%)	18 (9%)	0	100	100
2	GC	207/303 (68%)	192 (93%)	15 (7%)	0	100	100
2	HC	241/303 (80%)	227 (94%)	14 (6%)	0	100	100
2	IC	241/303 (80%)	226 (94%)	15 (6%)	0	100	100
2	JC	207/303 (68%)	187 (90%)	20 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	KC	207/303 (68%)	190 (92%)	17 (8%)	0	100	100
2	LC	241/303 (80%)	226 (94%)	15 (6%)	0	100	100
2	MC	241/303 (80%)	229 (95%)	12 (5%)	0	100	100
3	AF	61/269 (23%)	56 (92%)	5 (8%)	0	100	100
3	Af	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
3	BF	61/269 (23%)	60 (98%)	1 (2%)	0	100	100
3	Bf	57/269 (21%)	52 (91%)	5 (9%)	0	100	100
3	CF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
3	Cf	57/269 (21%)	51 (90%)	6 (10%)	0	100	100
3	DF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
3	Df	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
3	EF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
3	Ef	57/269 (21%)	52 (91%)	5 (9%)	0	100	100
3	FF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
3	Ff	57/269 (21%)	52 (91%)	5 (9%)	0	100	100
3	GF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
3	Gf	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
3	HF	61/269 (23%)	55 (90%)	6 (10%)	0	100	100
3	Hf	57/269 (21%)	52 (91%)	5 (9%)	0	100	100
3	IF	61/269 (23%)	56 (92%)	5 (8%)	0	100	100
3	If	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
3	JF	61/269 (23%)	56 (92%)	5 (8%)	0	100	100
3	Jf	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
3	KF	61/269 (23%)	60 (98%)	1 (2%)	0	100	100
3	Kf	57/269 (21%)	53 (93%)	4 (7%)	0	100	100
3	LF	61/269 (23%)	56 (92%)	5 (8%)	0	100	100
3	Lf	57/269 (21%)	55 (96%)	2 (4%)	0	100	100
3	MF	61/269 (23%)	55 (90%)	6 (10%)	0	100	100
3	Mf	57/269 (21%)	54 (95%)	3 (5%)	0	100	100
3	VF	61/269 (23%)	59 (97%)	2 (3%)	0	100	100
3	WF	61/269 (23%)	54 (88%)	7 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	XF	61/269 (23%)	58 (95%)	3 (5%)	0	100	100
3	YF	61/269 (23%)	56 (92%)	5 (8%)	0	100	100
3	ZF	61/269 (23%)	57 (93%)	4 (7%)	0	100	100
4	AD	138/163 (85%)	130 (94%)	8 (6%)	0	100	100
4	Ad	135/163 (83%)	133 (98%)	2 (2%)	0	100	100
4	BD	138/163 (85%)	127 (92%)	10 (7%)	1 (1%)	18	55
4	Bd	135/163 (83%)	130 (96%)	5 (4%)	0	100	100
4	CD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
4	Cd	135/163 (83%)	130 (96%)	5 (4%)	0	100	100
4	DD	138/163 (85%)	127 (92%)	11 (8%)	0	100	100
4	Dd	135/163 (83%)	129 (96%)	6 (4%)	0	100	100
4	ED	138/163 (85%)	132 (96%)	6 (4%)	0	100	100
4	Ed	135/163 (83%)	131 (97%)	4 (3%)	0	100	100
4	FD	138/163 (85%)	130 (94%)	8 (6%)	0	100	100
4	Fd	135/163 (83%)	128 (95%)	7 (5%)	0	100	100
4	GD	138/163 (85%)	128 (93%)	10 (7%)	0	100	100
4	Gd	135/163 (83%)	126 (93%)	9 (7%)	0	100	100
4	HD	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
4	Hd	135/163 (83%)	126 (93%)	9 (7%)	0	100	100
4	ID	138/163 (85%)	131 (95%)	7 (5%)	0	100	100
4	Id	135/163 (83%)	128 (95%)	7 (5%)	0	100	100
4	JD	138/163 (85%)	129 (94%)	9 (6%)	0	100	100
4	Jd	135/163 (83%)	127 (94%)	8 (6%)	0	100	100
4	KD	138/163 (85%)	129 (94%)	9 (6%)	0	100	100
4	Kd	135/163 (83%)	130 (96%)	5 (4%)	0	100	100
4	LD	138/163 (85%)	130 (94%)	8 (6%)	0	100	100
4	Ld	135/163 (83%)	131 (97%)	4 (3%)	0	100	100
4	MD	138/163 (85%)	133 (96%)	5 (4%)	0	100	100
4	Md	135/163 (83%)	126 (93%)	9 (7%)	0	100	100
5	AH	256/361 (71%)	235 (92%)	21 (8%)	0	100	100
5	BH	256/361 (71%)	244 (95%)	12 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	CH	256/361 (71%)	242 (94%)	14 (6%)	0	100	100
5	DH	256/361 (71%)	244 (95%)	12 (5%)	0	100	100
5	EH	256/361 (71%)	247 (96%)	9 (4%)	0	100	100
5	FH	256/361 (71%)	244 (95%)	12 (5%)	0	100	100
5	GH	256/361 (71%)	246 (96%)	10 (4%)	0	100	100
5	HH	256/361 (71%)	242 (94%)	14 (6%)	0	100	100
5	IH	256/361 (71%)	240 (94%)	16 (6%)	0	100	100
5	JH	256/361 (71%)	244 (95%)	12 (5%)	0	100	100
5	KH	256/361 (71%)	242 (94%)	14 (6%)	0	100	100
5	LH	256/361 (71%)	241 (94%)	15 (6%)	0	100	100
5	MH	256/361 (71%)	245 (96%)	11 (4%)	0	100	100
5	VH	239/361 (66%)	229 (96%)	10 (4%)	0	100	100
5	WH	239/361 (66%)	229 (96%)	10 (4%)	0	100	100
5	XH	239/361 (66%)	232 (97%)	7 (3%)	0	100	100
5	YH	239/361 (66%)	230 (96%)	9 (4%)	0	100	100
5	ZH	239/361 (66%)	229 (96%)	10 (4%)	0	100	100
6	AK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
6	BK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
6	CK	149/189 (79%)	142 (95%)	7 (5%)	0	100	100
6	DK	149/189 (79%)	142 (95%)	7 (5%)	0	100	100
6	EK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
6	FK	149/189 (79%)	142 (95%)	7 (5%)	0	100	100
6	GK	149/189 (79%)	139 (93%)	10 (7%)	0	100	100
6	HK	149/189 (79%)	146 (98%)	3 (2%)	0	100	100
6	IK	149/189 (79%)	144 (97%)	5 (3%)	0	100	100
6	JK	149/189 (79%)	144 (97%)	5 (3%)	0	100	100
6	KK	149/189 (79%)	139 (93%)	10 (7%)	0	100	100
6	LK	149/189 (79%)	140 (94%)	9 (6%)	0	100	100
6	MK	149/189 (79%)	143 (96%)	6 (4%)	0	100	100
7	AL	169/249 (68%)	162 (96%)	7 (4%)	0	100	100
7	BL	169/249 (68%)	161 (95%)	8 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	CL	169/249 (68%)	159 (94%)	10 (6%)	0	100	100
7	DL	169/249 (68%)	160 (95%)	9 (5%)	0	100	100
7	EL	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
7	FL	169/249 (68%)	163 (96%)	6 (4%)	0	100	100
7	GL	169/249 (68%)	162 (96%)	7 (4%)	0	100	100
7	HL	169/249 (68%)	160 (95%)	9 (5%)	0	100	100
7	IL	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
7	JL	169/249 (68%)	163 (96%)	6 (4%)	0	100	100
7	KL	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
7	LL	169/249 (68%)	161 (95%)	8 (5%)	0	100	100
7	ML	169/249 (68%)	159 (94%)	10 (6%)	0	100	100
8	AM	206/320 (64%)	190 (92%)	16 (8%)	0	100	100
8	BM	206/320 (64%)	187 (91%)	19 (9%)	0	100	100
8	CM	206/320 (64%)	187 (91%)	19 (9%)	0	100	100
8	DM	206/320 (64%)	189 (92%)	17 (8%)	0	100	100
8	EM	206/320 (64%)	191 (93%)	15 (7%)	0	100	100
8	FM	206/320 (64%)	185 (90%)	21 (10%)	0	100	100
8	GM	206/320 (64%)	191 (93%)	15 (7%)	0	100	100
8	HM	206/320 (64%)	195 (95%)	11 (5%)	0	100	100
8	IM	206/320 (64%)	186 (90%)	20 (10%)	0	100	100
8	JM	206/320 (64%)	188 (91%)	18 (9%)	0	100	100
8	KM	206/320 (64%)	190 (92%)	16 (8%)	0	100	100
8	LM	206/320 (64%)	185 (90%)	21 (10%)	0	100	100
8	MM	206/320 (64%)	189 (92%)	17 (8%)	0	100	100
9	AN	76/124 (61%)	68 (90%)	8 (10%)	0	100	100
9	BN	76/124 (61%)	67 (88%)	9 (12%)	0	100	100
9	CN	76/124 (61%)	66 (87%)	10 (13%)	0	100	100
9	DN	76/124 (61%)	66 (87%)	10 (13%)	0	100	100
9	EN	76/124 (61%)	68 (90%)	8 (10%)	0	100	100
9	FN	76/124 (61%)	68 (90%)	8 (10%)	0	100	100
9	GN	76/124 (61%)	71 (93%)	5 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	HN	76/124 (61%)	71 (93%)	5 (7%)	0	100	100
9	IN	76/124 (61%)	72 (95%)	4 (5%)	0	100	100
9	JN	76/124 (61%)	69 (91%)	7 (9%)	0	100	100
9	KN	76/124 (61%)	68 (90%)	8 (10%)	0	100	100
9	LN	76/124 (61%)	66 (87%)	10 (13%)	0	100	100
9	MN	76/124 (61%)	69 (91%)	7 (9%)	0	100	100
All	All	23724/70112 (34%)	22279 (94%)	1444 (6%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	BD	28	PRO

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%)	108 (80%)	27 (20%)	1	8
1	Ag	31/765 (4%)	27 (87%)	4 (13%)	4	17
1	BG	135/765 (18%)	113 (84%)	22 (16%)	2	12
1	Bg	31/765 (4%)	22 (71%)	9 (29%)	0	3
1	CG	135/765 (18%)	108 (80%)	27 (20%)	1	8
1	Cg	31/765 (4%)	27 (87%)	4 (13%)	4	17
1	DG	135/765 (18%)	114 (84%)	21 (16%)	2	13
1	Dg	31/765 (4%)	23 (74%)	8 (26%)	0	4
1	EG	135/765 (18%)	114 (84%)	21 (16%)	2	13
1	Eg	31/765 (4%)	27 (87%)	4 (13%)	4	17
1	FG	135/765 (18%)	112 (83%)	23 (17%)	2	11
1	Fg	31/765 (4%)	27 (87%)	4 (13%)	4	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	GG	135/765 (18%)	113 (84%)	22 (16%)	2	12
1	Gg	31/765 (4%)	25 (81%)	6 (19%)	1	8
1	HG	135/765 (18%)	114 (84%)	21 (16%)	2	13
1	Hg	31/765 (4%)	25 (81%)	6 (19%)	1	8
1	IG	135/765 (18%)	119 (88%)	16 (12%)	5	19
1	Ig	31/765 (4%)	26 (84%)	5 (16%)	2	12
1	JG	135/765 (18%)	115 (85%)	20 (15%)	3	14
1	Jg	31/765 (4%)	21 (68%)	10 (32%)	0	2
1	KG	135/765 (18%)	112 (83%)	23 (17%)	2	11
1	Kg	31/765 (4%)	22 (71%)	9 (29%)	0	3
1	LG	135/765 (18%)	117 (87%)	18 (13%)	4	16
1	Lg	31/765 (4%)	22 (71%)	9 (29%)	0	3
1	MG	135/765 (18%)	108 (80%)	27 (20%)	1	8
1	Mg	31/765 (4%)	24 (77%)	7 (23%)	1	6
1	NG	135/765 (18%)	110 (82%)	25 (18%)	1	9
1	OG	135/765 (18%)	112 (83%)	23 (17%)	2	11
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%)	28 (90%)	3 (10%)	8	25
1	XG	31/765 (4%)	25 (81%)	6 (19%)	1	8
1	YG	31/765 (4%)	28 (90%)	3 (10%)	8	25
1	ZG	31/765 (4%)	26 (84%)	5 (16%)	2	12
2	AC	178/257 (69%)	150 (84%)	28 (16%)	2	12
2	BC	178/257 (69%)	145 (82%)	33 (18%)	1	9
2	CC	178/257 (69%)	142 (80%)	36 (20%)	1	8
2	DC	203/257 (79%)	174 (86%)	29 (14%)	3	14
2	EC	178/257 (69%)	148 (83%)	30 (17%)	2	11
2	FC	178/257 (69%)	143 (80%)	35 (20%)	1	8
2	GC	178/257 (69%)	150 (84%)	28 (16%)	2	12
2	HC	203/257 (79%)	180 (89%)	23 (11%)	5	20
2	IC	203/257 (79%)	176 (87%)	27 (13%)	4	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	JC	178/257 (69%)	148 (83%)	30 (17%)	2	11
2	KC	178/257 (69%)	146 (82%)	32 (18%)	2	10
2	LC	203/257 (79%)	181 (89%)	22 (11%)	6	22
2	MC	203/257 (79%)	176 (87%)	27 (13%)	4	16
3	AF	53/237 (22%)	41 (77%)	12 (23%)	1	6
3	Af	49/237 (21%)	35 (71%)	14 (29%)	0	3
3	BF	53/237 (22%)	42 (79%)	11 (21%)	1	7
3	Bf	49/237 (21%)	43 (88%)	6 (12%)	5	18
3	CF	53/237 (22%)	43 (81%)	10 (19%)	1	9
3	Cf	49/237 (21%)	35 (71%)	14 (29%)	0	3
3	DF	53/237 (22%)	46 (87%)	7 (13%)	4	16
3	Df	49/237 (21%)	43 (88%)	6 (12%)	5	18
3	EF	53/237 (22%)	46 (87%)	7 (13%)	4	16
3	Ef	49/237 (21%)	40 (82%)	9 (18%)	1	10
3	FF	53/237 (22%)	45 (85%)	8 (15%)	3	13
3	Ff	49/237 (21%)	40 (82%)	9 (18%)	1	10
3	GF	53/237 (22%)	47 (89%)	6 (11%)	5	20
3	Gf	49/237 (21%)	41 (84%)	8 (16%)	2	12
3	HF	53/237 (22%)	45 (85%)	8 (15%)	3	13
3	Hf	49/237 (21%)	40 (82%)	9 (18%)	1	10
3	IF	53/237 (22%)	42 (79%)	11 (21%)	1	7
3	If	49/237 (21%)	37 (76%)	12 (24%)	1	4
3	JF	53/237 (22%)	45 (85%)	8 (15%)	3	13
3	Jf	49/237 (21%)	37 (76%)	12 (24%)	1	4
3	KF	53/237 (22%)	45 (85%)	8 (15%)	3	13
3	Kf	49/237 (21%)	41 (84%)	8 (16%)	2	12
3	LF	53/237 (22%)	47 (89%)	6 (11%)	5	20
3	Lf	49/237 (21%)	41 (84%)	8 (16%)	2	12
3	MF	53/237 (22%)	45 (85%)	8 (15%)	3	13
3	Mf	49/237 (21%)	40 (82%)	9 (18%)	1	10
3	VF	53/237 (22%)	43 (81%)	10 (19%)	1	9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	WF	53/237 (22%)	44 (83%)	9 (17%)	2	11
3	XF	53/237 (22%)	45 (85%)	8 (15%)	3	13
3	YF	53/237 (22%)	44 (83%)	9 (17%)	2	11
3	ZF	53/237 (22%)	43 (81%)	10 (19%)	1	9
4	AD	121/139 (87%)	99 (82%)	22 (18%)	2	10
4	Ad	118/139 (85%)	106 (90%)	12 (10%)	7	23
4	BD	121/139 (87%)	106 (88%)	15 (12%)	4	18
4	Bd	118/139 (85%)	100 (85%)	18 (15%)	3	13
4	CD	121/139 (87%)	100 (83%)	21 (17%)	2	11
4	Cd	118/139 (85%)	103 (87%)	15 (13%)	4	17
4	DD	121/139 (87%)	105 (87%)	16 (13%)	4	16
4	Dd	118/139 (85%)	102 (86%)	16 (14%)	3	15
4	ED	121/139 (87%)	107 (88%)	14 (12%)	5	19
4	Ed	118/139 (85%)	101 (86%)	17 (14%)	3	14
4	FD	121/139 (87%)	101 (84%)	20 (16%)	2	12
4	Fd	118/139 (85%)	102 (86%)	16 (14%)	3	15
4	GD	121/139 (87%)	101 (84%)	20 (16%)	2	12
4	Gd	118/139 (85%)	102 (86%)	16 (14%)	3	15
4	HD	121/139 (87%)	110 (91%)	11 (9%)	9	28
4	Hd	118/139 (85%)	98 (83%)	20 (17%)	2	11
4	ID	121/139 (87%)	108 (89%)	13 (11%)	6	22
4	Id	118/139 (85%)	101 (86%)	17 (14%)	3	14
4	JD	121/139 (87%)	102 (84%)	19 (16%)	2	12
4	Jd	118/139 (85%)	104 (88%)	14 (12%)	5	19
4	KD	121/139 (87%)	112 (93%)	9 (7%)	13	33
4	Kd	118/139 (85%)	104 (88%)	14 (12%)	5	19
4	LD	121/139 (87%)	101 (84%)	20 (16%)	2	12
4	Ld	118/139 (85%)	107 (91%)	11 (9%)	8	26
4	MD	121/139 (87%)	109 (90%)	12 (10%)	7	24
4	Md	118/139 (85%)	102 (86%)	16 (14%)	3	15
5	AH	220/300 (73%)	188 (86%)	32 (14%)	3	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	BH	220/300 (73%)	190 (86%)	30 (14%)	3	15
5	CH	220/300 (73%)	191 (87%)	29 (13%)	4	16
5	DH	220/300 (73%)	191 (87%)	29 (13%)	4	16
5	EH	220/300 (73%)	180 (82%)	40 (18%)	2	10
5	FH	220/300 (73%)	187 (85%)	33 (15%)	3	13
5	GH	220/300 (73%)	190 (86%)	30 (14%)	3	15
5	HH	220/300 (73%)	188 (86%)	32 (14%)	3	14
5	IH	220/300 (73%)	195 (89%)	25 (11%)	5	20
5	JH	220/300 (73%)	200 (91%)	20 (9%)	9	28
5	KH	220/300 (73%)	196 (89%)	24 (11%)	6	21
5	LH	220/300 (73%)	190 (86%)	30 (14%)	3	15
5	MH	220/300 (73%)	198 (90%)	22 (10%)	7	24
5	VH	207/300 (69%)	179 (86%)	28 (14%)	4	15
5	WH	207/300 (69%)	184 (89%)	23 (11%)	6	20
5	XH	207/300 (69%)	181 (87%)	26 (13%)	4	17
5	YH	207/300 (69%)	176 (85%)	31 (15%)	3	13
5	ZH	207/300 (69%)	176 (85%)	31 (15%)	3	13
6	AK	129/163 (79%)	107 (83%)	22 (17%)	2	11
6	BK	129/163 (79%)	108 (84%)	21 (16%)	2	12
6	CK	129/163 (79%)	110 (85%)	19 (15%)	3	14
6	DK	129/163 (79%)	114 (88%)	15 (12%)	5	19
6	EK	129/163 (79%)	105 (81%)	24 (19%)	1	9
6	FK	129/163 (79%)	104 (81%)	25 (19%)	1	8
6	GK	129/163 (79%)	113 (88%)	16 (12%)	4	18
6	HK	129/163 (79%)	107 (83%)	22 (17%)	2	11
6	IK	129/163 (79%)	114 (88%)	15 (12%)	5	19
6	JK	129/163 (79%)	105 (81%)	24 (19%)	1	9
6	KK	129/163 (79%)	102 (79%)	27 (21%)	1	6
6	LK	129/163 (79%)	107 (83%)	22 (17%)	2	11
6	MK	129/163 (79%)	110 (85%)	19 (15%)	3	14
7	AL	148/203 (73%)	131 (88%)	17 (12%)	5	19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	BL	148/203 (73%)	133 (90%)	15 (10%)	7	23
7	CL	148/203 (73%)	128 (86%)	20 (14%)	4	15
7	DL	148/203 (73%)	125 (84%)	23 (16%)	2	13
7	EL	148/203 (73%)	136 (92%)	12 (8%)	11	31
7	FL	148/203 (73%)	126 (85%)	22 (15%)	3	14
7	GL	148/203 (73%)	129 (87%)	19 (13%)	4	17
7	HL	148/203 (73%)	133 (90%)	15 (10%)	7	23
7	IL	148/203 (73%)	126 (85%)	22 (15%)	3	14
7	JL	148/203 (73%)	132 (89%)	16 (11%)	6	22
7	KL	148/203 (73%)	127 (86%)	21 (14%)	3	15
7	LL	148/203 (73%)	131 (88%)	17 (12%)	5	19
7	ML	148/203 (73%)	130 (88%)	18 (12%)	5	18
8	AM	175/276 (63%)	150 (86%)	25 (14%)	3	14
8	BM	175/276 (63%)	143 (82%)	32 (18%)	2	10
8	CM	175/276 (63%)	144 (82%)	31 (18%)	2	10
8	DM	175/276 (63%)	148 (85%)	27 (15%)	2	13
8	EM	175/276 (63%)	141 (81%)	34 (19%)	1	8
8	FM	175/276 (63%)	146 (83%)	29 (17%)	2	11
8	GM	175/276 (63%)	149 (85%)	26 (15%)	3	14
8	HM	175/276 (63%)	145 (83%)	30 (17%)	2	11
8	IM	175/276 (63%)	151 (86%)	24 (14%)	3	15
8	JM	175/276 (63%)	152 (87%)	23 (13%)	4	16
8	KM	175/276 (63%)	144 (82%)	31 (18%)	2	10
8	LM	175/276 (63%)	151 (86%)	24 (14%)	3	15
8	MM	175/276 (63%)	145 (83%)	30 (17%)	2	11
9	AN	66/107 (62%)	59 (89%)	7 (11%)	6	22
9	BN	66/107 (62%)	56 (85%)	10 (15%)	3	13
9	CN	66/107 (62%)	55 (83%)	11 (17%)	2	11
9	DN	66/107 (62%)	55 (83%)	11 (17%)	2	11
9	EN	66/107 (62%)	54 (82%)	12 (18%)	2	10
9	FN	66/107 (62%)	53 (80%)	13 (20%)	1	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	GN	66/107 (62%)	54 (82%)	12 (18%)	2	10
9	HN	66/107 (62%)	57 (86%)	9 (14%)	3	15
9	IN	66/107 (62%)	55 (83%)	11 (17%)	2	11
9	JN	66/107 (62%)	54 (82%)	12 (18%)	2	10
9	KN	66/107 (62%)	55 (83%)	11 (17%)	2	11
9	LN	66/107 (62%)	57 (86%)	9 (14%)	3	15
9	MN	66/107 (62%)	58 (88%)	8 (12%)	5	18
All	All	20484/55449 (37%)	17424 (85%)	3060 (15%)	5	14

All (3060) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AG	864	LYS
1	AG	865	THR
1	AG	869	MET
1	AG	875	THR
1	AG	886	LEU
1	AG	898	LYS
1	AG	900	ILE
1	AG	904	ASN
1	AG	910	ASP
1	AG	911	LYS
1	AG	913	VAL
1	AG	916	PHE
1	AG	930	ILE
1	AG	939	THR
1	AG	942	THR
1	AG	944	LEU
1	AG	948	THR
1	AG	962	SER
1	AG	963	SER
1	AG	965	LEU
1	AG	972	PHE
1	AG	1017	GLN
1	AG	1027	THR
1	AG	1028	THR
1	AG	1031	VAL
1	AG	1032	TYR
1	AG	1045	VAL
2	BC	68	GLN

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Mol	Chain	Res	Type
2	BC	96	ASN
2	BC	98	LEU
2	BC	103	ASN
2	BC	104	ILE
2	BC	108	VAL
2	BC	110	LEU
2	BC	111	GLU
2	BC	118	LEU
2	BC	128	ASP
2	BC	136	GLN
2	BC	140	ILE
2	BC	142	THR
2	BC	145	THR
2	BC	147	ARG
2	BC	162	VAL
2	BC	164	LEU
2	BC	165	LEU
2	BC	167	LYS
2	BC	168	THR
2	BC	180	GLU
2	BC	194	LEU
2	BC	203	GLU
2	BC	213	LYS
2	BC	215	LEU
2	BC	220	VAL
2	BC	227	HIS
2	BC	228	THR
2	BC	229	ASP
2	BC	239	ILE
2	BC	245	VAL
2	BC	262	ARG
2	BC	265	VAL
2	EC	69	GLN
2	EC	79	ILE
2	EC	97	ASN
2	EC	99	LEU
2	EC	105	ILE
2	EC	109	VAL
2	EC	111	LEU
2	EC	117	LEU
2	EC	119	LEU
2	EC	127	ILE

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Mol	Chain	Res	Type
2	EC	129	ASP
2	EC	140	PHE
2	EC	141	ILE
2	EC	142	THR
2	EC	143	THR
2	EC	146	THR
2	EC	148	ARG
2	EC	163	VAL
2	EC	166	LEU
2	EC	195	LEU
2	EC	204	GLU
2	EC	205	ASP
2	EC	214	LYS
2	EC	221	VAL
2	EC	228	HIS
2	EC	229	THR
2	EC	233	VAL
2	EC	234	THR
2	EC	247	LEU
2	EC	266	VAL
3	AF	208	ILE
3	AF	209	ILE
3	AF	215	VAL
3	AF	223	ILE
3	AF	229	THR
3	AF	230	LEU
3	AF	231	THR
3	AF	232	VAL
3	AF	238	ILE
3	AF	250	LEU
3	AF	256	THR
3	AF	258	SER
4	GD	30	ILE
4	GD	34	SER
4	GD	35	ASP
4	GD	43	GLU
4	GD	46	VAL
4	GD	47	SER
4	GD	51	SER
4	GD	55	MET
4	GD	78	ASN
4	GD	79	LEU

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Mol	Chain	Res	Type
4	GD	85	VAL
4	GD	112	SER
4	GD	127	SER
4	GD	147	VAL
4	GD	150	ASN
4	GD	154	VAL
4	GD	155	GLU
4	GD	156	LEU
4	GD	160	LYS
4	GD	162	TYR
3	GF	207	ARG
3	GF	208	ILE
3	GF	223	ILE
3	GF	231	THR
3	GF	255	LEU
3	GF	256	THR
1	Gg	794	ILE
1	Gg	803	THR
1	Gg	811	ASP
1	Gg	814	GLN
1	Gg	815	VAL
1	Gg	819	VAL
5	GH	107	ILE
5	GH	127	VAL
5	GH	135	GLU
5	GH	136	THR
5	GH	144	THR
5	GH	147	THR
5	GH	168	VAL
5	GH	171	LEU
5	GH	180	VAL
5	GH	215	ILE
5	GH	221	TYR
5	GH	233	LEU
5	GH	238	MET
5	GH	248	VAL
5	GH	253	ASP
5	GH	256	VAL
5	GH	264	LYS
5	GH	284	LEU
5	GH	313	VAL
5	GH	316	ASN

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Mol	Chain	Res	Type
5	GH	319	ILE
5	GH	334	THR
5	GH	344	VAL
5	GH	345	LEU
5	GH	346	LEU
5	GH	352	LYS
5	GH	353	VAL
5	GH	354	MET
5	GH	355	GLN
5	GH	356	LEU
6	GK	45	VAL
6	GK	50	ASP
6	GK	54	ILE
6	GK	70	VAL
6	GK	73	ASN
6	GK	75	LEU
6	GK	77	SER
6	GK	91	LEU
6	GK	112	ILE
6	GK	114	ILE
6	GK	116	VAL
6	GK	144	LEU
6	GK	149	VAL
6	GK	153	ILE
6	GK	156	THR
6	GK	170	LEU
7	GL	44	HIS
7	GL	47	TYR
7	GL	57	VAL
7	GL	93	LEU
7	GL	98	TYR
7	GL	100	ASP
7	GL	109	LEU
7	GL	129	THR
7	GL	130	ASP
7	GL	161	SER
7	GL	162	THR
7	GL	169	THR
7	GL	172	VAL
7	GL	174	SER
7	GL	182	SER
7	GL	188	THR

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Mol	Chain	Res	Type
7	GL	193	LEU
7	GL	212	ASN
7	GL	216	ASP
8	GM	129	LEU
8	GM	131	THR
8	GM	134	LEU
8	GM	136	LEU
8	GM	146	LEU
8	GM	149	ASN
8	GM	152	LEU
8	GM	153	GLN
8	GM	162	VAL
8	GM	175	ILE
8	GM	176	VAL
8	GM	178	LYS
8	GM	188	PHE
8	GM	190	ASN
8	GM	192	ARG
8	GM	199	LYS
8	GM	207	ILE
8	GM	212	LEU
8	GM	227	ILE
8	GM	259	SER
8	GM	263	ILE
8	GM	271	SER
8	GM	277	SER
8	GM	292	MET
8	GM	299	LEU
8	GM	301	MET
9	GN	48	ILE
9	GN	51	CYS
9	GN	52	ASP
9	GN	58	LEU
9	GN	62	ASN
9	GN	71	THR
9	GN	95	LEU
9	GN	96	ASN
9	GN	101	VAL
9	GN	102	VAL
9	GN	111	GLU
9	GN	116	LYS
4	Gd	58	VAL

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Mol	Chain	Res	Type
4	Gd	59	GLU
4	Gd	61	VAL
4	Gd	63	THR
4	Gd	72	THR
4	Gd	73	ILE
4	Gd	82	ARG
4	Gd	91	ILE
4	Gd	115	VAL
4	Gd	123	THR
4	Gd	128	LEU
4	Gd	132	LEU
4	Gd	142	LYS
4	Gd	145	ILE
4	Gd	147	VAL
4	Gd	150	ASN
3	Gf	211	TYR
3	Gf	216	ILE
3	Gf	222	LEU
3	Gf	238	ILE
3	Gf	244	VAL
3	Gf	245	LYS
3	Gf	246	LEU
3	Gf	261	VAL
4	HD	46	VAL
4	HD	63	THR
4	HD	70	THR
4	HD	86	ASP
4	HD	115	VAL
4	HD	118	LEU
4	HD	130	GLU
4	HD	147	VAL
4	HD	154	VAL
4	HD	156	LEU
4	HD	160	LYS
3	HF	208	ILE
3	HF	215	VAL
3	HF	223	ILE
3	HF	230	LEU
3	HF	233	ARG
3	HF	238	ILE
3	HF	250	LEU
3	HF	256	THR

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Mol	Chain	Res	Type
1	Hg	794	ILE
1	Hg	802	LEU
1	Hg	808	LEU
1	Hg	814	GLN
1	Hg	815	VAL
1	Hg	821	THR
5	HH	107	ILE
5	HH	108	ASP
5	HH	114	ASP
5	HH	126	GLN
5	HH	135	GLU
5	HH	138	GLU
5	HH	158	VAL
5	HH	178	SER
5	HH	180	VAL
5	HH	204	ILE
5	HH	207	ASP
5	HH	218	THR
5	HH	220	LEU
5	HH	228	VAL
5	HH	231	ARG
5	HH	238	MET
5	HH	240	THR
5	HH	241	LEU
5	HH	248	VAL
5	HH	251	ARG
5	HH	253	ASP
5	HH	278	ASP
5	HH	279	LEU
5	HH	284	LEU
5	HH	313	VAL
5	HH	317	LEU
5	HH	329	THR
5	HH	332	ASP
5	HH	342	SER
5	HH	344	VAL
5	HH	345	LEU
5	HH	348	SER
6	HK	41	LEU
6	HK	45	VAL
6	HK	50	ASP
6	HK	67	VAL

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Mol	Chain	Res	Type
6	HK	70	VAL
6	HK	73	ASN
6	HK	75	LEU
6	HK	83	LEU
6	HK	92	ASN
6	HK	99	LEU
6	HK	106	LEU
6	HK	111	LYS
6	HK	125	SER
6	HK	126	VAL
6	HK	144	LEU
6	HK	151	SER
6	HK	152	ARG
6	HK	156	THR
6	HK	159	LEU
6	HK	166	THR
6	HK	180	VAL
6	HK	182	ILE
7	HL	57	VAL
7	HL	108	ASP
7	HL	109	LEU
7	HL	130	ASP
7	HL	137	SER
7	HL	140	LEU
7	HL	148	LEU
7	HL	151	VAL
7	HL	161	SER
7	HL	162	THR
7	HL	172	VAL
7	HL	175	ARG
7	HL	182	SER
7	HL	212	ASN
7	HL	219	ILE
8	HM	129	LEU
8	HM	131	THR
8	HM	134	LEU
8	HM	138	LEU
8	HM	140	ASN
8	HM	146	LEU
8	HM	149	ASN
8	HM	160	ASN
8	HM	162	VAL

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Mol	Chain	Res	Type
8	HM	170	SER
8	HM	176	VAL
8	HM	178	LYS
8	HM	180	ASP
8	HM	184	LEU
8	HM	194	LEU
8	HM	201	THR
8	HM	212	LEU
8	HM	222	ILE
8	HM	228	VAL
8	HM	231	LEU
8	HM	242	LYS
8	HM	251	SER
8	HM	259	SER
8	HM	262	GLU
8	HM	269	GLN
8	HM	277	SER
8	HM	284	LEU
8	HM	292	MET
8	HM	298	VAL
8	HM	299	LEU
9	HN	44	LYS
9	HN	66	SER
9	HN	78	LEU
9	HN	91	VAL
9	HN	96	ASN
9	HN	101	VAL
9	HN	108	VAL
9	HN	110	GLU
9	HN	114	LEU
1	BG	865	THR
1	BG	876	SER
1	BG	886	LEU
1	BG	893	LYS
1	BG	898	LYS
1	BG	899	LEU
1	BG	904	ASN
1	BG	911	LYS
1	BG	913	VAL
1	BG	915	THR
1	BG	930	ILE
1	BG	939	THR

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Mol	Chain	Res	Type
1	BG	944	LEU
1	BG	953	LEU
1	BG	956	TYR
1	BG	962	SER
1	BG	963	SER
1	BG	965	LEU
1	BG	972	PHE
1	BG	1027	THR
1	BG	1031	VAL
1	BG	1045	VAL
4	Hd	30	ILE
4	Hd	41	LEU
4	Hd	58	VAL
4	Hd	61	VAL
4	Hd	63	THR
4	Hd	73	ILE
4	Hd	78	ASN
4	Hd	88	SER
4	Hd	93	GLU
4	Hd	94	LEU
4	Hd	115	VAL
4	Hd	121	ILE
4	Hd	127	SER
4	Hd	128	LEU
4	Hd	138	GLN
4	Hd	145	ILE
4	Hd	150	ASN
4	Hd	154	VAL
4	Hd	155	GLU
4	Hd	156	LEU
3	Hf	215	VAL
3	Hf	219	ARG
3	Hf	222	LEU
3	Hf	236	SER
3	Hf	244	VAL
3	Hf	245	LYS
3	Hf	261	VAL
3	Hf	262	ILE
3	Hf	265	SER
1	Bg	793	GLU
1	Bg	794	ILE
1	Bg	800	ASP

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Mol	Chain	Res	Type
1	Bg	806	THR
1	Bg	808	LEU
1	Bg	809	VAL
1	Bg	815	VAL
1	Bg	816	GLU
1	Bg	819	VAL
4	ID	62	ILE
4	ID	73	ILE
4	ID	79	LEU
4	ID	92	GLU
4	ID	93	GLU
4	ID	105	ARG
4	ID	109	LEU
4	ID	111	LYS
4	ID	115	VAL
4	ID	127	SER
4	ID	134	ASP
4	ID	135	ILE
4	ID	161	ILE
3	IF	207	ARG
3	IF	208	ILE
3	IF	223	ILE
3	IF	231	THR
3	IF	232	VAL
3	IF	243	MET
3	IF	246	LEU
3	IF	250	LEU
3	IF	255	LEU
3	IF	256	THR
3	IF	266	GLN
1	Ig	794	ILE
1	Ig	808	LEU
1	Ig	815	VAL
1	Ig	817	THR
1	Ig	819	VAL
5	IH	107	ILE
5	IH	108	ASP
5	IH	117	ARG
5	IH	147	THR
5	IH	178	SER
5	IH	180	VAL
5	IH	195	ASP

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Mol	Chain	Res	Type
5	IH	218	THR
5	IH	226	LEU
5	IH	231	ARG
5	IH	233	LEU
5	IH	238	MET
5	IH	245	GLN
5	IH	248	VAL
5	IH	250	TYR
5	IH	253	ASP
5	IH	278	ASP
5	IH	296	VAL
5	IH	313	VAL
5	IH	340	GLN
5	IH	342	SER
5	IH	344	VAL
5	IH	345	LEU
5	IH	353	VAL
5	IH	354	MET
6	IK	41	LEU
6	IK	45	VAL
6	IK	54	ILE
6	IK	70	VAL
6	IK	75	LEU
6	IK	83	LEU
6	IK	92	ASN
6	IK	111	LYS
6	IK	116	VAL
6	IK	142	GLU
6	IK	144	LEU
6	IK	149	VAL
6	IK	156	THR
6	IK	162	ASP
6	IK	170	LEU
7	IL	47	TYR
7	IL	51	GLN
7	IL	93	LEU
7	IL	98	TYR
7	IL	100	ASP
7	IL	101	SER
7	IL	109	LEU
7	IL	123	ARG
7	IL	129	THR

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Mol	Chain	Res	Type
7	IL	130	ASP
7	IL	133	PHE
7	IL	148	LEU
7	IL	155	LEU
7	IL	161	SER
7	IL	172	VAL
7	IL	174	SER
7	IL	181	LEU
7	IL	182	SER
7	IL	193	LEU
7	IL	203	LEU
7	IL	220	ILE
7	IL	229	ILE
8	IM	115	ARG
8	IM	129	LEU
8	IM	134	LEU
8	IM	144	THR
8	IM	149	ASN
8	IM	152	LEU
8	IM	160	ASN
8	IM	175	ILE
8	IM	176	VAL
8	IM	177	LEU
8	IM	180	ASP
8	IM	183	VAL
8	IM	184	LEU
8	IM	191	LEU
8	IM	202	LEU
8	IM	222	ILE
8	IM	224	LEU
8	IM	233	VAL
8	IM	253	VAL
8	IM	262	GLU
8	IM	263	ILE
8	IM	264	SER
8	IM	292	MET
8	IM	297	SER
9	IN	39	ASP
9	IN	48	ILE
9	IN	65	TYR
9	IN	67	THR
9	IN	71	THR

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Mol	Chain	Res	Type
9	IN	81	LEU
9	IN	84	CYS
9	IN	91	VAL
9	IN	95	LEU
9	IN	102	VAL
9	IN	110	GLU
4	Dd	26	LYS
4	Dd	53	LEU
4	Dd	58	VAL
4	Dd	61	VAL
4	Dd	62	ILE
4	Dd	63	THR
4	Dd	85	VAL
4	Dd	88	SER
4	Dd	91	ILE
4	Dd	92	GLU
4	Dd	93	GLU
4	Dd	115	VAL
4	Dd	138	GLN
4	Dd	146	HIS
4	Dd	150	ASN
4	Dd	154	VAL
4	Id	27	LYS
4	Id	30	ILE
4	Id	36	ASP
4	Id	52	MET
4	Id	60	LYS
4	Id	61	VAL
4	Id	63	THR
4	Id	72	THR
4	Id	78	ASN
4	Id	85	VAL
4	Id	92	GLU
4	Id	108	VAL
4	Id	115	VAL
4	Id	119	ILE
4	Id	128	LEU
4	Id	150	ASN
4	Id	154	VAL
3	If	212	ILE
3	If	215	VAL
3	If	216	ILE

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Mol	Chain	Res	Type
3	If	232	VAL
3	If	233	ARG
3	If	244	VAL
3	If	251	GLN
3	If	255	LEU
3	If	256	THR
3	If	260	GLN
3	If	261	VAL
3	If	266	GLN
4	JD	31	ASN
4	JD	35	ASP
4	JD	41	LEU
4	JD	43	GLU
4	JD	47	SER
4	JD	50	ASP
4	JD	55	MET
4	JD	71	LEU
4	JD	84	SER
4	JD	85	VAL
4	JD	91	ILE
4	JD	108	VAL
4	JD	115	VAL
4	JD	118	LEU
4	JD	124	LYS
4	JD	127	SER
4	JD	131	ILE
4	JD	132	LEU
4	JD	160	LYS
3	JF	211	TYR
3	JF	222	LEU
3	JF	223	ILE
3	JF	229	THR
3	JF	231	THR
3	JF	238	ILE
3	JF	250	LEU
3	JF	256	THR
1	Jg	794	ILE
1	Jg	801	MET
1	Jg	806	THR
1	Jg	808	LEU
1	Jg	810	GLN
1	Jg	811	ASP

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Mol	Chain	Res	Type
1	Jg	813	LYS
1	Jg	815	VAL
1	Jg	817	THR
1	Jg	819	VAL
5	JH	116	THR
5	JH	125	GLU
5	JH	147	THR
5	JH	203	ASN
5	JH	204	ILE
5	JH	205	GLN
5	JH	226	LEU
5	JH	233	LEU
5	JH	241	LEU
5	JH	248	VAL
5	JH	249	ASP
5	JH	253	ASP
5	JH	256	VAL
5	JH	262	ASN
5	JH	285	GLU
5	JH	313	VAL
5	JH	316	ASN
5	JH	319	ILE
5	JH	339	MET
5	JH	350	HIS
6	JK	45	VAL
6	JK	50	ASP
6	JK	70	VAL
6	JK	72	GLN
6	JK	75	LEU
6	JK	83	LEU
6	JK	88	SER
6	JK	91	LEU
6	JK	92	ASN
6	JK	99	LEU
6	JK	106	LEU
6	JK	107	LYS
6	JK	111	LYS
6	JK	114	ILE
6	JK	117	THR
6	JK	126	VAL
6	JK	144	LEU
6	JK	156	THR

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Mol	Chain	Res	Type
6	JK	157	GLN
6	JK	159	LEU
6	JK	170	LEU
6	JK	180	VAL
6	JK	182	ILE
6	JK	183	THR
7	JL	44	HIS
7	JL	47	TYR
7	JL	58	LYS
7	JL	101	SER
7	JL	109	LEU
7	JL	129	THR
7	JL	130	ASP
7	JL	133	PHE
7	JL	134	MET
7	JL	155	LEU
7	JL	172	VAL
7	JL	181	LEU
7	JL	193	LEU
7	JL	203	LEU
7	JL	212	ASN
7	JL	216	ASP
8	JM	129	LEU
8	JM	146	LEU
8	JM	149	ASN
8	JM	150	ILE
8	JM	160	ASN
8	JM	162	VAL
8	JM	173	LEU
8	JM	175	ILE
8	JM	177	LEU
8	JM	180	ASP
8	JM	184	LEU
8	JM	191	LEU
8	JM	207	ILE
8	JM	212	LEU
8	JM	229	ASN
8	JM	233	VAL
8	JM	253	VAL
8	JM	259	SER
8	JM	260	VAL
8	JM	271	SER

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Mol	Chain	Res	Type
8	JM	290	ASP
8	JM	292	MET
8	JM	308	ASP
9	JN	44	LYS
9	JN	58	LEU
9	JN	65	TYR
9	JN	77	ASP
9	JN	84	CYS
9	JN	86	LEU
9	JN	91	VAL
9	JN	100	LEU
9	JN	101	VAL
9	JN	102	VAL
9	JN	103	CYS
9	JN	104	ASN
1	CG	865	THR
1	CG	869	MET
1	CG	877	VAL
1	CG	886	LEU
1	CG	898	LYS
1	CG	900	ILE
1	CG	904	ASN
1	CG	910	ASP
1	CG	911	LYS
1	CG	913	VAL
1	CG	916	PHE
1	CG	930	ILE
1	CG	942	THR
1	CG	944	LEU
1	CG	956	TYR
1	CG	962	SER
1	CG	965	LEU
1	CG	966	GLN
1	CG	1010	THR
1	CG	1017	GLN
1	CG	1020	GLN
1	CG	1027	THR
1	CG	1028	THR
1	CG	1031	VAL
1	CG	1037	LEU
1	CG	1041	PHE
1	CG	1044	ASP

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Mol	Chain	Res	Type
4	Jd	30	ILE
4	Jd	36	ASP
4	Jd	51	SER
4	Jd	59	GLU
4	Jd	61	VAL
4	Jd	62	ILE
4	Jd	63	THR
4	Jd	108	VAL
4	Jd	115	VAL
4	Jd	118	LEU
4	Jd	119	ILE
4	Jd	121	ILE
4	Jd	142	LYS
4	Jd	150	ASN
3	Jf	208	ILE
3	Jf	209	ILE
3	Jf	213	GLN
3	Jf	216	ILE
3	Jf	237	LYS
3	Jf	238	ILE
3	Jf	245	LYS
3	Jf	246	LEU
3	Jf	255	LEU
3	Jf	260	GLN
3	Jf	261	VAL
3	Jf	263	LYS
5	AH	107	ILE
5	AH	109	LYS
5	AH	113	LYS
5	AH	135	GLU
5	AH	147	THR
5	AH	154	THR
5	AH	160	LEU
5	AH	180	VAL
5	AH	183	ASP
5	AH	201	SER
5	AH	202	PHE
5	AH	207	ASP
5	AH	218	THR
5	AH	226	LEU
5	AH	230	LEU
5	AH	233	LEU

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Mol	Chain	Res	Type
5	AH	235	THR
5	AH	237	VAL
5	AH	239	LEU
5	AH	241	LEU
5	AH	245	GLN
5	AH	248	VAL
5	AH	262	ASN
5	AH	277	ASN
5	AH	280	LEU
5	AH	283	VAL
5	AH	284	LEU
5	AH	316	ASN
5	AH	344	VAL
5	AH	345	LEU
5	AH	347	VAL
5	AH	356	LEU
4	KD	23	MET
4	KD	38	THR
4	KD	63	THR
4	KD	79	LEU
4	KD	85	VAL
4	KD	91	ILE
4	KD	108	VAL
4	KD	156	LEU
4	KD	160	LYS
2	CC	62	THR
2	CC	65	SER
2	CC	80	ASP
2	CC	83	LEU
2	CC	84	ASN
2	CC	99	LEU
2	CC	102	GLU
2	CC	103	HIS
2	CC	105	ILE
2	CC	111	LEU
2	CC	116	THR
2	CC	117	LEU
2	CC	127	ILE
2	CC	143	THR
2	CC	146	THR
2	CC	148	ARG
2	CC	151	LEU

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Mol	Chain	Res	Type
2	CC	153	MET
2	CC	156	VAL
2	CC	163	VAL
2	CC	168	LYS
2	CC	170	LYS
2	CC	176	TRP
2	CC	181	GLU
2	CC	185	LYS
2	CC	204	GLU
2	CC	218	MET
2	CC	221	VAL
2	CC	226	VAL
2	CC	240	ILE
2	CC	247	LEU
2	CC	248	ARG
2	CC	249	ILE
2	CC	258	ASN
2	CC	259	SER
2	CC	266	VAL
3	KF	207	ARG
3	KF	215	VAL
3	KF	222	LEU
3	KF	229	THR
3	KF	230	LEU
3	KF	231	THR
3	KF	238	ILE
3	KF	262	ILE
1	Kg	793	GLU
1	Kg	806	THR
1	Kg	808	LEU
1	Kg	809	VAL
1	Kg	811	ASP
1	Kg	815	VAL
1	Kg	817	THR
1	Kg	819	VAL
1	Kg	824	THR
5	KH	122	LEU
5	KH	123	ASN
5	KH	147	THR
5	KH	158	VAL
5	KH	164	SER
5	KH	180	VAL

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Mol	Chain	Res	Type
5	KH	183	ASP
5	KH	218	THR
5	KH	222	ASN
5	KH	228	VAL
5	KH	234	ASN
5	KH	242	ILE
5	KH	248	VAL
5	KH	249	ASP
5	KH	259	TYR
5	KH	270	GLU
5	KH	279	LEU
5	KH	285	GLU
5	KH	305	TRP
5	KH	313	VAL
5	KH	321	SER
5	KH	329	THR
5	KH	342	SER
5	KH	346	LEU
6	KK	45	VAL
6	KK	50	ASP
6	KK	55	LYS
6	KK	60	LEU
6	KK	66	LYS
6	KK	70	VAL
6	KK	72	GLN
6	KK	75	LEU
6	KK	76	ILE
6	KK	83	LEU
6	KK	91	LEU
6	KK	95	SER
6	KK	102	ILE
6	KK	106	LEU
6	KK	111	LYS
6	KK	112	ILE
6	KK	125	SER
6	KK	133	THR
6	KK	134	LEU
6	KK	144	LEU
6	KK	149	VAL
6	KK	152	ARG
6	KK	156	THR
6	KK	159	LEU

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Mol	Chain	Res	Type
6	KK	166	THR
6	KK	180	VAL
6	KK	183	THR
7	KL	44	HIS
7	KL	54	ARG
7	KL	57	VAL
7	KL	91	VAL
7	KL	109	LEU
7	KL	112	GLN
7	KL	113	ASP
7	KL	121	ASP
7	KL	130	ASP
7	KL	140	LEU
7	KL	143	ILE
7	KL	155	LEU
7	KL	160	GLN
7	KL	165	VAL
7	KL	172	VAL
7	KL	174	SER
7	KL	193	LEU
7	KL	204	LYS
7	KL	210	ASP
7	KL	212	ASN
7	KL	217	ASN
8	KM	124	VAL
8	KM	127	ASN
8	KM	129	LEU
8	KM	131	THR
8	KM	134	LEU
8	KM	136	LEU
8	KM	146	LEU
8	KM	149	ASN
8	KM	152	LEU
8	KM	155	LEU
8	KM	160	ASN
8	KM	162	VAL
8	KM	171	ARG
8	KM	173	LEU
8	KM	178	LYS
8	KM	180	ASP
8	KM	183	VAL
8	KM	184	LEU

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Mol	Chain	Res	Type
8	KM	205	TYR
8	KM	207	ILE
8	KM	212	LEU
8	KM	222	ILE
8	KM	231	LEU
8	KM	259	SER
8	KM	263	ILE
8	KM	271	SER
8	KM	290	ASP
8	KM	292	MET
8	KM	299	LEU
8	KM	303	GLU
8	KM	308	ASP
9	KN	62	ASN
9	KN	69	TYR
9	KN	70	CYS
9	KN	71	THR
9	KN	78	LEU
9	KN	81	LEU
9	KN	95	LEU
9	KN	100	LEU
9	KN	110	GLU
9	KN	114	LEU
9	KN	115	GLN
4	Kd	30	ILE
4	Kd	61	VAL
4	Kd	63	THR
4	Kd	67	LYS
4	Kd	72	THR
4	Kd	73	ILE
4	Kd	93	GLU
4	Kd	108	VAL
4	Kd	111	LYS
4	Kd	115	VAL
4	Kd	132	LEU
4	Kd	147	VAL
4	Kd	150	ASN
4	Kd	154	VAL
3	Kf	208	ILE
3	Kf	209	ILE
3	Kf	215	VAL
3	Kf	216	ILE

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Mol	Chain	Res	Type
3	Kf	232	VAL
3	Kf	250	LEU
3	Kf	261	VAL
3	Kf	266	GLN
4	LD	23	MET
4	LD	30	ILE
4	LD	32	ASN
4	LD	36	ASP
4	LD	43	GLU
4	LD	61	VAL
4	LD	71	LEU
4	LD	73	ILE
4	LD	75	ASN
4	LD	85	VAL
4	LD	86	ASP
4	LD	91	ILE
4	LD	95	THR
4	LD	108	VAL
4	LD	123	THR
4	LD	131	ILE
4	LD	152	GLN
4	LD	154	VAL
4	LD	160	LYS
4	LD	162	TYR
3	LF	215	VAL
3	LF	223	ILE
3	LF	230	LEU
3	LF	231	THR
3	LF	238	ILE
3	LF	250	LEU
1	Lg	795	GLN
1	Lg	796	GLN
1	Lg	798	THR
1	Lg	806	THR
1	Lg	808	LEU
1	Lg	809	VAL
1	Lg	810	GLN
1	Lg	811	ASP
1	Lg	817	THR
5	LH	105	GLU
5	LH	107	ILE
5	LH	115	MET

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Mol	Chain	Res	Type
5	LH	119	LEU
5	LH	130	LEU
5	LH	137	SER
5	LH	138	GLU
5	LH	147	THR
5	LH	154	THR
5	LH	160	LEU
5	LH	180	VAL
5	LH	196	LEU
5	LH	209	THR
5	LH	230	LEU
5	LH	239	LEU
5	LH	241	LEU
5	LH	248	VAL
5	LH	251	ARG
5	LH	254	LEU
5	LH	256	VAL
5	LH	270	GLU
5	LH	280	LEU
5	LH	313	VAL
5	LH	317	LEU
5	LH	329	THR
5	LH	339	MET
5	LH	345	LEU
5	LH	347	VAL
5	LH	353	VAL
5	LH	356	LEU
6	LK	41	LEU
6	LK	45	VAL
6	LK	50	ASP
6	LK	53	ILE
6	LK	58	THR
6	LK	63	LYS
6	LK	76	ILE
6	LK	83	LEU
6	LK	95	SER
6	LK	106	LEU
6	LK	111	LYS
6	LK	116	VAL
6	LK	124	VAL
6	LK	125	SER
6	LK	126	VAL

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Mol	Chain	Res	Type
6	LK	134	LEU
6	LK	144	LEU
6	LK	149	VAL
6	LK	156	THR
6	LK	162	ASP
6	LK	177	ASN
6	LK	183	THR
7	LL	51	GLN
7	LL	103	ARG
7	LL	105	ILE
7	LL	109	LEU
7	LL	113	ASP
7	LL	115	GLN
7	LL	133	PHE
7	LL	148	LEU
7	LL	155	LEU
7	LL	172	VAL
7	LL	174	SER
7	LL	187	GLU
7	LL	193	LEU
7	LL	204	LYS
7	LL	210	ASP
7	LL	212	ASN
7	LL	230	GLU
8	LM	115	ARG
8	LM	134	LEU
8	LM	149	ASN
8	LM	152	LEU
8	LM	160	ASN
8	LM	162	VAL
8	LM	176	VAL
8	LM	180	ASP
8	LM	182	LYS
8	LM	183	VAL
8	LM	184	LEU
8	LM	190	ASN
8	LM	192	ARG
8	LM	202	LEU
8	LM	205	TYR
8	LM	212	LEU
8	LM	228	VAL
8	LM	263	ILE

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Mol	Chain	Res	Type
8	LM	292	MET
8	LM	297	SER
8	LM	299	LEU
8	LM	300	ASP
8	LM	301	MET
8	LM	303	GLU
9	LN	59	VAL
9	LN	78	LEU
9	LN	81	LEU
9	LN	91	VAL
9	LN	101	VAL
9	LN	102	VAL
9	LN	110	GLU
9	LN	114	LEU
9	LN	115	GLN
1	DG	865	THR
1	DG	874	ASP
1	DG	877	VAL
1	DG	885	ILE
1	DG	886	LEU
1	DG	889	ILE
1	DG	898	LYS
1	DG	913	VAL
1	DG	925	GLU
1	DG	928	ILE
1	DG	930	ILE
1	DG	935	ILE
1	DG	944	LEU
1	DG	947	ARG
1	DG	956	TYR
1	DG	962	SER
1	DG	963	SER
1	DG	965	LEU
1	DG	1031	VAL
1	DG	1037	LEU
1	DG	1044	ASP
4	Ld	41	LEU
4	Ld	55	MET
4	Ld	58	VAL
4	Ld	61	VAL
4	Ld	85	VAL
4	Ld	103	HIS

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Mol	Chain	Res	Type
4	Ld	111	LYS
4	Ld	112	SER
4	Ld	115	VAL
4	Ld	147	VAL
4	Ld	156	LEU
3	Lf	208	ILE
3	Lf	212	ILE
3	Lf	215	VAL
3	Lf	216	ILE
3	Lf	223	ILE
3	Lf	246	LEU
3	Lf	251	GLN
3	Lf	262	ILE
6	AK	45	VAL
6	AK	46	ASP
6	AK	50	ASP
6	AK	60	LEU
6	AK	83	LEU
6	AK	92	ASN
6	AK	95	SER
6	AK	98	LEU
6	AK	99	LEU
6	AK	101	GLU
6	AK	106	LEU
6	AK	111	LYS
6	AK	125	SER
6	AK	126	VAL
6	AK	129	GLU
6	AK	144	LEU
6	AK	149	VAL
6	AK	156	THR
6	AK	162	ASP
6	AK	163	LYS
6	AK	170	LEU
6	AK	180	VAL
4	MD	38	THR
4	MD	41	LEU
4	MD	47	SER
4	MD	54	GLU
4	MD	78	ASN
4	MD	115	VAL
4	MD	117	VAL

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Mol	Chain	Res	Type
4	MD	118	LEU
4	MD	123	THR
4	MD	127	SER
4	MD	130	GLU
4	MD	161	ILE
3	MF	207	ARG
3	MF	215	VAL
3	MF	223	ILE
3	MF	230	LEU
3	MF	232	VAL
3	MF	238	ILE
3	MF	250	LEU
3	MF	256	THR
1	Cg	802	LEU
1	Cg	806	THR
1	Cg	808	LEU
1	Cg	815	VAL
1	Mg	800	ASP
1	Mg	802	LEU
1	Mg	806	THR
1	Mg	814	GLN
1	Mg	815	VAL
1	Mg	817	THR
1	Mg	819	VAL
1	Ag	811	ASP
1	Ag	815	VAL
1	Ag	817	THR
1	Ag	819	VAL
5	MH	115	MET
5	MH	141	LYS
5	MH	147	THR
5	MH	154	THR
5	MH	160	LEU
5	MH	205	GLN
5	MH	209	THR
5	MH	226	LEU
5	MH	228	VAL
5	MH	240	THR
5	MH	241	LEU
5	MH	248	VAL
5	MH	257	GLN
5	MH	268	THR

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Mol	Chain	Res	Type
5	MH	278	ASP
5	MH	280	LEU
5	MH	285	GLU
5	MH	287	VAL
5	MH	296	VAL
5	MH	313	VAL
5	MH	348	SER
5	MH	361	LEU
6	MK	41	LEU
6	MK	66	LYS
6	MK	70	VAL
6	MK	75	LEU
6	MK	83	LEU
6	MK	86	ASP
6	MK	92	ASN
6	MK	98	LEU
6	MK	99	LEU
6	MK	101	GLU
6	MK	111	LYS
6	MK	112	ILE
6	MK	125	SER
6	MK	126	VAL
6	MK	127	LYS
6	MK	144	LEU
6	MK	149	VAL
6	MK	156	THR
6	MK	180	VAL
7	ML	47	TYR
7	ML	49	ASN
7	ML	51	GLN
7	ML	62	VAL
7	ML	93	LEU
7	ML	96	SER
7	ML	98	TYR
7	ML	109	LEU
7	ML	151	VAL
7	ML	154	LEU
7	ML	160	GLN
7	ML	172	VAL
7	ML	189	MET
7	ML	193	LEU
7	ML	212	ASN

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Mol	Chain	Res	Type
7	ML	219	ILE
7	ML	225	GLN
7	ML	235	THR
8	MM	129	LEU
8	MM	131	THR
8	MM	134	LEU
8	MM	144	THR
8	MM	149	ASN
8	MM	152	LEU
8	MM	155	LEU
8	MM	162	VAL
8	MM	171	ARG
8	MM	173	LEU
8	MM	175	ILE
8	MM	176	VAL
8	MM	177	LEU
8	MM	180	ASP
8	MM	183	VAL
8	MM	195	ASP
8	MM	202	LEU
8	MM	204	LEU
8	MM	207	ILE
8	MM	212	LEU
8	MM	224	LEU
8	MM	259	SER
8	MM	271	SER
8	MM	275	ASP
8	MM	277	SER
8	MM	290	ASP
8	MM	292	MET
8	MM	299	LEU
8	MM	301	MET
8	MM	303	GLU
9	MN	48	ILE
9	MN	52	ASP
9	MN	91	VAL
9	MN	95	LEU
9	MN	101	VAL
9	MN	102	VAL
9	MN	108	VAL
9	MN	114	LEU
4	Md	31	ASN

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Mol	Chain	Res	Type
4	Md	36	ASP
4	Md	41	LEU
4	Md	55	MET
4	Md	61	VAL
4	Md	63	THR
4	Md	91	ILE
4	Md	92	GLU
4	Md	100	LYS
4	Md	108	VAL
4	Md	115	VAL
4	Md	123	THR
4	Md	128	LEU
4	Md	134	ASP
4	Md	142	LYS
4	Md	155	GLU
3	Mf	209	ILE
3	Mf	216	ILE
3	Mf	230	LEU
3	Mf	232	VAL
3	Mf	236	SER
3	Mf	250	LEU
3	Mf	255	LEU
3	Mf	260	GLN
3	Mf	261	VAL
3	VF	207	ARG
3	VF	208	ILE
3	VF	215	VAL
3	VF	223	ILE
3	VF	229	THR
3	VF	230	LEU
3	VF	231	THR
3	VF	238	ILE
3	VF	256	THR
3	VF	262	ILE
1	VG	793	GLU
1	VG	796	GLN
1	VG	802	LEU
1	VG	817	THR
5	VH	105	GLU
5	VH	108	ASP
5	VH	109	LYS
5	VH	115	MET

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Mol	Chain	Res	Type
5	VH	138	GLU
5	VH	147	THR
5	VH	154	THR
5	VH	160	LEU
5	VH	168	VAL
5	VH	180	VAL
5	VH	204	ILE
5	VH	226	LEU
5	VH	238	MET
5	VH	240	THR
5	VH	241	LEU
5	VH	248	VAL
5	VH	250	TYR
5	VH	257	GLN
5	VH	281	LEU
5	VH	287	VAL
5	VH	296	VAL
5	VH	297	VAL
5	VH	313	VAL
5	VH	318	THR
5	VH	329	THR
5	VH	338	GLU
5	VH	347	VAL
5	VH	358	VAL
3	WF	207	ARG
3	WF	223	ILE
3	WF	229	THR
3	WF	232	VAL
3	WF	234	GLU
3	WF	238	ILE
3	WF	256	THR
3	WF	264	PHE
3	WF	266	GLN
1	WG	815	VAL
1	WG	816	GLU
1	WG	817	THR
5	WH	105	GLU
5	WH	107	ILE
5	WH	108	ASP
5	WH	114	ASP
5	WH	116	THR
5	WH	119	LEU

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Mol	Chain	Res	Type
5	WH	147	THR
5	WH	176	VAL
5	WH	180	VAL
5	WH	182	LEU
5	WH	185	THR
5	WH	215	ILE
5	WH	228	VAL
5	WH	240	THR
5	WH	242	ILE
5	WH	253	ASP
5	WH	262	ASN
5	WH	279	LEU
5	WH	297	VAL
5	WH	313	VAL
5	WH	315	THR
5	WH	345	LEU
5	WH	354	MET
4	CD	26	LYS
4	CD	30	ILE
4	CD	41	LEU
4	CD	47	SER
4	CD	50	ASP
4	CD	51	SER
4	CD	52	MET
4	CD	70	THR
4	CD	73	ILE
4	CD	85	VAL
4	CD	91	ILE
4	CD	95	THR
4	CD	98	ILE
4	CD	109	LEU
4	CD	111	LYS
4	CD	115	VAL
4	CD	124	LYS
4	CD	145	ILE
4	CD	154	VAL
4	CD	156	LEU
4	CD	161	ILE
1	EG	865	THR
1	EG	869	MET
1	EG	873	LEU
1	EG	885	ILE

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Mol	Chain	Res	Type
1	EG	886	LEU
1	EG	898	LYS
1	EG	913	VAL
1	EG	916	PHE
1	EG	930	ILE
1	EG	935	ILE
1	EG	939	THR
1	EG	942	THR
1	EG	944	LEU
1	EG	948	THR
1	EG	956	TYR
1	EG	962	SER
1	EG	963	SER
1	EG	965	LEU
1	EG	1027	THR
1	EG	1028	THR
1	EG	1045	VAL
3	XF	215	VAL
3	XF	216	ILE
3	XF	223	ILE
3	XF	230	LEU
3	XF	232	VAL
3	XF	238	ILE
3	XF	250	LEU
3	XF	256	THR
1	XG	793	GLU
1	XG	802	LEU
1	XG	815	VAL
1	XG	817	THR
1	XG	819	VAL
1	XG	821	THR
5	XH	107	ILE
5	XH	108	ASP
5	XH	113	LYS
5	XH	132	GLN
5	XH	138	GLU
5	XH	147	THR
5	XH	207	ASP
5	XH	211	ASN
5	XH	218	THR
5	XH	225	ASN
5	XH	226	LEU

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Mol	Chain	Res	Type
5	XH	229	ARG
5	XH	242	ILE
5	XH	248	VAL
5	XH	250	TYR
5	XH	253	ASP
5	XH	256	VAL
5	XH	259	TYR
5	XH	278	ASP
5	XH	296	VAL
5	XH	297	VAL
5	XH	317	LEU
5	XH	329	THR
5	XH	338	GLU
5	XH	353	VAL
5	XH	358	VAL
3	YF	207	ARG
3	YF	208	ILE
3	YF	215	VAL
3	YF	223	ILE
3	YF	230	LEU
3	YF	231	THR
3	YF	238	ILE
3	YF	256	THR
3	YF	258	SER
7	AL	49	ASN
7	AL	93	LEU
7	AL	102	LYS
7	AL	109	LEU
7	AL	110	GLN
7	AL	114	ILE
7	AL	125	LEU
7	AL	155	LEU
7	AL	162	THR
7	AL	165	VAL
7	AL	172	VAL
7	AL	177	HIS
7	AL	189	MET
7	AL	193	LEU
7	AL	203	LEU
7	AL	210	ASP
7	AL	229	ILE
1	YG	815	VAL

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Mol	Chain	Res	Type
1	YG	816	GLU
1	YG	817	THR
5	YH	107	ILE
5	YH	115	MET
5	YH	125	GLU
5	YH	129	LYS
5	YH	136	THR
5	YH	147	THR
5	YH	160	LEU
5	YH	171	LEU
5	YH	176	VAL
5	YH	179	LEU
5	YH	209	THR
5	YH	211	ASN
5	YH	214	MET
5	YH	218	THR
5	YH	228	VAL
5	YH	240	THR
5	YH	248	VAL
5	YH	249	ASP
5	YH	255	ARG
5	YH	256	VAL
5	YH	281	LEU
5	YH	282	HIS
5	YH	283	VAL
5	YH	295	LEU
5	YH	301	ASP
5	YH	306	LEU
5	YH	329	THR
5	YH	332	ASP
5	YH	338	GLU
5	YH	345	LEU
5	YH	358	VAL
3	Df	216	ILE
3	Df	232	VAL
3	Df	236	SER
3	Df	250	LEU
3	Df	255	LEU
3	Df	262	ILE
2	DC	28	ASP
2	DC	29	THR
2	DC	32	LEU

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Mol	Chain	Res	Type
2	DC	57	GLU
2	DC	60	LEU
2	DC	61	LYS
2	DC	86	LYS
2	DC	87	GLN
2	DC	90	ASN
2	DC	100	LEU
2	DC	101	VAL
2	DC	104	HIS
2	DC	111	LEU
2	DC	117	THR
2	DC	118	LEU
2	DC	126	ILE
2	DC	142	ILE
2	DC	147	THR
2	DC	150	GLN
2	DC	152	LEU
2	DC	170	THR
2	DC	191	GLN
2	DC	203	ILE
2	DC	222	VAL
2	DC	227	VAL
2	DC	241	ILE
2	DC	244	ASP
2	DC	250	ILE
2	DC	267	VAL
3	ZF	207	ARG
3	ZF	208	ILE
3	ZF	215	VAL
3	ZF	223	ILE
3	ZF	230	LEU
3	ZF	231	THR
3	ZF	238	ILE
3	ZF	247	ILE
3	ZF	250	LEU
3	ZF	256	THR
1	ZG	793	GLU
1	ZG	806	THR
1	ZG	813	LYS
1	ZG	815	VAL
1	ZG	821	THR
5	ZH	105	GLU

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Mol	Chain	Res	Type
5	ZH	113	LYS
5	ZH	114	ASP
5	ZH	122	LEU
5	ZH	138	GLU
5	ZH	147	THR
5	ZH	159	ASN
5	ZH	180	VAL
5	ZH	191	ILE
5	ZH	195	ASP
5	ZH	215	ILE
5	ZH	218	THR
5	ZH	225	ASN
5	ZH	226	LEU
5	ZH	231	ARG
5	ZH	233	LEU
5	ZH	238	MET
5	ZH	239	LEU
5	ZH	241	LEU
5	ZH	249	ASP
5	ZH	253	ASP
5	ZH	262	ASN
5	ZH	278	ASP
5	ZH	281	LEU
5	ZH	297	VAL
5	ZH	306	LEU
5	ZH	311	MET
5	ZH	321	SER
5	ZH	325	LEU
5	ZH	329	THR
5	ZH	358	VAL
8	AM	129	LEU
8	AM	131	THR
8	AM	134	LEU
8	AM	136	LEU
8	AM	149	ASN
8	AM	176	VAL
8	AM	184	LEU
8	AM	194	LEU
8	AM	204	LEU
8	AM	207	ILE
8	AM	208	LYS
8	AM	212	LEU

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Mol	Chain	Res	Type
8	AM	228	VAL
8	AM	235	LEU
8	AM	251	SER
8	AM	253	VAL
8	AM	259	SER
8	AM	262	GLU
8	AM	263	ILE
8	AM	266	VAL
8	AM	269	GLN
8	AM	277	SER
8	AM	292	MET
8	AM	297	SER
8	AM	299	LEU
9	AN	62	ASN
9	AN	69	TYR
9	AN	81	LEU
9	AN	84	CYS
9	AN	86	LEU
9	AN	100	LEU
9	AN	102	VAL
4	Ad	32	ASN
4	Ad	53	LEU
4	Ad	61	VAL
4	Ad	63	THR
4	Ad	69	ASN
4	Ad	91	ILE
4	Ad	108	VAL
4	Ad	115	VAL
4	Ad	117	VAL
4	Ad	128	LEU
4	Ad	150	ASN
4	Ad	153	VAL
3	Af	208	ILE
3	Af	215	VAL
3	Af	216	ILE
3	Af	222	LEU
3	Af	225	SER
3	Af	230	LEU
3	Af	238	ILE
3	Af	243	MET
3	Af	244	VAL
3	Af	246	LEU

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Mol	Chain	Res	Type
3	Af	247	ILE
3	Af	253	ARG
3	Af	261	VAL
3	Af	263	LYS
4	BD	31	ASN
4	BD	36	ASP
4	BD	38	THR
4	BD	47	SER
4	BD	53	LEU
4	BD	70	THR
4	BD	84	SER
4	BD	98	ILE
4	BD	109	LEU
4	BD	123	THR
4	BD	127	SER
4	BD	128	LEU
4	BD	154	VAL
4	BD	156	LEU
4	BD	161	ILE
3	BF	207	ARG
3	BF	208	ILE
3	BF	215	VAL
3	BF	223	ILE
3	BF	230	LEU
3	BF	231	THR
3	BF	232	VAL
3	BF	238	ILE
3	BF	244	VAL
3	BF	255	LEU
3	BF	256	THR
5	BH	117	ARG
5	BH	119	LEU
5	BH	122	LEU
5	BH	138	GLU
5	BH	147	THR
5	BH	154	THR
5	BH	160	LEU
5	BH	168	VAL
5	BH	182	LEU
5	BH	204	ILE
5	BH	207	ASP
5	BH	209	THR

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Mol	Chain	Res	Type
5	BH	220	LEU
5	BH	228	VAL
5	BH	233	LEU
5	BH	241	LEU
5	BH	242	ILE
5	BH	248	VAL
5	BH	249	ASP
5	BH	254	LEU
5	BH	266	MET
5	BH	280	LEU
5	BH	284	LEU
5	BH	297	VAL
5	BH	315	THR
5	BH	318	THR
5	BH	321	SER
5	BH	329	THR
5	BH	334	THR
5	BH	338	GLU
6	BK	41	LEU
6	BK	56	MET
6	BK	58	THR
6	BK	67	VAL
6	BK	75	LEU
6	BK	88	SER
6	BK	91	LEU
6	BK	95	SER
6	BK	98	LEU
6	BK	112	ILE
6	BK	126	VAL
6	BK	134	LEU
6	BK	142	GLU
6	BK	144	LEU
6	BK	149	VAL
6	BK	153	ILE
6	BK	156	THR
6	BK	170	LEU
6	BK	179	ARG
6	BK	180	VAL
6	BK	182	ILE
3	CF	207	ARG
3	CF	208	ILE
3	CF	215	VAL

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Mol	Chain	Res	Type
3	CF	230	LEU
3	CF	238	ILE
3	CF	244	VAL
3	CF	250	LEU
3	CF	256	THR
3	CF	265	SER
3	CF	266	GLN
1	FG	865	THR
1	FG	867	ASP
1	FG	869	MET
1	FG	885	ILE
1	FG	886	LEU
1	FG	898	LYS
1	FG	900	ILE
1	FG	910	ASP
1	FG	911	LYS
1	FG	913	VAL
1	FG	916	PHE
1	FG	930	ILE
1	FG	935	ILE
1	FG	939	THR
1	FG	942	THR
1	FG	944	LEU
1	FG	962	SER
1	FG	963	SER
1	FG	965	LEU
1	FG	972	PHE
1	FG	1020	GLN
1	FG	1022	LEU
1	FG	1028	THR
7	BL	43	PHE
7	BL	57	VAL
7	BL	93	LEU
7	BL	109	LEU
7	BL	125	LEU
7	BL	127	ILE
7	BL	129	THR
7	BL	133	PHE
7	BL	161	SER
7	BL	170	ASP
7	BL	172	VAL
7	BL	174	SER

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Mol	Chain	Res	Type
7	BL	190	MET
7	BL	216	ASP
7	BL	230	GLU
8	BM	123	VAL
8	BM	134	LEU
8	BM	136	LEU
8	BM	138	LEU
8	BM	140	ASN
8	BM	146	LEU
8	BM	149	ASN
8	BM	152	LEU
8	BM	171	ARG
8	BM	176	VAL
8	BM	177	LEU
8	BM	180	ASP
8	BM	182	LYS
8	BM	184	LEU
8	BM	191	LEU
8	BM	205	TYR
8	BM	207	ILE
8	BM	210	ASP
8	BM	212	LEU
8	BM	233	VAL
8	BM	246	LEU
8	BM	257	ASP
8	BM	259	SER
8	BM	263	ILE
8	BM	269	GLN
8	BM	271	SER
8	BM	277	SER
8	BM	285	SER
8	BM	292	MET
8	BM	297	SER
8	BM	298	VAL
8	BM	318	GLN
9	BN	44	LYS
9	BN	62	ASN
9	BN	66	SER
9	BN	71	THR
9	BN	81	LEU
9	BN	84	CYS
9	BN	91	VAL

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Mol	Chain	Res	Type
9	BN	94	GLN
9	BN	101	VAL
9	BN	110	GLU
4	Bd	38	THR
4	Bd	41	LEU
4	Bd	52	MET
4	Bd	61	VAL
4	Bd	63	THR
4	Bd	70	THR
4	Bd	73	ILE
4	Bd	78	ASN
4	Bd	108	VAL
4	Bd	115	VAL
4	Bd	118	LEU
4	Bd	127	SER
4	Bd	128	LEU
4	Bd	142	LYS
4	Bd	147	VAL
4	Bd	154	VAL
4	Bd	155	GLU
4	Bd	156	LEU
3	Bf	208	ILE
3	Bf	216	ILE
3	Bf	230	LEU
3	Bf	232	VAL
3	Bf	245	LYS
3	Bf	255	LEU
1	Dg	792	GLN
1	Dg	794	ILE
1	Dg	808	LEU
1	Dg	811	ASP
1	Dg	814	GLN
1	Dg	815	VAL
1	Dg	817	THR
1	Dg	822	GLU
4	AD	24	LYS
4	AD	35	ASP
4	AD	41	LEU
4	AD	43	GLU
4	AD	47	SER
4	AD	50	ASP
4	AD	51	SER

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Mol	Chain	Res	Type
4	AD	53	LEU
4	AD	62	ILE
4	AD	73	ILE
4	AD	79	LEU
4	AD	85	VAL
4	AD	86	ASP
4	AD	91	ILE
4	AD	92	GLU
4	AD	93	GLU
4	AD	115	VAL
4	AD	117	VAL
4	AD	127	SER
4	AD	132	LEU
4	AD	154	VAL
4	AD	160	LYS
2	FC	68	GLN
2	FC	80	GLU
2	FC	84	LYS
2	FC	89	LEU
2	FC	95	PHE
2	FC	99	VAL
2	FC	104	ILE
2	FC	109	LEU
2	FC	110	LEU
2	FC	116	LEU
2	FC	120	ASP
2	FC	141	THR
2	FC	142	THR
2	FC	145	THR
2	FC	147	ARG
2	FC	150	LEU
2	FC	153	ASP
2	FC	162	VAL
2	FC	164	LEU
2	FC	165	LEU
2	FC	172	LYS
2	FC	173	GLU
2	FC	179	THR
2	FC	183	TRP
2	FC	189	GLN
2	FC	192	THR
2	FC	203	GLU

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Mol	Chain	Res	Type
2	FC	209	ILE
2	FC	214	LEU
2	FC	225	VAL
2	FC	232	VAL
2	FC	239	ILE
2	FC	248	ILE
2	FC	254	LEU
2	FC	265	VAL
2	GC	60	LYS
2	GC	83	LEU
2	GC	85	LYS
2	GC	95	ASP
2	GC	99	LEU
2	GC	105	ILE
2	GC	109	VAL
2	GC	110	LEU
2	GC	111	LEU
2	GC	116	THR
2	GC	143	THR
2	GC	146	THR
2	GC	166	LEU
2	GC	169	THR
2	GC	190	GLN
2	GC	193	THR
2	GC	195	LEU
2	GC	204	GLU
2	GC	209	MET
2	GC	221	VAL
2	GC	225	TYR
2	GC	229	THR
2	GC	240	ILE
2	GC	241	HIS
2	GC	243	ASP
2	GC	249	ILE
2	GC	250	THR
2	GC	266	VAL
2	IC	28	ASP
2	IC	29	THR
2	IC	36	GLN
2	IC	43	TYR
2	IC	60	LEU
2	IC	90	ASN

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Mol	Chain	Res	Type
2	IC	92	ASP
2	IC	100	LEU
2	IC	101	VAL
2	IC	106	ILE
2	IC	117	THR
2	IC	126	ILE
2	IC	128	ILE
2	IC	132	THR
2	IC	147	THR
2	IC	152	LEU
2	IC	154	MET
2	IC	155	ASP
2	IC	167	LEU
2	IC	170	THR
2	IC	171	LYS
2	IC	206	ASP
2	IC	212	LEU
2	IC	227	VAL
2	IC	235	THR
2	IC	241	ILE
2	IC	259	ASN
2	JC	61	THR
2	JC	96	ASN
2	JC	99	VAL
2	JC	104	ILE
2	JC	110	LEU
2	JC	115	THR
2	JC	118	LEU
2	JC	126	ILE
2	JC	141	THR
2	JC	150	LEU
2	JC	154	TYR
2	JC	155	VAL
2	JC	161	ASN
2	JC	162	VAL
2	JC	165	LEU
2	JC	171	GLU
2	JC	179	THR
2	JC	203	GLU
2	JC	209	ILE
2	JC	214	LEU
2	JC	217	MET

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Mol	Chain	Res	Type
2	JC	225	VAL
2	JC	229	ASP
2	JC	232	VAL
2	JC	242	ASP
2	JC	243	ASP
2	JC	248	ILE
2	JC	253	GLU
2	JC	254	LEU
2	JC	265	VAL
2	KC	64	LEU
2	KC	79	ILE
2	KC	83	LEU
2	KC	84	ASN
2	KC	89	ASN
2	KC	97	ASN
2	KC	105	ILE
2	KC	111	LEU
2	KC	116	THR
2	KC	123	GLN
2	KC	125	ILE
2	KC	127	ILE
2	KC	143	THR
2	KC	146	THR
2	KC	148	ARG
2	KC	151	LEU
2	KC	156	VAL
2	KC	163	VAL
2	KC	165	LEU
2	KC	176	TRP
2	KC	189	ASP
2	KC	214	LYS
2	KC	220	MET
2	KC	221	VAL
2	KC	225	TYR
2	KC	226	VAL
2	KC	230	ASP
2	KC	238	SER
2	KC	240	ILE
2	KC	249	ILE
2	KC	256	ASN
2	KC	257	VAL
2	MC	29	THR

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Mol	Chain	Res	Type
2	MC	35	LEU
2	MC	47	GLN
2	MC	56	ARG
2	MC	58	MET
2	MC	86	LYS
2	MC	100	LEU
2	MC	104	HIS
2	MC	106	ILE
2	MC	111	LEU
2	MC	113	GLU
2	MC	117	THR
2	MC	126	ILE
2	MC	128	ILE
2	MC	132	THR
2	MC	143	THR
2	MC	152	LEU
2	MC	154	MET
2	MC	157	VAL
2	MC	167	LEU
2	MC	194	THR
2	MC	196	LEU
2	MC	222	VAL
2	MC	234	VAL
2	MC	235	THR
2	MC	242	HIS
2	MC	250	ILE
5	CH	115	MET
5	CH	123	ASN
5	CH	130	LEU
5	CH	147	THR
5	CH	152	THR
5	CH	154	THR
5	CH	180	VAL
5	CH	182	LEU
5	CH	196	LEU
5	CH	204	ILE
5	CH	207	ASP
5	CH	209	THR
5	CH	226	LEU
5	CH	233	LEU
5	CH	241	LEU
5	CH	248	VAL

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Mol	Chain	Res	Type
5	CH	249	ASP
5	CH	250	TYR
5	CH	253	ASP
5	CH	256	VAL
5	CH	278	ASP
5	CH	284	LEU
5	CH	292	SER
5	CH	313	VAL
5	CH	315	THR
5	CH	316	ASN
5	CH	320	LEU
5	CH	338	GLU
5	CH	344	VAL
6	CK	41	LEU
6	CK	43	CYS
6	CK	54	ILE
6	CK	60	LEU
6	CK	62	LYS
6	CK	83	LEU
6	CK	88	SER
6	CK	106	LEU
6	CK	125	SER
6	CK	126	VAL
6	CK	127	LYS
6	CK	144	LEU
6	CK	149	VAL
6	CK	151	SER
6	CK	153	ILE
6	CK	156	THR
6	CK	170	LEU
6	CK	173	ASP
6	CK	180	VAL
7	CL	57	VAL
7	CL	93	LEU
7	CL	96	SER
7	CL	100	ASP
7	CL	109	LEU
7	CL	127	ILE
7	CL	133	PHE
7	CL	140	LEU
7	CL	161	SER
7	CL	162	THR

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Mol	Chain	Res	Type
7	CL	172	VAL
7	CL	174	SER
7	CL	175	ARG
7	CL	181	LEU
7	CL	188	THR
7	CL	193	LEU
7	CL	212	ASN
7	CL	216	ASP
7	CL	225	GLN
7	CL	229	ILE
8	CM	127	ASN
8	CM	129	LEU
8	CM	134	LEU
8	CM	136	LEU
8	CM	144	THR
8	CM	149	ASN
8	CM	150	ILE
8	CM	152	LEU
8	CM	153	GLN
8	CM	162	VAL
8	CM	171	ARG
8	CM	173	LEU
8	CM	177	LEU
8	CM	183	VAL
8	CM	184	LEU
8	CM	191	LEU
8	CM	201	THR
8	CM	204	LEU
8	CM	205	TYR
8	CM	212	LEU
8	CM	221	LYS
8	CM	224	LEU
8	CM	231	LEU
8	CM	263	ILE
8	CM	271	SER
8	CM	285	SER
8	CM	287	THR
8	CM	292	MET
8	CM	299	LEU
8	CM	303	GLU
8	CM	308	ASP
9	CN	44	LYS

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Mol	Chain	Res	Type
9	CN	66	SER
9	CN	78	LEU
9	CN	81	LEU
9	CN	94	GLN
9	CN	95	LEU
9	CN	101	VAL
9	CN	102	VAL
9	CN	108	VAL
9	CN	110	GLU
9	CN	114	LEU
4	Cd	30	ILE
4	Cd	35	ASP
4	Cd	43	GLU
4	Cd	61	VAL
4	Cd	63	THR
4	Cd	68	ASP
4	Cd	69	ASN
4	Cd	85	VAL
4	Cd	111	LYS
4	Cd	119	ILE
4	Cd	123	THR
4	Cd	126	GLU
4	Cd	142	LYS
4	Cd	147	VAL
4	Cd	150	ASN
3	Cf	211	TYR
3	Cf	216	ILE
3	Cf	223	ILE
3	Cf	232	VAL
3	Cf	238	ILE
3	Cf	245	LYS
3	Cf	247	ILE
3	Cf	248	ASP
3	Cf	250	LEU
3	Cf	254	ILE
3	Cf	255	LEU
3	Cf	258	SER
3	Cf	260	GLN
3	Cf	261	VAL
4	DD	38	THR
4	DD	50	ASP
4	DD	51	SER

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Mol	Chain	Res	Type
4	DD	54	GLU
4	DD	55	MET
4	DD	75	ASN
4	DD	79	LEU
4	DD	85	VAL
4	DD	91	ILE
4	DD	109	LEU
4	DD	115	VAL
4	DD	118	LEU
4	DD	127	SER
4	DD	150	ASN
4	DD	160	LYS
4	DD	161	ILE
3	DF	207	ARG
3	DF	208	ILE
3	DF	215	VAL
3	DF	231	THR
3	DF	238	ILE
3	DF	250	LEU
3	DF	255	LEU
1	GG	865	THR
1	GG	867	ASP
1	GG	869	MET
1	GG	873	LEU
1	GG	886	LEU
1	GG	900	ILE
1	GG	904	ASN
1	GG	910	ASP
1	GG	913	VAL
1	GG	930	ILE
1	GG	944	LEU
1	GG	962	SER
1	GG	963	SER
1	GG	965	LEU
1	GG	972	PHE
1	GG	1001	LEU
1	GG	1010	THR
1	GG	1011	VAL
1	GG	1020	GLN
1	GG	1028	THR
1	GG	1037	LEU
1	GG	1045	VAL

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Mol	Chain	Res	Type
5	DH	107	ILE
5	DH	114	ASP
5	DH	115	MET
5	DH	122	LEU
5	DH	130	LEU
5	DH	147	THR
5	DH	154	THR
5	DH	180	VAL
5	DH	201	SER
5	DH	207	ASP
5	DH	210	SER
5	DH	220	LEU
5	DH	238	MET
5	DH	240	THR
5	DH	241	LEU
5	DH	249	ASP
5	DH	253	ASP
5	DH	272	ILE
5	DH	280	LEU
5	DH	284	LEU
5	DH	285	GLU
5	DH	287	VAL
5	DH	292	SER
5	DH	297	VAL
5	DH	313	VAL
5	DH	342	SER
5	DH	344	VAL
5	DH	353	VAL
5	DH	354	MET
6	DK	41	LEU
6	DK	45	VAL
6	DK	83	LEU
6	DK	91	LEU
6	DK	111	LYS
6	DK	125	SER
6	DK	126	VAL
6	DK	142	GLU
6	DK	144	LEU
6	DK	149	VAL
6	DK	153	ILE
6	DK	156	THR
6	DK	162	ASP

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Mol	Chain	Res	Type
6	DK	180	VAL
6	DK	183	THR
7	DL	57	VAL
7	DL	93	LEU
7	DL	100	ASP
7	DL	109	LEU
7	DL	121	ASP
7	DL	125	LEU
7	DL	127	ILE
7	DL	133	PHE
7	DL	143	ILE
7	DL	154	LEU
7	DL	163	ILE
7	DL	165	VAL
7	DL	169	THR
7	DL	174	SER
7	DL	175	ARG
7	DL	182	SER
7	DL	193	LEU
7	DL	201	LYS
7	DL	204	LYS
7	DL	210	ASP
7	DL	212	ASN
7	DL	216	ASP
7	DL	229	ILE
8	DM	127	ASN
8	DM	129	LEU
8	DM	131	THR
8	DM	134	LEU
8	DM	146	LEU
8	DM	149	ASN
8	DM	152	LEU
8	DM	155	LEU
8	DM	177	LEU
8	DM	180	ASP
8	DM	183	VAL
8	DM	184	LEU
8	DM	185	ILE
8	DM	189	VAL
8	DM	192	ARG
8	DM	204	LEU
8	DM	207	ILE

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Mol	Chain	Res	Type
8	DM	212	LEU
8	DM	221	LYS
8	DM	259	SER
8	DM	260	VAL
8	DM	263	ILE
8	DM	277	SER
8	DM	284	LEU
8	DM	292	MET
8	DM	306	GLN
8	DM	308	ASP
9	DN	51	CYS
9	DN	58	LEU
9	DN	59	VAL
9	DN	62	ASN
9	DN	66	SER
9	DN	75	VAL
9	DN	91	VAL
9	DN	101	VAL
9	DN	102	VAL
9	DN	108	VAL
9	DN	116	LYS
4	ED	34	SER
4	ED	47	SER
4	ED	50	ASP
4	ED	53	LEU
4	ED	60	LYS
4	ED	85	VAL
4	ED	115	VAL
4	ED	117	VAL
4	ED	123	THR
4	ED	126	GLU
4	ED	127	SER
4	ED	132	LEU
4	ED	156	LEU
4	ED	161	ILE
3	EF	207	ARG
3	EF	208	ILE
3	EF	215	VAL
3	EF	223	ILE
3	EF	231	THR
3	EF	238	ILE
3	EF	256	THR

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Mol	Chain	Res	Type
1	Eg	808	LEU
1	Eg	811	ASP
1	Eg	815	VAL
1	Eg	819	VAL
5	EH	105	GLU
5	EH	107	ILE
5	EH	108	ASP
5	EH	119	LEU
5	EH	147	THR
5	EH	160	LEU
5	EH	173	GLN
5	EH	176	VAL
5	EH	180	VAL
5	EH	182	LEU
5	EH	218	THR
5	EH	225	ASN
5	EH	226	LEU
5	EH	233	LEU
5	EH	237	VAL
5	EH	238	MET
5	EH	240	THR
5	EH	248	VAL
5	EH	249	ASP
5	EH	250	TYR
5	EH	253	ASP
5	EH	254	LEU
5	EH	266	MET
5	EH	269	GLU
5	EH	278	ASP
5	EH	279	LEU
5	EH	280	LEU
5	EH	287	VAL
5	EH	292	SER
5	EH	314	ARG
5	EH	315	THR
5	EH	325	LEU
5	EH	329	THR
5	EH	334	THR
5	EH	344	VAL
5	EH	346	LEU
5	EH	347	VAL
5	EH	348	SER

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Mol	Chain	Res	Type
5	EH	353	VAL
5	EH	356	LEU
6	EK	50	ASP
6	EK	63	LYS
6	EK	65	ILE
6	EK	70	VAL
6	EK	75	LEU
6	EK	78	ILE
6	EK	83	LEU
6	EK	91	LEU
6	EK	92	ASN
6	EK	95	SER
6	EK	98	LEU
6	EK	111	LYS
6	EK	112	ILE
6	EK	115	THR
6	EK	117	THR
6	EK	125	SER
6	EK	126	VAL
6	EK	142	GLU
6	EK	144	LEU
6	EK	145	TRP
6	EK	149	VAL
6	EK	152	ARG
6	EK	156	THR
6	EK	162	ASP
7	EL	57	VAL
7	EL	91	VAL
7	EL	93	LEU
7	EL	101	SER
7	EL	109	LEU
7	EL	124	THR
7	EL	125	LEU
7	EL	127	ILE
7	EL	140	LEU
7	EL	172	VAL
7	EL	193	LEU
7	EL	212	ASN
8	EM	127	ASN
8	EM	129	LEU
8	EM	131	THR
8	EM	132	SER

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Mol	Chain	Res	Type
8	EM	134	LEU
8	EM	136	LEU
8	EM	146	LEU
8	EM	149	ASN
8	EM	152	LEU
8	EM	154	LYS
8	EM	155	LEU
8	EM	173	LEU
8	EM	175	ILE
8	EM	177	LEU
8	EM	182	LYS
8	EM	183	VAL
8	EM	194	LEU
8	EM	202	LEU
8	EM	215	ARG
8	EM	222	ILE
8	EM	235	LEU
8	EM	253	VAL
8	EM	259	SER
8	EM	262	GLU
8	EM	263	ILE
8	EM	266	VAL
8	EM	269	GLN
8	EM	271	SER
8	EM	290	ASP
8	EM	292	MET
8	EM	298	VAL
8	EM	299	LEU
8	EM	303	GLU
8	EM	309	LEU
9	EN	48	ILE
9	EN	59	VAL
9	EN	62	ASN
9	EN	65	TYR
9	EN	73	HIS
9	EN	75	VAL
9	EN	81	LEU
9	EN	95	LEU
9	EN	101	VAL
9	EN	102	VAL
9	EN	110	GLU
9	EN	114	LEU

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Mol	Chain	Res	Type
4	Ed	36	ASP
4	Ed	38	THR
4	Ed	50	ASP
4	Ed	52	MET
4	Ed	58	VAL
4	Ed	61	VAL
4	Ed	63	THR
4	Ed	70	THR
4	Ed	91	ILE
4	Ed	92	GLU
4	Ed	109	LEU
4	Ed	115	VAL
4	Ed	119	ILE
4	Ed	126	GLU
4	Ed	127	SER
4	Ed	150	ASN
4	Ed	153	VAL
3	Ef	209	ILE
3	Ef	216	ILE
3	Ef	222	LEU
3	Ef	223	ILE
3	Ef	232	VAL
3	Ef	233	ARG
3	Ef	244	VAL
3	Ef	247	ILE
3	Ef	265	SER
4	FD	30	ILE
4	FD	34	SER
4	FD	35	ASP
4	FD	41	LEU
4	FD	47	SER
4	FD	51	SER
4	FD	55	MET
4	FD	63	THR
4	FD	69	ASN
4	FD	86	ASP
4	FD	91	ILE
4	FD	108	VAL
4	FD	109	LEU
4	FD	118	LEU
4	FD	123	THR
4	FD	132	LEU

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Mol	Chain	Res	Type
4	FD	137	TYR
4	FD	154	VAL
4	FD	155	GLU
4	FD	156	LEU
3	FF	208	ILE
3	FF	215	VAL
3	FF	222	LEU
3	FF	223	ILE
3	FF	230	LEU
3	FF	238	ILE
3	FF	250	LEU
3	FF	258	SER
1	Fg	808	LEU
1	Fg	815	VAL
1	Fg	817	THR
1	Fg	819	VAL
5	FH	105	GLU
5	FH	108	ASP
5	FH	119	LEU
5	FH	125	GLU
5	FH	129	LYS
5	FH	130	LEU
5	FH	134	TYR
5	FH	137	SER
5	FH	147	THR
5	FH	159	ASN
5	FH	168	VAL
5	FH	180	VAL
5	FH	196	LEU
5	FH	203	ASN
5	FH	220	LEU
5	FH	226	LEU
5	FH	237	VAL
5	FH	239	LEU
5	FH	248	VAL
5	FH	250	TYR
5	FH	262	ASN
5	FH	269	GLU
5	FH	272	ILE
5	FH	278	ASP
5	FH	284	LEU
5	FH	285	GLU

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Mol	Chain	Res	Type
5	FH	313	VAL
5	FH	320	LEU
5	FH	328	MET
5	FH	329	THR
5	FH	338	GLU
5	FH	342	SER
5	FH	348	SER
6	FK	45	VAL
6	FK	58	THR
6	FK	60	LEU
6	FK	65	ILE
6	FK	67	VAL
6	FK	70	VAL
6	FK	76	ILE
6	FK	83	LEU
6	FK	92	ASN
6	FK	99	LEU
6	FK	106	LEU
6	FK	107	LYS
6	FK	108	GLN
6	FK	111	LYS
6	FK	112	ILE
6	FK	125	SER
6	FK	126	VAL
6	FK	127	LYS
6	FK	144	LEU
6	FK	149	VAL
6	FK	152	ARG
6	FK	156	THR
6	FK	162	ASP
6	FK	166	THR
6	FK	180	VAL
1	HG	865	THR
1	HG	867	ASP
1	HG	869	MET
1	HG	875	THR
1	HG	877	VAL
1	HG	885	ILE
1	HG	898	LYS
1	HG	900	ILE
1	HG	913	VAL
1	HG	920	SER

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Mol	Chain	Res	Type
1	HG	930	ILE
1	HG	939	THR
1	HG	944	LEU
1	HG	962	SER
1	HG	965	LEU
1	HG	1020	GLN
1	HG	1027	THR
1	HG	1031	VAL
1	HG	1037	LEU
1	HG	1041	PHE
1	HG	1045	VAL
1	IG	867	ASP
1	IG	875	THR
1	IG	877	VAL
1	IG	885	ILE
1	IG	886	LEU
1	IG	898	LYS
1	IG	900	ILE
1	IG	916	PHE
1	IG	920	SER
1	IG	930	ILE
1	IG	944	LEU
1	IG	962	SER
1	IG	963	SER
1	IG	965	LEU
1	IG	972	PHE
1	IG	1027	THR
1	JG	864	LYS
1	JG	869	MET
1	JG	885	ILE
1	JG	886	LEU
1	JG	898	LYS
1	JG	900	ILE
1	JG	913	VAL
1	JG	916	PHE
1	JG	930	ILE
1	JG	944	LEU
1	JG	949	ASN
1	JG	962	SER
1	JG	965	LEU
1	JG	972	PHE
1	JG	999	SER

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Mol	Chain	Res	Type
1	JG	1020	GLN
1	JG	1024	ASN
1	JG	1027	THR
1	JG	1028	THR
1	JG	1040	LEU
1	KG	865	THR
1	KG	867	ASP
1	KG	869	MET
1	KG	877	VAL
1	KG	885	ILE
1	KG	886	LEU
1	KG	895	LYS
1	KG	898	LYS
1	KG	910	ASP
1	KG	913	VAL
1	KG	916	PHE
1	KG	925	GLU
1	KG	930	ILE
1	KG	935	ILE
1	KG	944	LEU
1	KG	962	SER
1	KG	963	SER
1	KG	965	LEU
1	KG	972	PHE
1	KG	1027	THR
1	KG	1030	GLU
1	KG	1031	VAL
1	KG	1037	LEU
1	LG	865	THR
1	LG	885	ILE
1	LG	898	LYS
1	LG	910	ASP
1	LG	913	VAL
1	LG	920	SER
1	LG	930	ILE
1	LG	935	ILE
1	LG	939	THR
1	LG	944	LEU
1	LG	947	ARG
1	LG	949	ASN
1	LG	965	LEU
1	LG	972	PHE

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Mol	Chain	Res	Type
1	LG	1020	GLN
1	LG	1032	TYR
1	LG	1040	LEU
1	LG	1045	VAL
1	MG	864	LYS
1	MG	867	ASP
1	MG	869	MET
1	MG	874	ASP
1	MG	875	THR
1	MG	886	LEU
1	MG	891	THR
1	MG	898	LYS
1	MG	911	LYS
1	MG	913	VAL
1	MG	915	THR
1	MG	916	PHE
1	MG	925	GLU
1	MG	926	LYS
1	MG	930	ILE
1	MG	933	TYR
1	MG	939	THR
1	MG	944	LEU
1	MG	948	THR
1	MG	963	SER
1	MG	965	LEU
1	MG	972	PHE
1	MG	1027	THR
1	MG	1028	THR
1	MG	1031	VAL
1	MG	1044	ASP
1	MG	1045	VAL
1	NG	864	LYS
1	NG	865	THR
1	NG	869	MET
1	NG	876	SER
1	NG	886	LEU
1	NG	889	ILE
1	NG	891	THR
1	NG	893	LYS
1	NG	904	ASN
1	NG	910	ASP
1	NG	911	LYS

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Mol	Chain	Res	Type
1	NG	912	MET
1	NG	913	VAL
1	NG	916	PHE
1	NG	925	GLU
1	NG	930	ILE
1	NG	935	ILE
1	NG	939	THR
1	NG	944	LEU
1	NG	962	SER
1	NG	963	SER
1	NG	965	LEU
1	NG	1010	THR
1	NG	1041	PHE
1	NG	1044	ASP
1	OG	864	LYS
1	OG	873	LEU
1	OG	875	THR
1	OG	886	LEU
1	OG	891	THR
1	OG	895	LYS
1	OG	898	LYS
1	OG	911	LYS
1	OG	913	VAL
1	OG	915	THR
1	OG	916	PHE
1	OG	928	ILE
1	OG	930	ILE
1	OG	944	LEU
1	OG	962	SER
1	OG	963	SER
1	OG	965	LEU
1	OG	972	PHE
1	OG	1001	LEU
1	OG	1017	GLN
1	OG	1028	THR
1	OG	1031	VAL
1	OG	1040	LEU
1	PG	865	THR
1	PG	885	ILE
1	PG	886	LEU
1	PG	889	ILE
1	PG	898	LYS

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Mol	Chain	Res	Type
1	PG	910	ASP
1	PG	911	LYS
1	PG	913	VAL
1	PG	916	PHE
1	PG	930	ILE
1	PG	939	THR
1	PG	944	LEU
1	PG	962	SER
1	PG	963	SER
1	PG	965	LEU
1	PG	972	PHE
1	PG	1028	THR
1	PG	1031	VAL
1	PG	1045	VAL
2	HC	29	THR
2	HC	36	GLN
2	HC	51	LYS
2	HC	57	GLU
2	HC	84	LEU
2	HC	111	LEU
2	HC	143	THR
2	HC	144	THR
2	HC	152	LEU
2	HC	167	LEU
2	HC	169	LYS
2	HC	170	THR
2	HC	171	LYS
2	HC	206	ASP
2	HC	211	ILE
2	HC	215	LYS
2	HC	222	VAL
2	HC	227	VAL
2	HC	231	ASP
2	HC	235	THR
2	HC	244	ASP
2	HC	255	GLU
2	HC	256	LEU
7	FL	51	GLN
7	FL	57	VAL
7	FL	58	LYS
7	FL	93	LEU
7	FL	109	LEU

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Mol	Chain	Res	Type
7	FL	125	LEU
7	FL	133	PHE
7	FL	140	LEU
7	FL	155	LEU
7	FL	163	ILE
7	FL	172	VAL
7	FL	174	SER
7	FL	177	HIS
7	FL	181	LEU
7	FL	193	LEU
7	FL	203	LEU
7	FL	204	LYS
7	FL	212	ASN
7	FL	217	ASN
7	FL	220	ILE
7	FL	225	GLN
7	FL	230	GLU
8	FM	114	ASN
8	FM	127	ASN
8	FM	129	LEU
8	FM	141	GLU
8	FM	146	LEU
8	FM	149	ASN
8	FM	152	LEU
8	FM	160	ASN
8	FM	162	VAL
8	FM	170	SER
8	FM	176	VAL
8	FM	177	LEU
8	FM	183	VAL
8	FM	184	LEU
8	FM	192	ARG
8	FM	205	TYR
8	FM	207	ILE
8	FM	212	LEU
8	FM	214	ILE
8	FM	215	ARG
8	FM	221	LYS
8	FM	231	LEU
8	FM	259	SER
8	FM	266	VAL
8	FM	271	SER

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Mol	Chain	Res	Type
8	FM	283	ASN
8	FM	292	MET
8	FM	303	GLU
8	FM	316	ASN
9	FN	48	ILE
9	FN	65	TYR
9	FN	66	SER
9	FN	71	THR
9	FN	81	LEU
9	FN	86	LEU
9	FN	91	VAL
9	FN	94	GLN
9	FN	101	VAL
9	FN	112	CYS
9	FN	114	LEU
9	FN	115	GLN
9	FN	116	LYS
2	LC	29	THR
2	LC	36	GLN
2	LC	56	ARG
2	LC	65	LEU
2	LC	80	ILE
2	LC	84	LEU
2	LC	100	LEU
2	LC	101	VAL
2	LC	104	HIS
2	LC	111	LEU
2	LC	128	ILE
2	LC	141	PHE
2	LC	147	THR
2	LC	152	LEU
2	LC	167	LEU
2	LC	171	LYS
2	LC	181	THR
2	LC	215	LYS
2	LC	227	VAL
2	LC	244	ASP
2	LC	255	GLU
2	LC	256	LEU
4	Fd	30	ILE
4	Fd	41	LEU
4	Fd	43	GLU

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Mol	Chain	Res	Type
4	Fd	54	GLU
4	Fd	61	VAL
4	Fd	62	ILE
4	Fd	63	THR
4	Fd	85	VAL
4	Fd	93	GLU
4	Fd	115	VAL
4	Fd	118	LEU
4	Fd	119	ILE
4	Fd	123	THR
4	Fd	126	GLU
4	Fd	134	ASP
4	Fd	145	ILE
3	Ff	208	ILE
3	Ff	213	GLN
3	Ff	216	ILE
3	Ff	232	VAL
3	Ff	244	VAL
3	Ff	245	LYS
3	Ff	249	SER
3	Ff	250	LEU
3	Ff	261	VAL
2	AC	79	ASP
2	AC	96	ASN
2	AC	98	LEU
2	AC	101	GLU
2	AC	103	ASN
2	AC	104	ILE
2	AC	108	VAL
2	AC	110	LEU
2	AC	111	GLU
2	AC	115	THR
2	AC	118	LEU
2	AC	124	ILE
2	AC	126	ILE
2	AC	139	PHE
2	AC	142	THR
2	AC	145	THR
2	AC	147	ARG
2	AC	153	ASP
2	AC	162	VAL
2	AC	165	LEU

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Mol	Chain	Res	Type
2	AC	181	ARG
2	AC	203	GLU
2	AC	213	LYS
2	AC	215	LEU
2	AC	220	VAL
2	AC	227	HIS
2	AC	242	ASP
2	AC	265	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (257) such sidechains are listed below:

Mol	Chain	Res	Type
2	BC	117	ASN
2	EC	86	GLN
2	EC	103	HIS
2	EC	104	ASN
4	GD	80	GLN
1	Gg	814	GLN
1	Gg	818	GLN
5	GH	118	ASN
5	GH	205	GLN
5	GH	308	ASN
6	GK	73	ASN
7	GL	112	GLN
9	GN	61	ASN
9	GN	79	GLN
9	GN	94	GLN
9	GN	104	ASN
4	Gd	32	ASN
3	Gf	266	GLN
4	HD	80	GLN
4	HD	152	GLN
5	HH	234	ASN
5	HH	340	GLN
7	HL	217	ASN
8	HM	166	ASN
9	HN	61	ASN
1	BG	938	ASN
1	BG	1003	ASN
1	BG	1018	GLN
4	Hd	138	GLN
4	Hd	152	GLN

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Mol	Chain	Res	Type
1	Bg	796	GLN
1	Bg	807	GLN
1	Ig	807	GLN
1	Ig	818	GLN
5	IH	159	ASN
5	IH	203	ASN
5	IH	262	ASN
7	IL	112	GLN
7	IL	150	ASN
7	IL	217	ASN
8	IM	174	GLN
8	IM	268	HIS
8	IM	295	ASN
9	IN	73	HIS
9	IN	104	ASN
4	Dd	80	GLN
4	Id	31	ASN
4	JD	78	ASN
4	JD	80	GLN
3	JF	251	GLN
1	Jg	807	GLN
1	Jg	810	GLN
5	JH	156	GLN
5	JH	234	ASN
5	JH	308	ASN
7	JL	150	ASN
1	CG	938	ASN
1	CG	966	GLN
4	Jd	32	ASN
4	Jd	78	ASN
4	Jd	103	HIS
3	Jf	266	GLN
5	AH	234	ASN
4	KD	80	GLN
2	CC	84	ASN
2	CC	89	ASN
2	CC	97	ASN
3	KF	266	GLN
1	Kg	807	GLN
1	Kg	818	GLN
5	KH	205	GLN
5	KH	222	ASN

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Mol	Chain	Res	Type
6	KK	100	ASN
7	KL	217	ASN
8	KM	269	GLN
8	KM	295	ASN
8	KM	316	ASN
9	KN	61	ASN
4	LD	80	GLN
4	LD	152	GLN
3	LF	260	GLN
3	LF	266	GLN
1	Lg	807	GLN
5	LH	205	GLN
5	LH	222	ASN
5	LH	355	GLN
6	LK	147	GLN
7	LL	51	GLN
8	LM	295	ASN
9	LN	94	GLN
1	DG	904	ASN
4	Ld	152	GLN
4	MD	78	ASN
1	Cg	818	GLN
1	Mg	807	GLN
1	Ag	807	GLN
1	Ag	810	GLN
5	MH	118	ASN
5	MH	156	GLN
5	MH	222	ASN
6	MK	100	ASN
7	ML	44	HIS
7	ML	49	ASN
7	ML	217	ASN
7	ML	226	ASN
8	MM	140	ASN
8	MM	174	GLN
8	MM	318	GLN
9	MN	79	GLN
4	Md	32	ASN
4	Md	75	ASN
3	Mf	213	GLN
1	VG	807	GLN
1	VG	810	GLN

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Mol	Chain	Res	Type
1	VG	814	GLN
5	VH	118	ASN
5	VH	126	GLN
5	VH	132	GLN
5	VH	205	GLN
5	VH	222	ASN
5	VH	245	GLN
5	VH	257	GLN
3	WF	266	GLN
1	WG	796	GLN
1	WG	818	GLN
5	WH	118	ASN
5	WH	123	ASN
5	WH	340	GLN
4	CD	32	ASN
4	CD	78	ASN
4	CD	80	GLN
1	EG	878	ASN
1	XG	814	GLN
5	XH	118	ASN
1	YG	792	GLN
1	YG	807	GLN
5	YH	123	ASN
5	YH	132	GLN
5	YH	159	ASN
5	YH	355	GLN
3	Df	251	GLN
2	DC	50	GLN
2	DC	70	GLN
2	DC	83	GLN
2	DC	87	GLN
2	DC	105	ASN
2	DC	191	GLN
1	ZG	807	GLN
5	ZH	234	ASN
9	AN	96	ASN
4	Ad	103	HIS
4	Ad	152	GLN
5	BH	118	ASN
5	BH	308	ASN
6	BK	73	ASN
1	FG	878	ASN

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Mol	Chain	Res	Type
1	FG	908	ASN
7	BL	51	GLN
7	BL	110	GLN
8	BM	318	GLN
9	BN	79	GLN
9	BN	94	GLN
9	BN	115	GLN
4	AD	32	ASN
4	AD	80	GLN
2	FC	83	ASN
2	FC	85	GLN
2	FC	185	ASN
2	GC	118	ASN
2	GC	123	GLN
2	GC	162	ASN
2	GC	198	ASN
2	JC	85	GLN
2	JC	103	ASN
2	JC	148	GLN
2	JC	189	GLN
2	JC	218	ASN
2	KC	86	GLN
2	KC	123	GLN
2	MC	163	ASN
5	CH	205	GLN
5	CH	225	ASN
5	CH	340	GLN
6	CK	108	GLN
7	CL	115	GLN
9	CN	79	GLN
4	Cd	75	ASN
3	Cf	266	GLN
4	DD	75	ASN
4	DD	78	ASN
4	DD	80	GLN
1	GG	908	ASN
5	DH	118	ASN
5	DH	132	GLN
6	DK	61	ASN
6	DK	87	GLN
7	DL	49	ASN
7	DL	110	GLN

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Mol	Chain	Res	Type
7	DL	112	GLN
8	DM	190	ASN
8	DM	295	ASN
9	DN	79	GLN
9	DN	96	ASN
9	DN	104	ASN
4	ED	78	ASN
4	ED	138	GLN
3	EF	251	GLN
1	Eg	807	GLN
1	Eg	814	GLN
5	EH	173	GLN
5	EH	245	GLN
7	EL	49	ASN
7	EL	112	GLN
7	EL	226	ASN
9	EN	61	ASN
9	EN	115	GLN
4	Ed	32	ASN
4	Ed	138	GLN
4	FD	32	ASN
1	Fg	814	GLN
5	FH	156	GLN
5	FH	159	ASN
5	FH	222	ASN
5	FH	245	GLN
5	FH	335	HIS
1	IG	908	ASN
1	IG	938	ASN
1	JG	878	ASN
1	JG	908	ASN
1	JG	938	ASN
1	JG	1003	ASN
1	JG	1020	GLN
1	KG	908	ASN
1	KG	1003	ASN
1	LG	938	ASN
1	MG	976	ASN
1	MG	1003	ASN
1	NG	1003	ASN
1	OG	976	ASN
1	OG	1017	GLN

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Mol	Chain	Res	Type
1	OG	1043	GLN
1	PG	938	ASN
1	PG	1020	GLN
2	HC	36	GLN
2	HC	83	GLN
2	HC	163	ASN
7	FL	51	GLN
7	FL	112	GLN
7	FL	149	ASN
7	FL	217	ASN
2	LC	36	GLN
2	LC	83	GLN
2	LC	163	ASN
2	LC	199	ASN
4	Fd	75	ASN
3	Ff	213	GLN
2	AC	81	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

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

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	JX	38:UNK	C	70:UNK	N	26.33
1	BX	38:UNK	C	70:UNK	N	25.95
1	VX	38:UNK	C	70:UNK	N	25.89
1	KX	38:UNK	C	70:UNK	N	25.61
1	DX	38:UNK	C	70:UNK	N	25.45
1	YX	38:UNK	C	70:UNK	N	25.38
1	XX	38:UNK	C	70:UNK	N	25.33
1	ZX	38:UNK	C	70:UNK	N	25.15
1	LX	38:UNK	C	70:UNK	N	25.12
1	GX	38:UNK	C	70:UNK	N	24.88
1	EX	38:UNK	C	70:UNK	N	24.75
1	MX	38:UNK	C	70:UNK	N	24.71
1	WX	38:UNK	C	70:UNK	N	24.65
1	HX	38:UNK	C	70:UNK	N	23.96
1	CX	38:UNK	C	70:UNK	N	23.84
1	IX	38:UNK	C	70:UNK	N	23.62
1	FX	38:UNK	C	70:UNK	N	23.09
1	AX	38:UNK	C	70:UNK	N	22.49

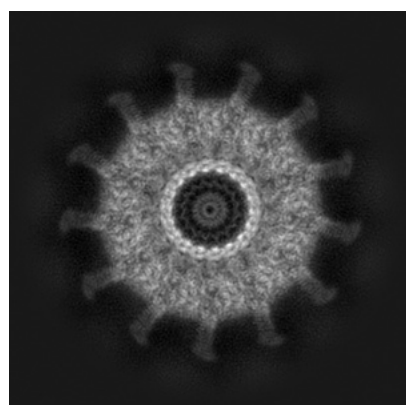
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24018. These allow visual inspection of the internal detail of the map and identification of artifacts.

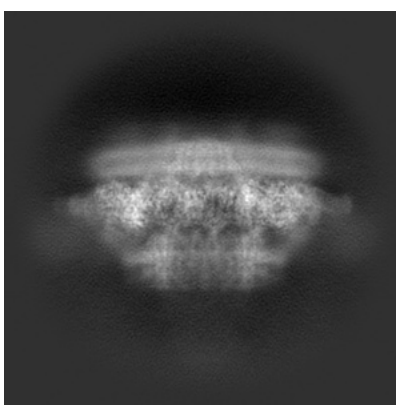
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

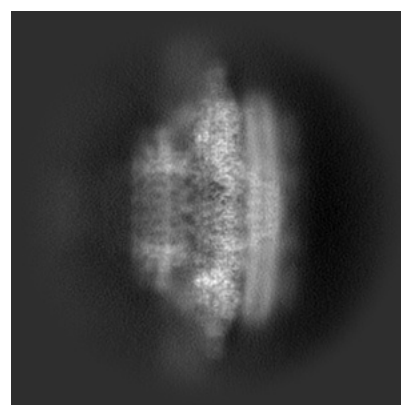
6.1.1 Primary map



X



Y

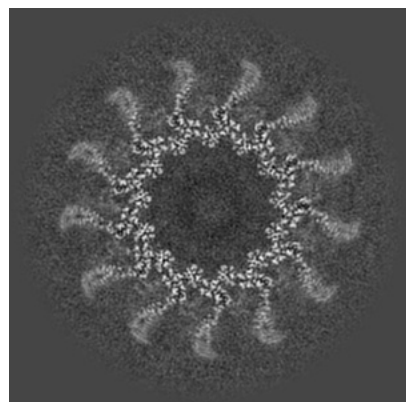


Z

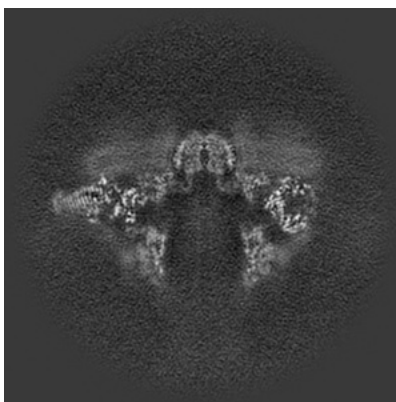
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

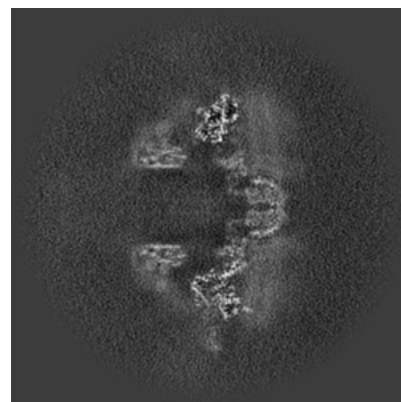
6.2.1 Primary map



X Index: 125



Y Index: 125

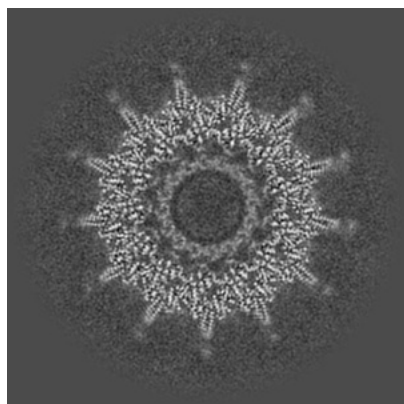


Z Index: 125

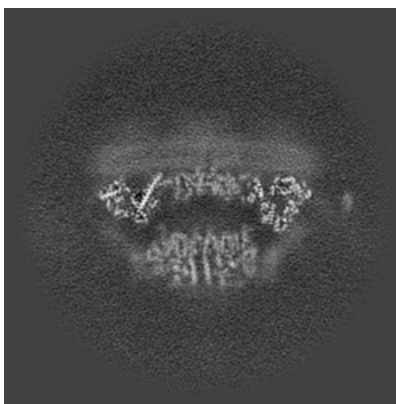
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

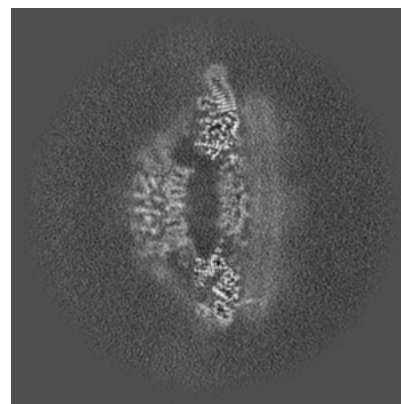
6.3.1 Primary map



X Index: 134



Y Index: 101

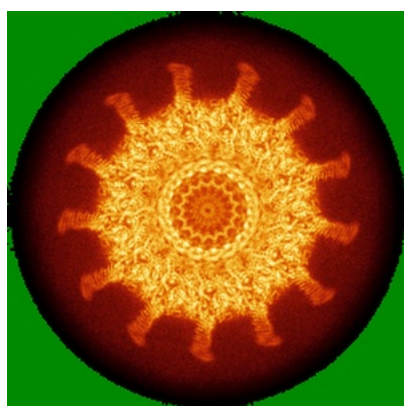


Z Index: 151

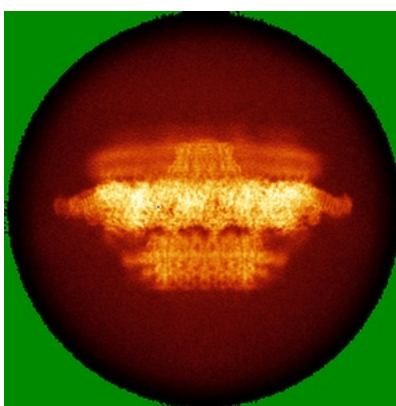
The images above show the largest variance slices of the map in three orthogonal directions.

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

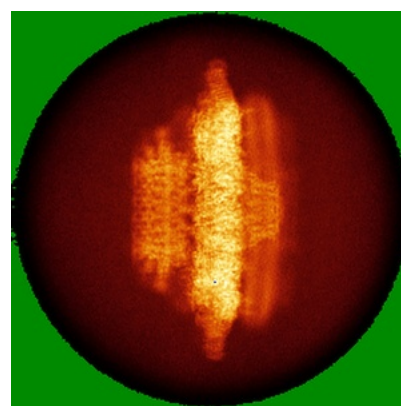
6.4.1 Primary map



X



Y

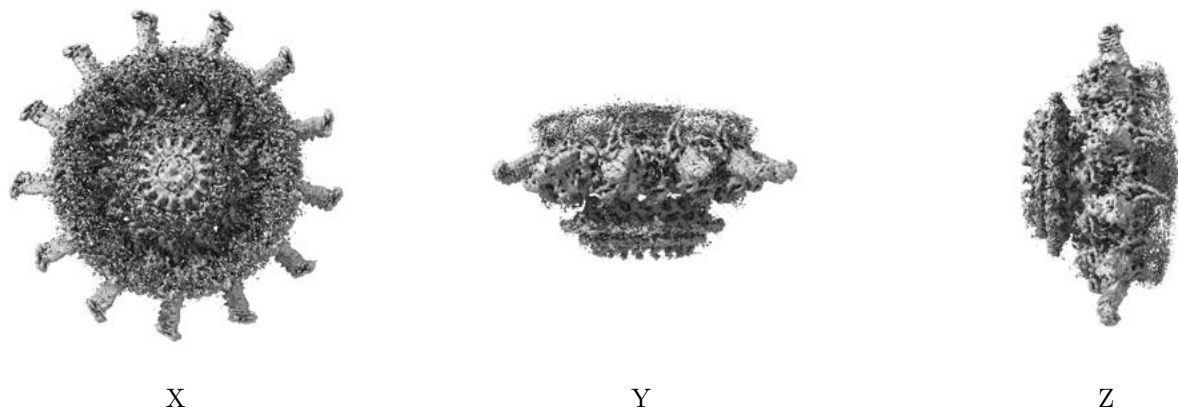


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

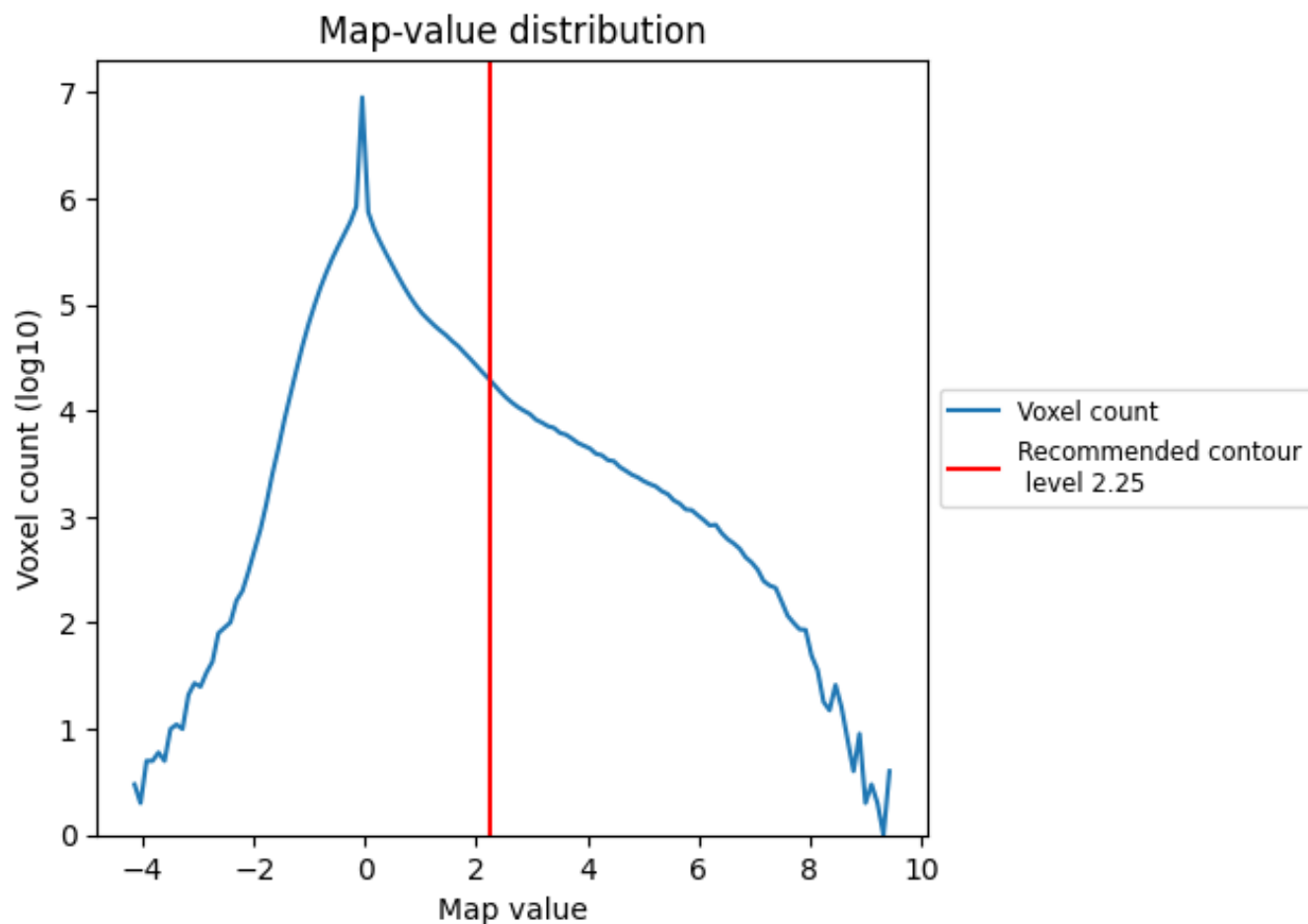
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

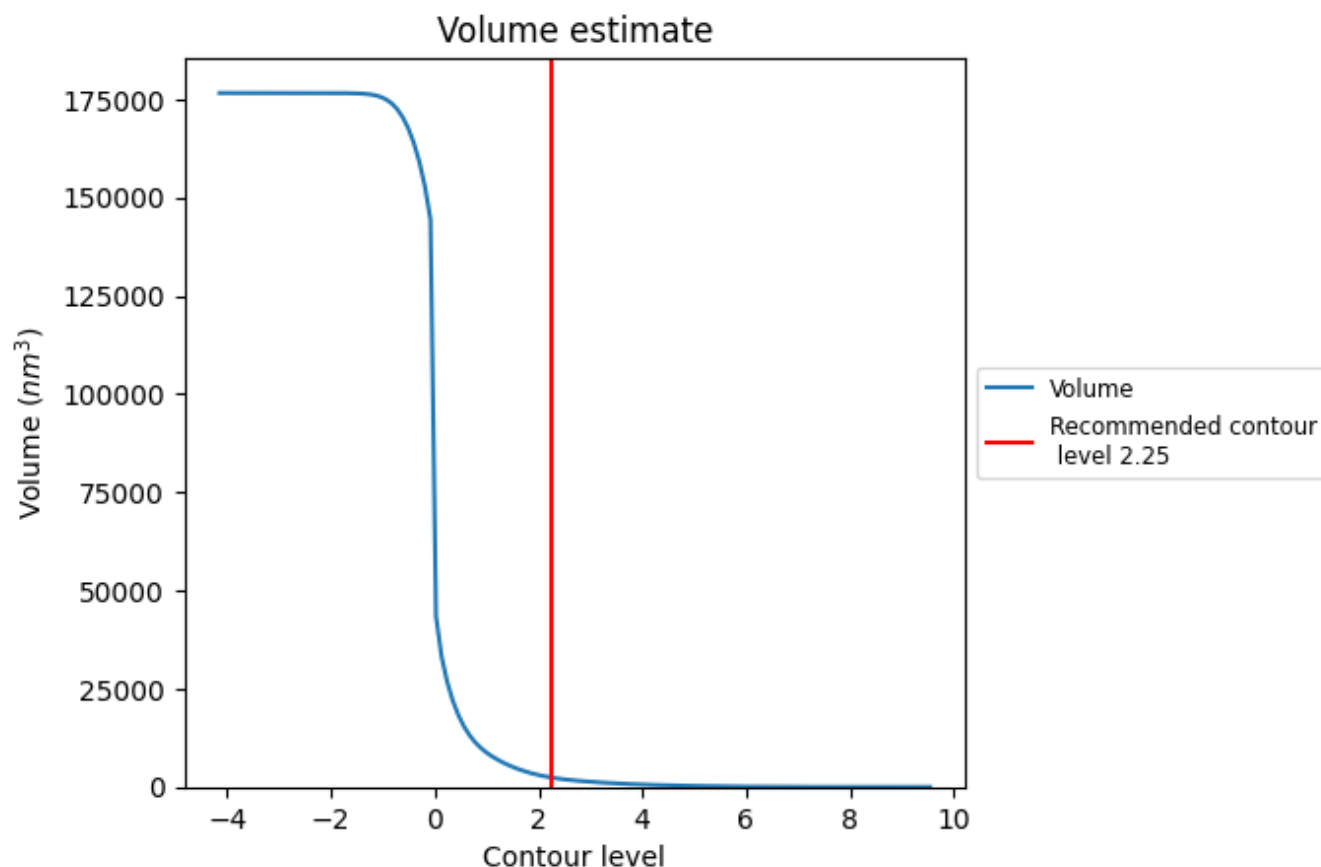
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

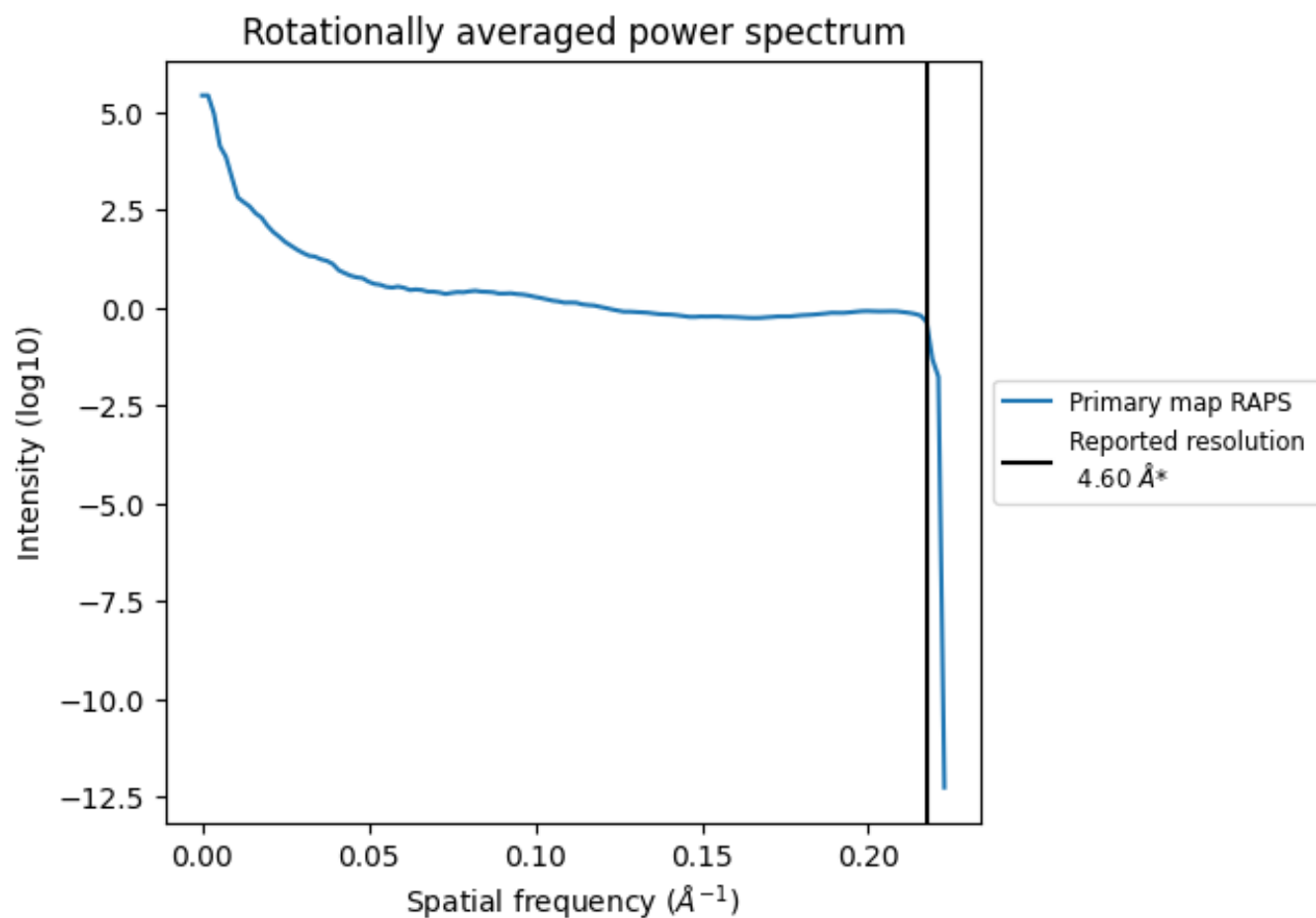
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2389 nm^3 ; this corresponds to an approximate mass of 2158 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



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

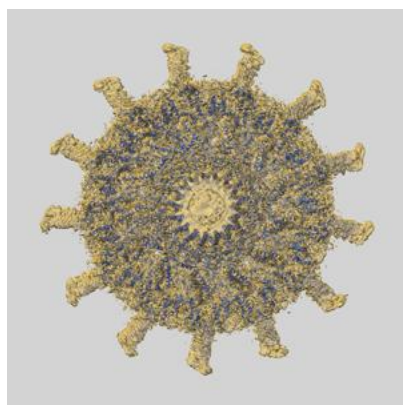
8 Fourier-Shell correlation

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

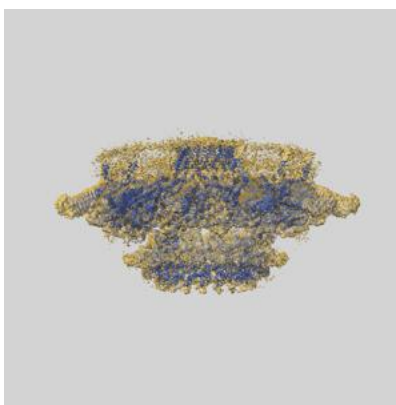
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24018 and PDB model 7MUQ. Per-residue inclusion information can be found in section [3](#) on page [23](#).

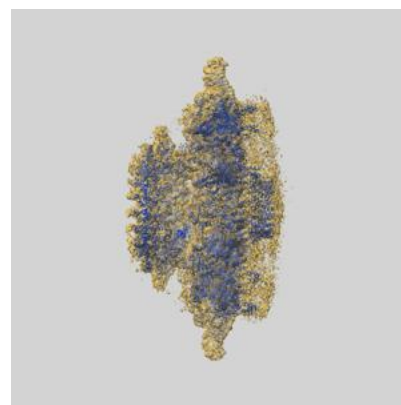
9.1 Map-model overlay [i](#)



X



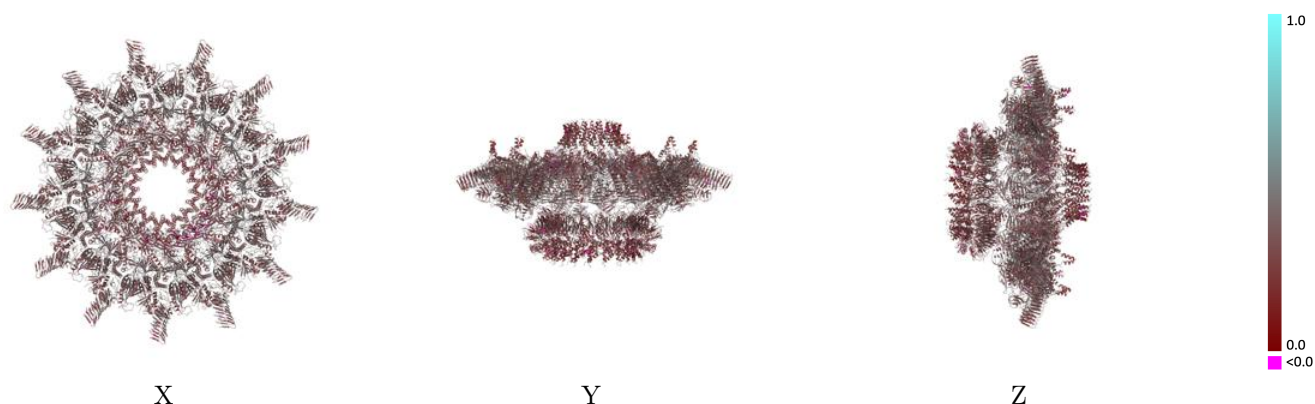
Y



Z

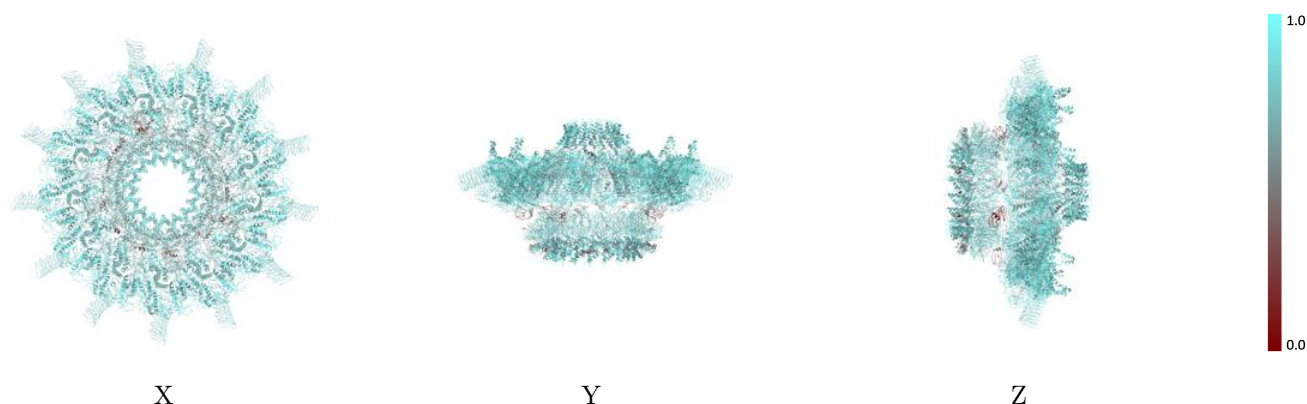
The images above show the 3D surface view of the map at the recommended contour level 2.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



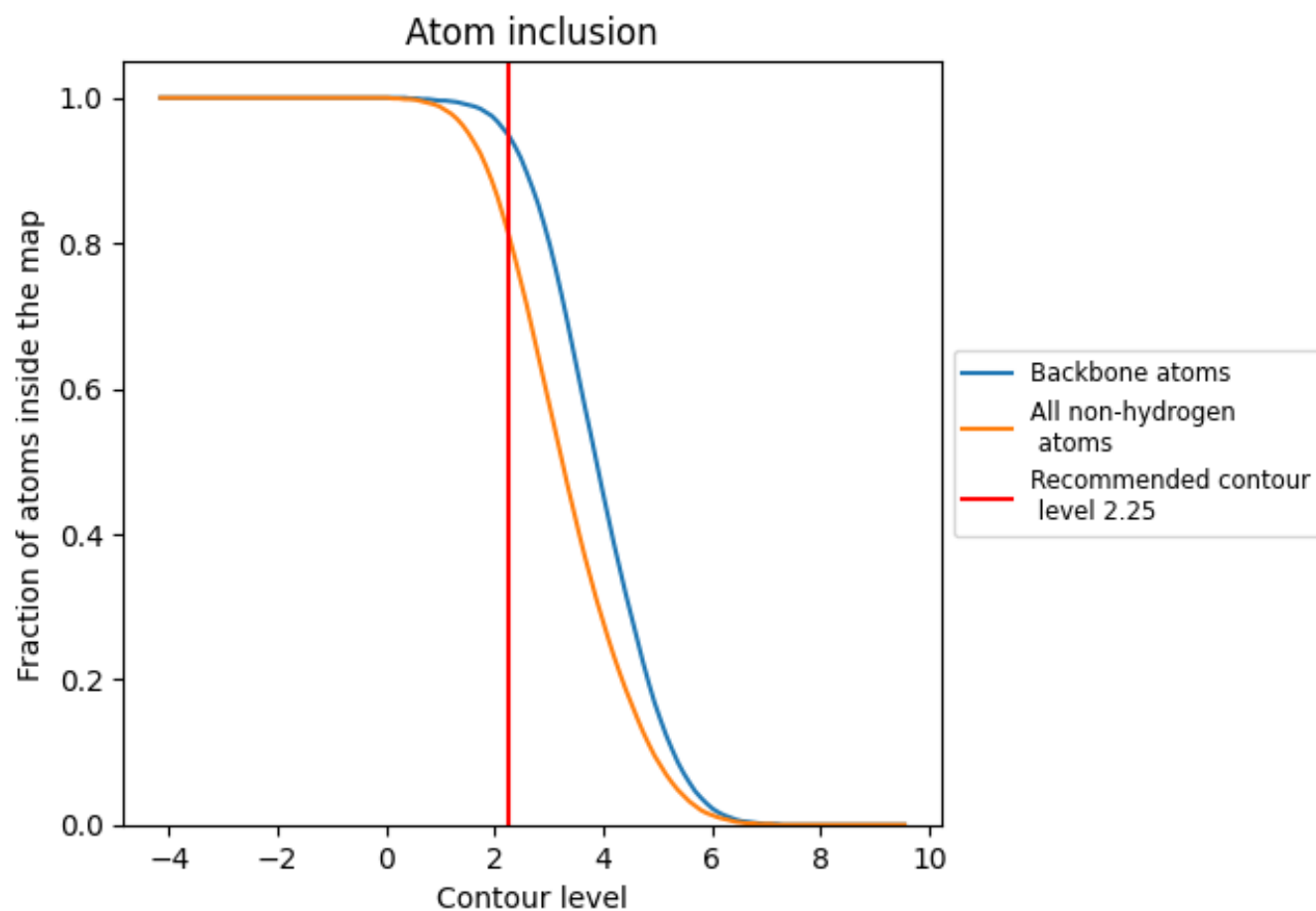
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 82% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (2.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8150	 0.3350
AC	 0.8600	 0.3620
AD	 0.8420	 0.3710
AF	 0.7790	 0.2470
AG	 0.7070	 0.2330
AH	 0.8130	 0.3320
AK	 0.8490	 0.3780
AL	 0.8630	 0.3550
AM	 0.8350	 0.3520
AN	 0.8020	 0.3790
AU	 1.0000	 0.4870
AX	 0.5670	 0.2380
Ad	 0.8570	 0.3580
Af	 0.8040	 0.3300
Ag	 0.8490	 0.3040
BC	 0.8730	 0.3660
BD	 0.8460	 0.3790
BF	 0.7790	 0.2670
BG	 0.6860	 0.2220
BH	 0.8100	 0.3300
BK	 0.8510	 0.3730
BL	 0.8640	 0.3530
BM	 0.8420	 0.3600
BN	 0.8550	 0.3800
BU	 1.0000	 0.5100
BX	 0.5580	 0.2280
Bd	 0.8450	 0.3640
Bf	 0.8410	 0.3260
Bg	 0.8240	 0.3030
CC	 0.8620	 0.3660
CD	 0.8650	 0.3770
CF	 0.7920	 0.2800
CG	 0.6740	 0.2220
CH	 0.8380	 0.3380
CK	 0.8610	 0.3650



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Chain	Atom inclusion	Q-score
CL	 0.8660	 0.3510
CM	 0.8540	 0.3480
CN	 0.8440	 0.3790
CU	 1.0000	 0.4610
CX	 0.7250	 0.3180
Cd	 0.8520	 0.3640
Cf	 0.8200	 0.3220
Cg	 0.8490	 0.2960
DC	 0.8100	 0.3530
DD	 0.8560	 0.3670
DF	 0.7640	 0.2450
DG	 0.7190	 0.2400
DH	 0.8280	 0.3300
DK	 0.8480	 0.3720
DL	 0.8540	 0.3500
DM	 0.8500	 0.3510
DN	 0.8180	 0.3700
DU	 1.0000	 0.4710
DX	 0.6170	 0.2590
Dd	 0.8660	 0.3620
Df	 0.8360	 0.3250
Dg	 0.8270	 0.2810
EC	 0.8380	 0.3520
ED	 0.8440	 0.3740
EF	 0.8130	 0.2610
EG	 0.7070	 0.2470
EH	 0.8310	 0.3220
EK	 0.8510	 0.3730
EL	 0.8470	 0.3520
EM	 0.8470	 0.3520
EN	 0.8110	 0.3730
EU	 1.0000	 0.4780
EX	 0.7210	 0.2470
Ed	 0.8440	 0.3490
Ef	 0.8250	 0.3470
Eg	 0.8050	 0.2740
FC	 0.8620	 0.3580
FD	 0.8440	 0.3680
FF	 0.7660	 0.2560
FG	 0.7180	 0.2540
FH	 0.8420	 0.3240
FK	 0.8580	 0.3710

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Chain	Atom inclusion	Q-score
FL	 0.8600	 0.3500
FM	 0.8550	 0.3540
FN	 0.8550	 0.3970
FU	 1.0000	 0.5090
FX	 0.5960	 0.2440
Fd	 0.8460	 0.3530
Ff	 0.8570	 0.3430
Fg	 0.7980	 0.2630
GC	 0.8550	 0.3660
GD	 0.8480	 0.3710
GF	 0.7960	 0.2650
GG	 0.7270	 0.2700
GH	 0.8210	 0.3260
GK	 0.8700	 0.3790
GL	 0.8750	 0.3560
GM	 0.8420	 0.3520
GN	 0.8530	 0.3860
GU	 0.9780	 0.4780
GX	 0.7330	 0.2880
Gd	 0.8560	 0.3620
Gf	 0.7990	 0.3160
Gg	 0.8570	 0.2720
HC	 0.8190	 0.3550
HD	 0.8400	 0.3820
HF	 0.7500	 0.2500
HG	 0.7410	 0.2810
HH	 0.8390	 0.3350
HK	 0.8570	 0.3750
HL	 0.8760	 0.3540
HM	 0.8520	 0.3550
HN	 0.8360	 0.3850
HU	 0.9780	 0.5230
HX	 0.6370	 0.2570
Hd	 0.8520	 0.3510
Hf	 0.8200	 0.3240
Hg	 0.8750	 0.3090
IC	 0.8060	 0.3470
ID	 0.8360	 0.3690
IF	 0.7600	 0.2630
IG	 0.7360	 0.2920
IH	 0.8210	 0.3290
IK	 0.8550	 0.3760

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Chain	Atom inclusion	Q-score
IL	 0.8550	 0.3550
IM	 0.8490	 0.3540
IN	 0.8110	 0.3860
IU	 1.0000	 0.5190
IX	 0.6790	 0.2750
Id	 0.8540	 0.3610
If	 0.8470	 0.3300
Ig	 0.8380	 0.2770
JC	 0.8470	 0.3620
JD	 0.8380	 0.3750
JF	 0.8020	 0.2510
JG	 0.7540	 0.2950
JH	 0.8260	 0.3320
JK	 0.8540	 0.3750
JL	 0.8610	 0.3600
JM	 0.8590	 0.3540
JN	 0.8250	 0.3750
JU	 0.9780	 0.5050
JX	 0.6250	 0.2110
Jd	 0.8500	 0.3660
Jf	 0.8180	 0.3440
Jg	 0.8380	 0.2980
KC	 0.8540	 0.3650
KD	 0.8420	 0.3680
KF	 0.7880	 0.2610
KG	 0.7540	 0.3050
KH	 0.8320	 0.3340
KK	 0.8690	 0.3770
KL	 0.8640	 0.3520
KM	 0.8320	 0.3570
KN	 0.8580	 0.3910
KU	 0.9780	 0.4860
KX	 0.6620	 0.2820
Kd	 0.8630	 0.3620
Kf	 0.7930	 0.3310
Kg	 0.8380	 0.3100
LC	 0.8150	 0.3410
LD	 0.8500	 0.3630
LF	 0.7920	 0.2840
LG	 0.7540	 0.3100
LH	 0.8150	 0.3330
LK	 0.8600	 0.3690

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Chain	Atom inclusion	Q-score
LL	 0.8750	 0.3590
LM	 0.8280	 0.3450
LN	 0.8370	 0.3890
LU	 1.0000	 0.4790
LX	 0.6370	 0.2470
Ld	 0.8640	 0.3640
Lf	 0.8500	 0.3280
Lg	 0.8460	 0.2740
MC	 0.8210	 0.3530
MD	 0.8460	 0.3630
MF	 0.7370	 0.2480
MG	 0.7350	 0.2550
MH	 0.8040	 0.3280
MK	 0.8590	 0.3770
ML	 0.8640	 0.3650
MM	 0.8430	 0.3620
MN	 0.8230	 0.3820
MU	 1.0000	 0.4830
MX	 0.5670	 0.2530
Md	 0.8520	 0.3590
Mf	 0.8270	 0.3410
Mg	 0.8380	 0.2750
NG	 0.7270	 0.2380
OG	 0.7790	 0.2970
PG	 0.7340	 0.2450
VF	 0.7980	 0.2570
VG	 0.7680	 0.2800
VH	 0.7210	 0.3100
VX	 0.6370	 0.2660
WF	 0.8050	 0.2480
WG	 0.7720	 0.2560
WH	 0.6650	 0.3050
WX	 0.6620	 0.2720
XF	 0.8130	 0.2470
XG	 0.7980	 0.2560
XH	 0.6070	 0.2980
XX	 0.6620	 0.2760
YF	 0.8090	 0.2640
YG	 0.8120	 0.2890
YH	 0.7270	 0.3090
YX	 0.6170	 0.2650
ZF	 0.7450	 0.2580

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Chain	Atom inclusion	Q-score
ZG	 0.7980	 0.2780
ZH	 0.5240	 0.2790
ZX	 0.7460	 0.3150