



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 15, 2026 – 01:44 AM UTC

PDB ID : 5V74 / pdb_00005v74
Title : Structure of the intact Haliangium ochraceum microcompartment shell
Authors : Sutter, M.; Kerfeld, C.A.
Deposited on : 2017-03-17
Resolution : 3.51 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

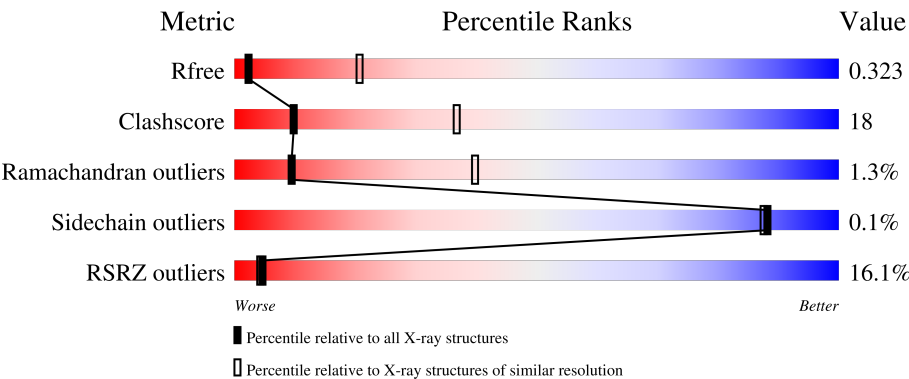
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.51 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.



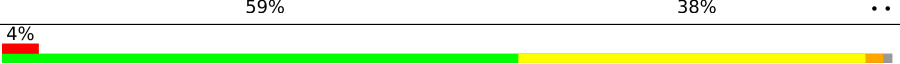
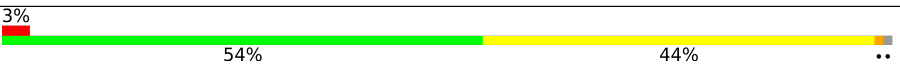
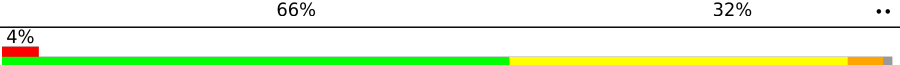
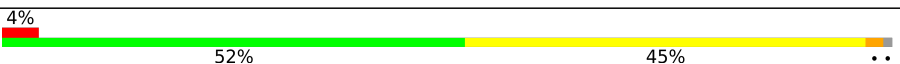
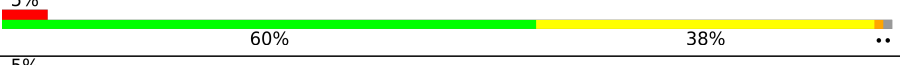
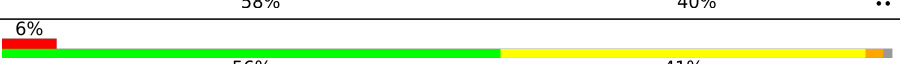
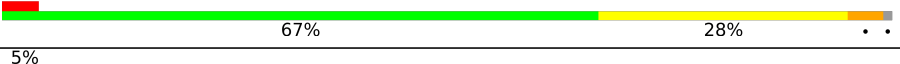
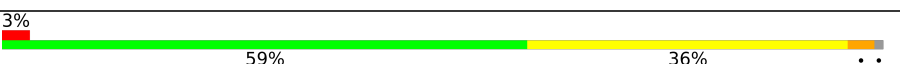
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	1025 (3.56-3.48)
Clashscore	190562	1079 (3.56-3.48)
Ramachandran outliers	187476	1052 (3.56-3.48)
Sidechain outliers	187428	1053 (3.56-3.48)
RSRZ outliers	180081	1024 (3.56-3.48)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	11	96	3% 59% 36% ..
1	21	96	5% 63% 35% ..
1	31	96	4% 48% 46% ..
1	41	96	3% 65% 32% ..
1	A1	96	5% 51% 45% ..

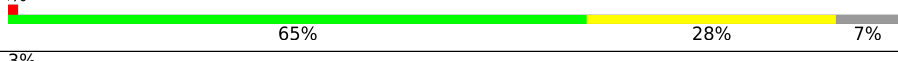
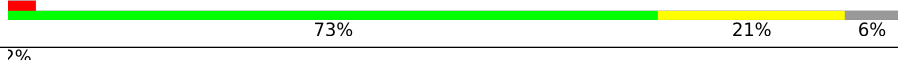
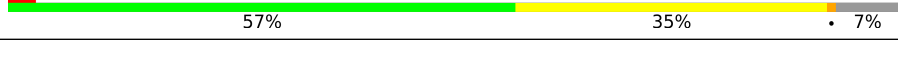
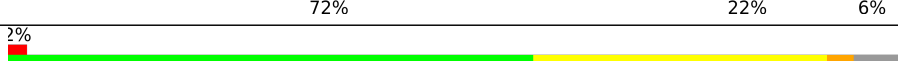
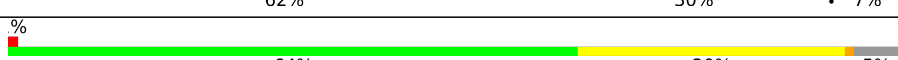
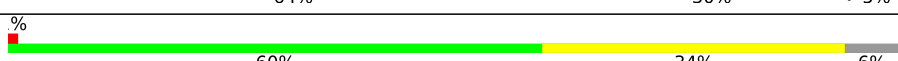
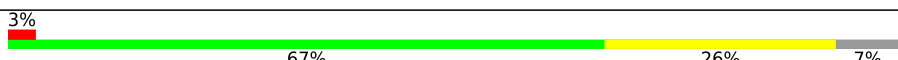
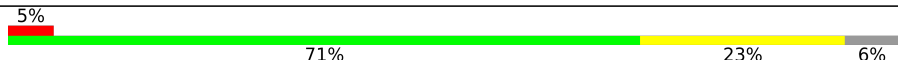
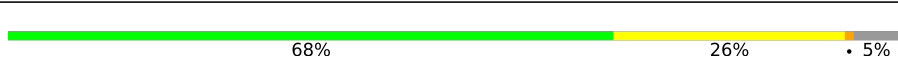
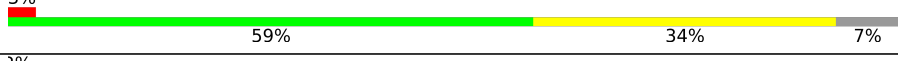
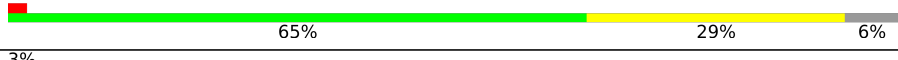
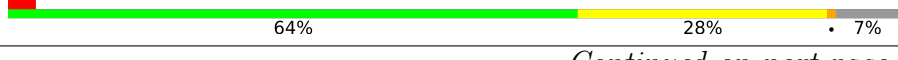
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Mol	Chain	Length	Quality of chain	
1	B1	96	5% 	..
1	C1	96	3% 	..
1	D1	96	5% 	..
1	E1	96	4% 	..
1	F1	96	3% 	..
1	G1	96	5% 	..
1	H1	96	7% 	..
1	I1	96	6% 	..
1	J1	96	4% 	..
1	K1	96	3% 	..
1	L1	96	3% 	..
1	M1	96	3% 	..
1	N1	96	4% 	..
1	O1	96	4% 	..
1	P1	96	5% 	..
1	Q1	96	5% 	..
1	R1	96	3% 	..
1	S1	96	6% 	..
1	T1	96	7% 	..
1	U1	96	4% 	..
1	V1	96	5% 	..
1	W1	96	7% 	..
1	X1	96	3% 	..
1	Y1	96	4% 	..
1	Z1	96	4% 	..

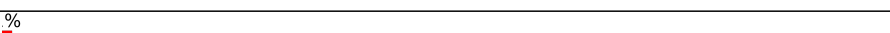
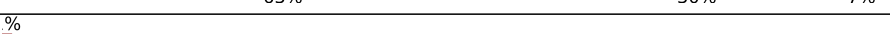
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Mol	Chain	Length	Quality of chain
2	12	99	
2	13	99	
2	14	99	
2	15	99	
2	16	99	
2	17	99	
2	22	99	
2	23	99	
2	24	99	
2	25	99	
2	26	99	
2	27	99	
2	32	99	
2	33	99	
2	34	99	
2	35	99	
2	36	99	
2	37	99	
2	42	99	
2	43	99	
2	44	99	
2	45	99	
2	46	99	
2	47	99	
2	A2	99	

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Mol	Chain	Length	Quality of chain
2	A3	99	
2	A4	99	
2	A5	99	
2	A6	99	
2	A7	99	
2	B2	99	
2	B3	99	
2	B4	99	
2	B5	99	
2	B6	99	
2	B7	99	
2	C2	99	
2	C3	99	
2	C4	99	
2	C5	99	
2	C6	99	
2	C7	99	
2	D2	99	
2	D3	99	
2	D4	99	
2	D5	99	
2	D6	99	
2	D7	99	
2	E2	99	
2	E3	99	

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Mol	Chain	Length	Quality of chain
2	E4	99	
2	E5	99	
2	E6	99	
2	E7	99	
2	F2	99	
2	F3	99	
2	F4	99	
2	F5	99	
2	F6	99	
2	F7	99	
2	G2	99	
2	G3	99	
2	G4	99	
2	G5	99	
2	G6	99	
2	G7	99	
2	H2	99	
2	H3	99	
2	H4	99	
2	H5	99	
2	H6	99	
2	H7	99	
2	I2	99	
2	I3	99	
2	I4	99	

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Mol	Chain	Length	Quality of chain
2	I5	99	
2	I6	99	
2	I7	99	
2	J2	99	
2	J3	99	
2	J4	99	
2	J5	99	
2	J6	99	
2	J7	99	
2	K2	99	
2	K3	99	
2	K4	99	
2	K5	99	
2	K6	99	
2	K7	99	
2	L2	99	
2	L3	99	
2	L4	99	
2	L5	99	
2	L6	99	
2	L7	99	
2	M2	99	
2	M3	99	
2	M4	99	
2	M5	99	

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Mol	Chain	Length	Quality of chain
2	M6	99	
2	M7	99	
2	N2	99	
2	N3	99	
2	N4	99	
2	N5	99	
2	N6	99	
2	N7	99	
2	O2	99	
2	O3	99	
2	O4	99	
2	O5	99	
2	O6	99	
2	O7	99	
2	P2	99	
2	P3	99	
2	P4	99	
2	P5	99	
2	P6	99	
2	P7	99	
2	Q2	99	
2	Q3	99	
2	Q4	99	
2	Q5	99	
2	Q6	99	

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Mol	Chain	Length	Quality of chain
2	Q7	99	
2	R2	99	
2	R3	99	
2	R4	99	
2	R5	99	
2	R6	99	
2	R7	99	
2	S2	99	
2	S3	99	
2	S4	99	
2	S5	99	
2	S6	99	
2	S7	99	
2	T2	99	
2	T3	99	
2	T4	99	
2	T5	99	
2	T6	99	
2	T7	99	
2	U2	99	
2	U3	99	
2	U4	99	
2	U5	99	
2	U6	99	
2	U7	99	

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Mol	Chain	Length	Quality of chain
2	V2	99	
2	V3	99	
2	V4	99	
2	V5	99	
2	V6	99	
2	V7	99	
2	W2	99	
2	W3	99	
2	W4	99	
2	W5	99	
2	W6	99	
2	W7	99	
2	X2	99	
2	X3	99	
2	X4	99	
2	X5	99	
2	X6	99	
2	X7	99	
2	Y2	99	
2	Y3	99	
2	Y4	99	
2	Y5	99	
2	Y6	99	
2	Y7	99	
2	Z2	99	

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Mol	Chain	Length	Quality of chain
2	Z3	99	
2	Z4	99	
2	Z5	99	
2	Z6	99	
2	Z7	99	
3	18	212	
3	19	212	
3	28	212	
3	29	212	
3	38	212	
3	39	212	
3	48	212	
3	49	212	
3	A8	212	
3	A9	212	
3	B8	212	
3	B9	212	
3	C8	212	
3	C9	212	
3	D8	212	
3	D9	212	
3	E8	212	
3	E9	212	
3	F8	212	
3	F9	212	

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Mol	Chain	Length	Quality of chain
3	G8	212	
3	G9	212	
3	H8	212	
3	H9	212	
3	I8	212	
3	I9	212	
3	J8	212	
3	J9	212	
3	K8	212	
3	K9	212	
3	L8	212	
3	L9	212	
3	M8	212	
3	M9	212	
3	N8	212	
3	N9	212	
3	O8	212	
3	O9	212	
3	P8	212	
3	P9	212	
3	Q8	212	
3	Q9	212	
3	R8	212	
3	R9	212	
3	S8	212	

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Mol	Chain	Length	Quality of chain
3	S9	212	48% 87% 9% .
3	T8	212	29% 51% 42% .
3	T9	212	56% 83% 13% .
3	U8	212	26% 46% 49% .
3	U9	212	50% 86% 9% .
3	V8	212	23% 49% 46% .
3	V9	212	46% 91% 5% .
3	W8	212	21% 44% 50% .
3	W9	212	51% 84% 12% .
3	X8	212	24% 50% 45% .
3	X9	212	43% 84% 11% .
3	Y8	212	25% 50% 45% .
3	Y9	212	44% 88% 8% .
3	Z8	212	28% 54% 40% .
3	Z9	212	53% 86% 9% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 215283 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Ethanolamine utilization protein EutN/carboxysome structural protein Ccml.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A1	95	Total	C	N	O	S	0	0	0
			678	419	122	132	5			
1	B1	95	Total	C	N	O	S	0	0	0
			678	419	122	132	5			
1	C1	95	Total	C	N	O	S	0	0	0
			678	419	122	132	5			
1	D1	95	Total	C	N	O	S	0	0	0
			678	419	122	132	5			
1	E1	95	Total	C	N	O	S	0	0	0
			678	419	122	132	5			
1	F1	95	Total	C	N	O	S	0	0	0
			678	419	122	132	5			
1	G1	95	Total	C	N	O	S	0	0	0
			678	419	122	132	5			
1	H1	95	Total	C	N	O	S	0	0	0
			678	419	122	132	5			
1	I1	95	Total	C	N	O	S	0	0	0
			678	419	122	132	5			
1	J1	95	Total	C	N	O	S	0	0	0
			678	419	122	132	5			
1	K1	95	Total	C	N	O	S	0	0	0
			678	419	122	132	5			
1	L1	95	Total	C	N	O	S	0	0	0
			678	419	122	132	5			
1	M1	95	Total	C	N	O	S	0	0	0
			678	419	122	132	5			
1	N1	95	Total	C	N	O	S	0	0	0
			678	419	122	132	5			
1	O1	95	Total	C	N	O	S	0	0	0
			678	419	122	132	5			
1	P1	95	Total	C	N	O	S	0	0	0
			678	419	122	132	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q1	95	Total 678	C 419	N 122	O 132	S 5	0	0	0
1	R1	95	Total 678	C 419	N 122	O 132	S 5	0	0	0
1	S1	95	Total 678	C 419	N 122	O 132	S 5	0	0	0
1	T1	95	Total 678	C 419	N 122	O 132	S 5	0	0	0
1	U1	95	Total 678	C 419	N 122	O 132	S 5	0	0	0
1	V1	95	Total 678	C 419	N 122	O 132	S 5	0	0	0
1	W1	95	Total 678	C 419	N 122	O 132	S 5	0	0	0
1	X1	95	Total 678	C 419	N 122	O 132	S 5	0	0	0
1	Y1	95	Total 678	C 419	N 122	O 132	S 5	0	0	0
1	Z1	95	Total 678	C 419	N 122	O 132	S 5	0	0	0
1	11	95	Total 678	C 419	N 122	O 132	S 5	0	0	0
1	21	95	Total 678	C 419	N 122	O 132	S 5	0	0	0
1	31	94	Total 669	C 413	N 120	O 131	S 5	0	0	0
1	41	95	Total 678	C 419	N 122	O 132	S 5	0	0	0

- Molecule 2 is a protein called Microcompartments protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A2	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	A3	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	A4	93	Total 662	C 415	N 121	O 123	S 3	0	0	0
2	A5	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	A6	92	Total 658	C 413	N 120	O 122	S 3	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A7	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	B2	91	Total 651	C 408	N 119	O 121	S 3	0	0	0
2	B3	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	B4	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	B5	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	B6	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	B7	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	C2	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	C3	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	C4	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	C5	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	C6	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	C7	93	Total 662	C 415	N 121	O 123	S 3	0	0	0
2	D2	93	Total 662	C 415	N 121	O 123	S 3	0	0	0
2	D3	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	D4	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	D5	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	D6	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	D7	93	Total 662	C 415	N 121	O 123	S 3	0	0	0
2	E2	94	Total 670	C 420	N 122	O 124	S 4	0	0	0
2	E3	92	Total 658	C 413	N 120	O 122	S 3	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E4	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	E5	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	E6	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	E7	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	F2	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	F3	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	F4	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	F5	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	F6	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	F7	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	G2	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	G3	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	G4	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	G5	91	Total	C	N	O	S	0	0	0
			653	410	119	121	3			
2	G6	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	G7	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	H2	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	H3	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	H4	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	H5	91	Total	C	N	O	S	0	0	0
			653	410	119	121	3			
2	H6	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H7	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	I2	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	I3	91	Total 653	C 410	N 119	O 121	S 3	0	0	0
2	I4	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	I5	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	I6	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	I7	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	J2	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	J3	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	J4	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	J5	91	Total 653	C 410	N 119	O 121	S 3	0	0	0
2	J6	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	J7	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	K2	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	K3	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	K4	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	K5	93	Total 662	C 415	N 121	O 123	S 3	0	0	0
2	K6	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	K7	93	Total 662	C 415	N 121	O 123	S 3	0	0	0
2	L2	94	Total 670	C 420	N 122	O 124	S 4	0	0	0
2	L3	92	Total 658	C 413	N 120	O 122	S 3	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L4	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	L5	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	L6	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	L7	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	M2	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	M3	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	M4	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	M5	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	M6	91	Total	C	N	O	S	0	0	0
			653	410	119	121	3			
2	M7	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	N2	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	N3	91	Total	C	N	O	S	0	0	0
			653	410	119	121	3			
2	N4	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	N5	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	N6	91	Total	C	N	O	S	0	0	0
			653	410	119	121	3			
2	N7	92	Total	C	N	O	S	0	0	0
			657	412	120	122	3			
2	O2	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	O3	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	O4	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	O5	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	O6	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	O7	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	P2	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	P3	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	P4	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	P5	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	P6	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	P7	91	Total	C	N	O	S	0	0	0
			649	408	119	119	3			
2	Q2	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	Q3	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	Q4	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	Q5	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	Q6	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	Q7	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	R2	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	R3	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	R4	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	R5	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	R6	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	R7	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	S2	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	S3	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	S4	94	Total 670	C 420	N 122	O 124	S 4	0	0	0
2	S5	93	Total 662	C 415	N 121	O 123	S 3	0	0	0
2	S6	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	S7	93	Total 662	C 415	N 121	O 123	S 3	0	0	0
2	T2	94	Total 670	C 420	N 122	O 124	S 4	0	0	0
2	T3	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	T4	94	Total 670	C 420	N 122	O 124	S 4	0	0	0
2	T5	93	Total 662	C 415	N 121	O 123	S 3	0	0	0
2	T6	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	T7	93	Total 662	C 415	N 121	O 123	S 3	0	0	0
2	U2	94	Total 670	C 420	N 122	O 124	S 4	0	0	0
2	U3	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	U4	94	Total 670	C 420	N 122	O 124	S 4	0	0	0
2	U5	93	Total 662	C 415	N 121	O 123	S 3	0	0	0
2	U6	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	U7	93	Total 662	C 415	N 121	O 123	S 3	0	0	0
2	V2	94	Total 670	C 420	N 122	O 124	S 4	0	0	0
2	V3	92	Total 658	C 413	N 120	O 122	S 3	0	0	0
2	V4	94	Total 670	C 420	N 122	O 124	S 4	0	0	0
2	V5	93	Total 662	C 415	N 121	O 123	S 3	0	0	0
2	V6	92	Total 658	C 413	N 120	O 122	S 3	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	V7	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	W2	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	W3	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	W4	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	W5	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	W6	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	W7	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	X2	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	X3	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	X4	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	X5	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	X6	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	X7	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	Y2	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	Y3	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	Y4	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	Y5	92	Total	C	N	O	S	0	0	0
			657	412	120	122	3			
2	Y6	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	Y7	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	Z2	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	Z3	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	Z4	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	Z5	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	Z6	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	Z7	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	12	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	13	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	14	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	15	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	16	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	17	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	22	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	23	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	24	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	25	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	26	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	27	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	32	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	33	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	34	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	35	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	36	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	37	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	42	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	43	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	44	94	Total	C	N	O	S	0	0	0
			670	420	122	124	4			
2	45	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			
2	46	92	Total	C	N	O	S	0	0	0
			658	413	120	122	3			
2	47	93	Total	C	N	O	S	0	0	0
			662	415	121	123	3			

- Molecule 3 is a protein called Microcompartments protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A8	203	Total	C	N	O	S	0	0	0
			1533	977	266	287	3			
3	A9	203	Total	C	N	O		0	0	0
			1000	594	203	203				
3	B8	203	Total	C	N	O	S	0	0	0
			1533	977	266	287	3			
3	B9	203	Total	C	N	O		0	0	0
			1000	594	203	203				
3	C8	203	Total	C	N	O	S	0	0	0
			1533	977	266	287	3			
3	C9	203	Total	C	N	O		0	0	0
			1000	594	203	203				
3	D8	203	Total	C	N	O	S	0	0	0
			1533	977	266	287	3			
3	D9	203	Total	C	N	O		0	0	0
			1000	594	203	203				
3	E8	203	Total	C	N	O	S	0	0	0
			1533	977	266	287	3			
3	E9	203	Total	C	N	O		0	0	0
			1000	594	203	203				
3	F8	203	Total	C	N	O	S	0	0	0
			1533	977	266	287	3			
3	F9	203	Total	C	N	O		0	0	0
			1000	594	203	203				

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G8	203	Total	C	N	O	S	0	0	0
			1533	977	266	287	3			
3	G9	203	Total	C	N	O		0	0	0
			1000	594	203	203				
3	H8	203	Total	C	N	O	S	0	0	0
			1533	977	266	287	3			
3	H9	203	Total	C	N	O		0	0	0
			1000	594	203	203				
3	I8	203	Total	C	N	O	S	0	0	0
			1533	977	266	287	3			
3	I9	203	Total	C	N	O		0	0	0
			1000	594	203	203				
3	J8	203	Total	C	N	O	S	0	0	0
			1533	977	266	287	3			
3	J9	203	Total	C	N	O		0	0	0
			1000	594	203	203				
3	K8	203	Total	C	N	O	S	0	0	0
			1533	977	266	287	3			
3	K9	203	Total	C	N	O		0	0	0
			1000	594	203	203				
3	L8	203	Total	C	N	O	S	0	0	0
			1533	977	266	287	3			
3	L9	203	Total	C	N	O		0	0	0
			1000	594	203	203				
3	M8	203	Total	C	N	O	S	0	0	0
			1533	977	266	287	3			
3	M9	203	Total	C	N	O		0	0	0
			1000	594	203	203				
3	N8	203	Total	C	N	O	S	0	0	0
			1533	977	266	287	3			
3	N9	203	Total	C	N	O		0	0	0
			1000	594	203	203				
3	O8	203	Total	C	N	O	S	0	0	0
			1533	977	266	287	3			
3	O9	203	Total	C	N	O		0	0	0
			1000	594	203	203				
3	P8	203	Total	C	N	O	S	0	0	0
			1533	977	266	287	3			
3	P9	203	Total	C	N	O		0	0	0
			1000	594	203	203				
3	Q8	203	Total	C	N	O	S	0	0	0
			1533	977	266	287	3			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	Q9	203	Total 1000	C 594	N 203	O 203	0	0	0
3	R8	203	Total 1533	C 977	N 266	O 287 S 3	0	0	0
3	R9	203	Total 1000	C 594	N 203	O 203	0	0	0
3	S8	203	Total 1533	C 977	N 266	O 287 S 3	0	0	0
3	S9	203	Total 1000	C 594	N 203	O 203	0	0	0
3	T8	203	Total 1533	C 977	N 266	O 287 S 3	0	0	0
3	T9	203	Total 1000	C 594	N 203	O 203	0	0	0
3	U8	203	Total 1533	C 977	N 266	O 287 S 3	0	0	0
3	U9	203	Total 1000	C 594	N 203	O 203	0	0	0
3	V8	203	Total 1533	C 977	N 266	O 287 S 3	0	0	0
3	V9	203	Total 1000	C 594	N 203	O 203	0	0	0
3	W8	203	Total 1533	C 977	N 266	O 287 S 3	0	0	0
3	W9	203	Total 1000	C 594	N 203	O 203	0	0	0
3	X8	203	Total 1533	C 977	N 266	O 287 S 3	0	0	0
3	X9	203	Total 1000	C 594	N 203	O 203	0	0	0
3	Y8	203	Total 1533	C 977	N 266	O 287 S 3	0	0	0
3	Y9	203	Total 1000	C 594	N 203	O 203	0	0	0
3	Z8	203	Total 1533	C 977	N 266	O 287 S 3	0	0	0
3	Z9	203	Total 1000	C 594	N 203	O 203	0	0	0
3	18	203	Total 1533	C 977	N 266	O 287 S 3	0	0	0
3	19	198	Total 975	C 579	N 198	O 198	0	0	0

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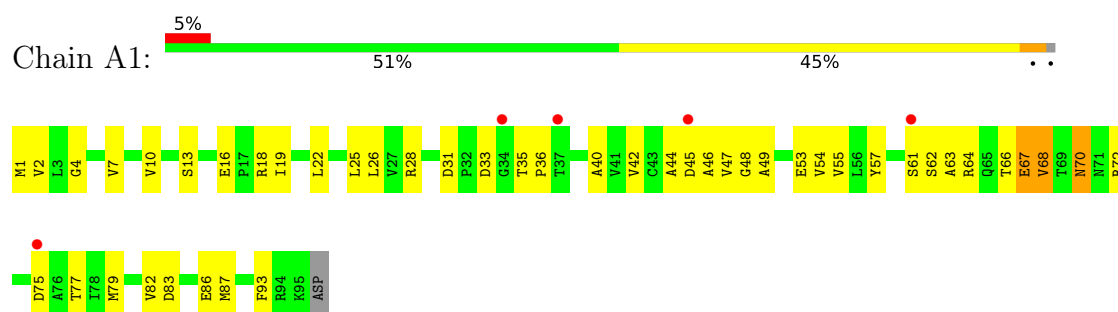
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	28	203	Total 1533	C 977	N 266	O 287	S 3	0	0	0
3	29	203	Total 1000	C 594	N 203	O 203		0	0	0
3	38	203	Total 1533	C 977	N 266	O 287	S 3	0	0	0
3	39	203	Total 1000	C 594	N 203	O 203		0	0	0
3	48	203	Total 1533	C 977	N 266	O 287	S 3	0	0	0
3	49	203	Total 1000	C 594	N 203	O 203		0	0	0

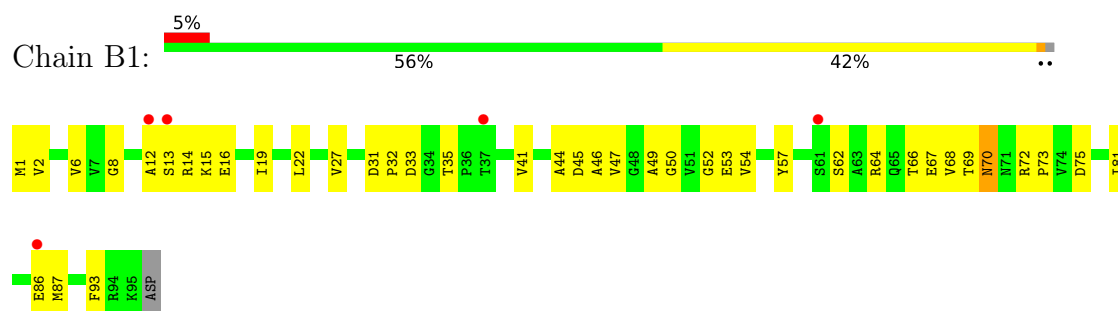
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

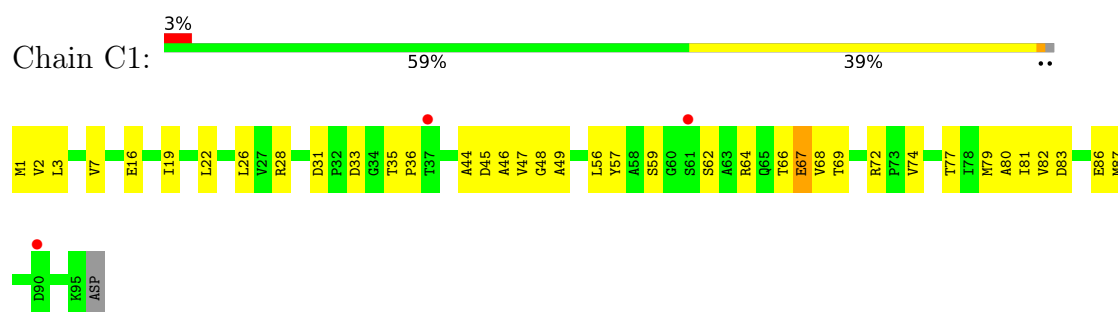
- Molecule 1: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI



- Molecule 1: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI

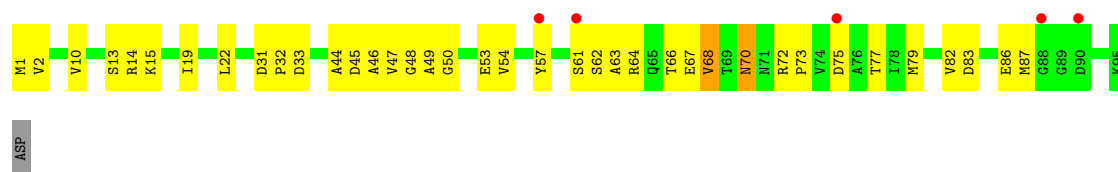


- Molecule 1: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI

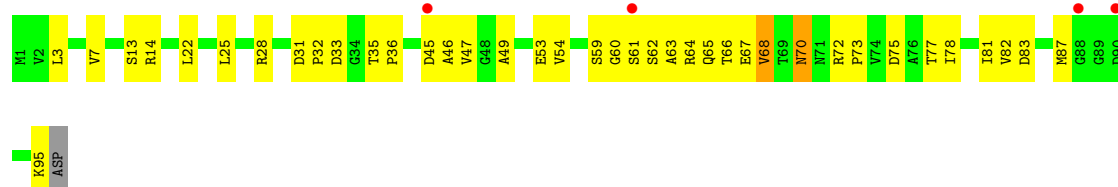


- Molecule 1: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI

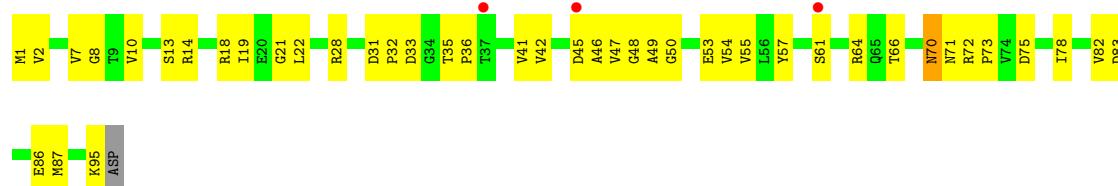




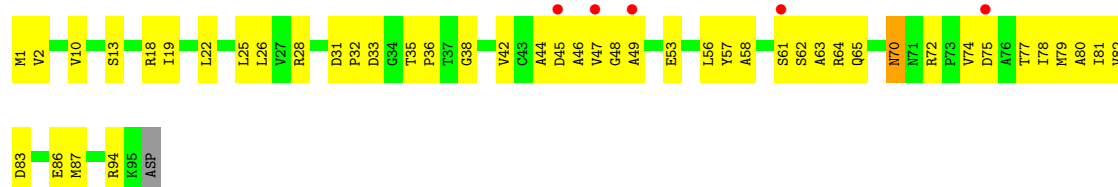
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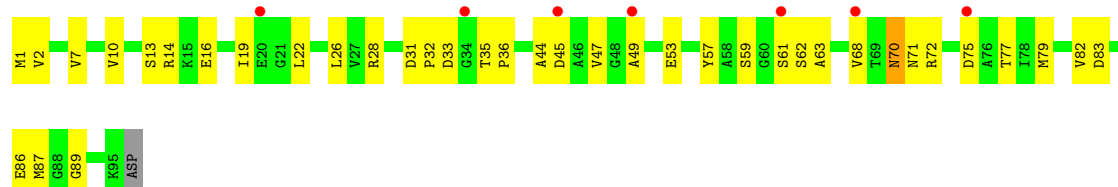
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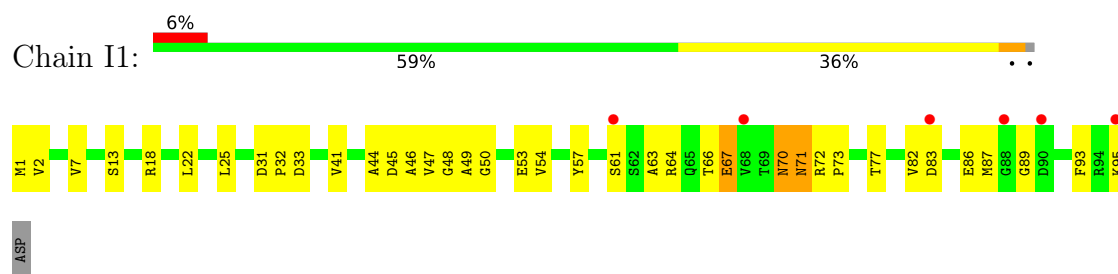
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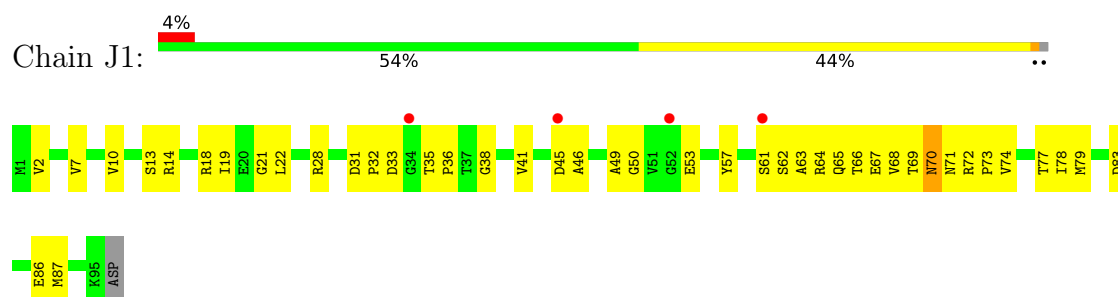
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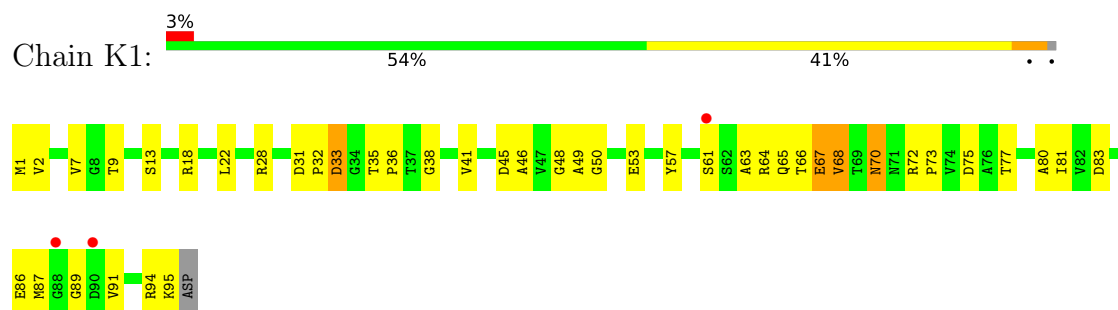
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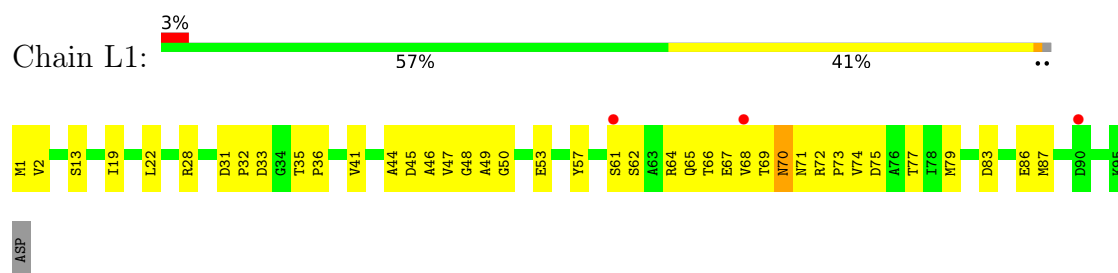
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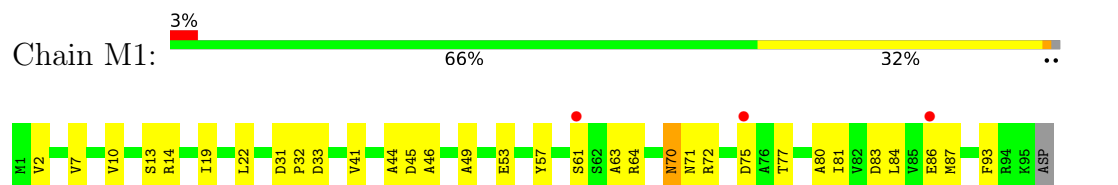
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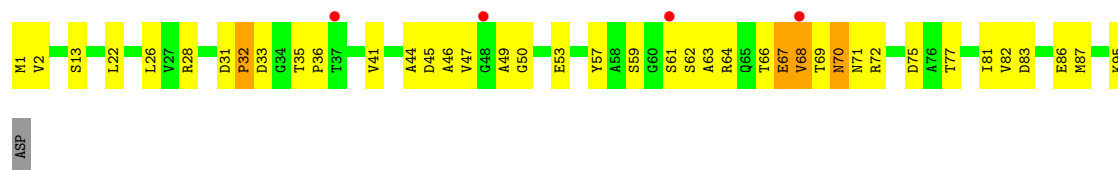


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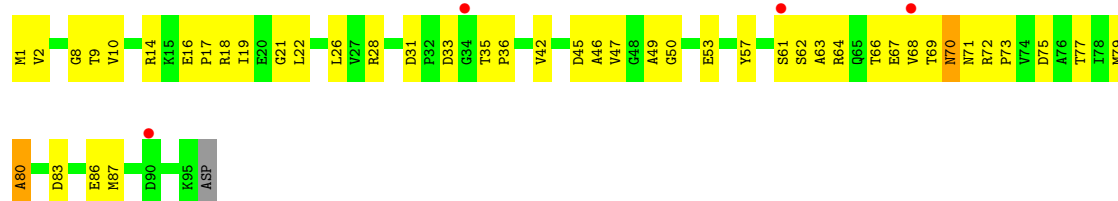


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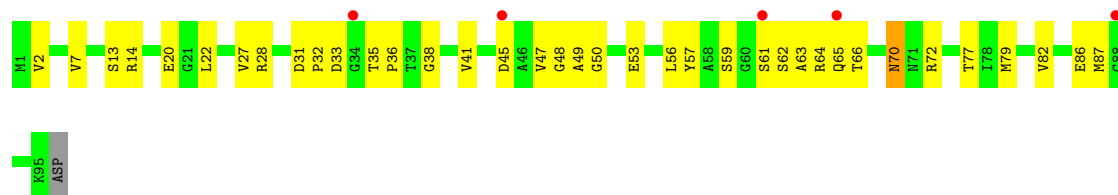




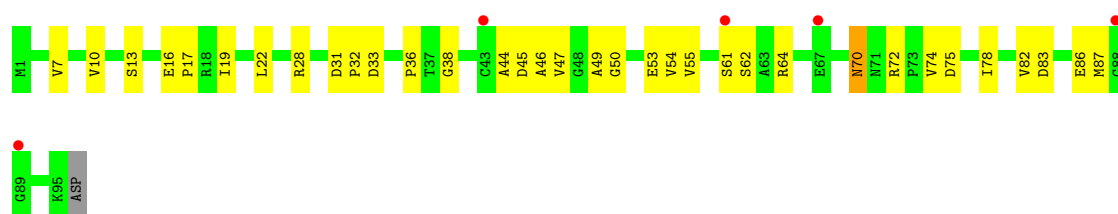
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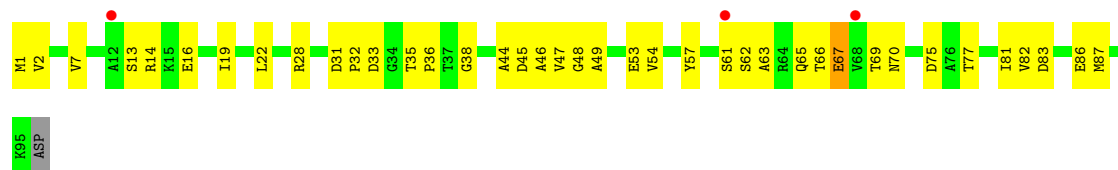
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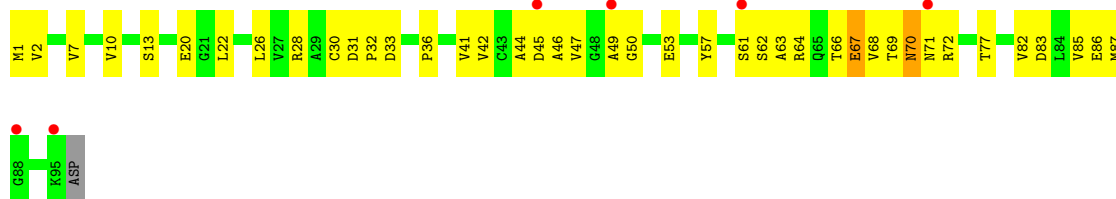


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Chain S1: 



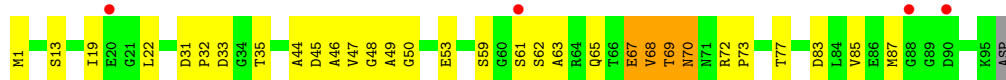
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Chain T1: 



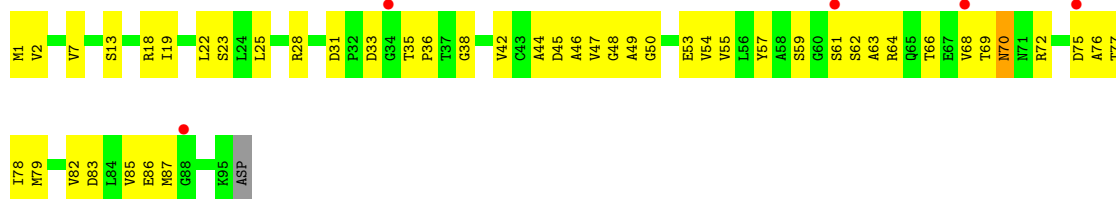
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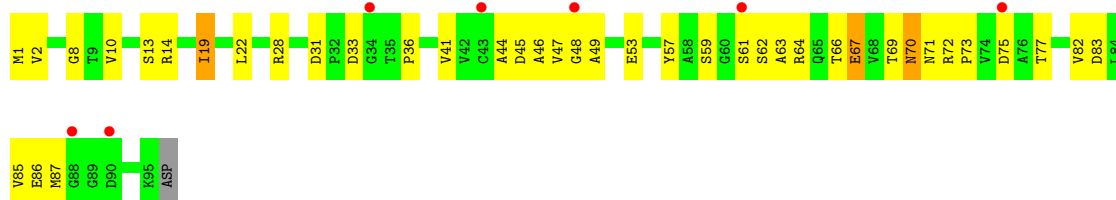
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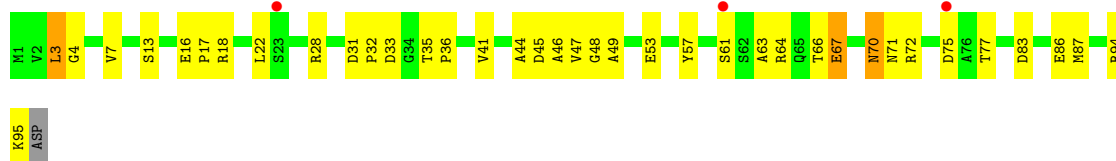
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Chain W1: 



- Molecule 1: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI

Chain X1:  3% 59% 36% ..



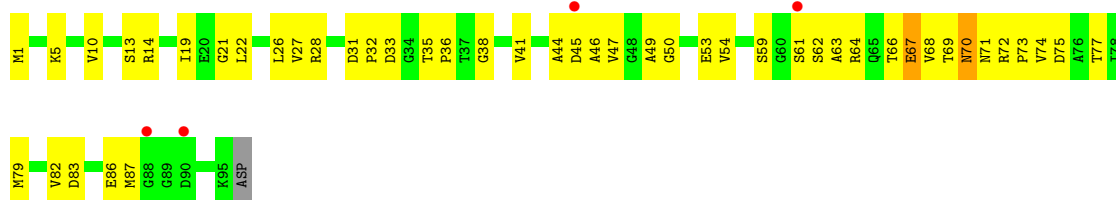
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Chain Y1:  4% 61% 36% ..



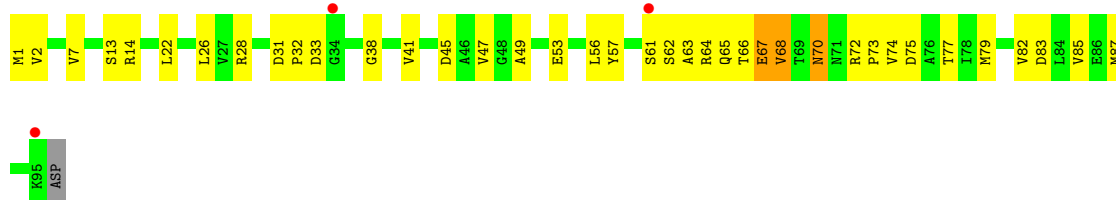
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Chain Z1:  4% 50% 47% ..



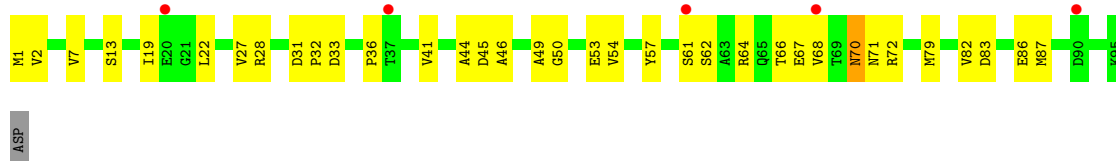
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Chain 11:  3% 59% 36% ..

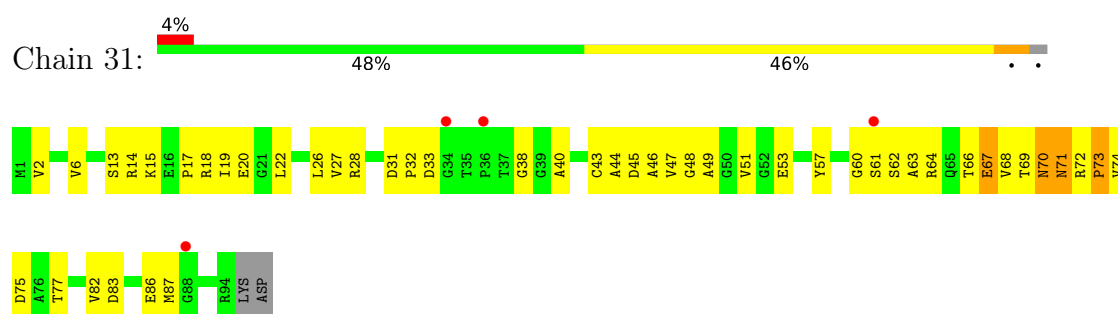


- Molecule 1: Ethanolamine utilization protein EutN/carboxysome structural protein CcmI

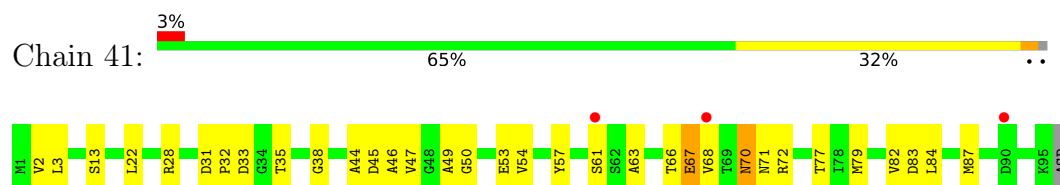
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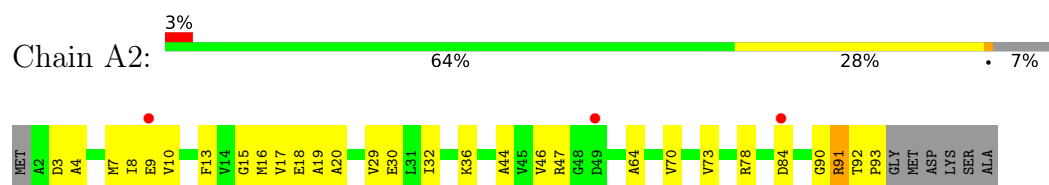
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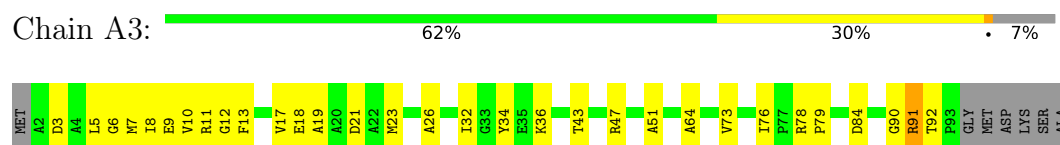
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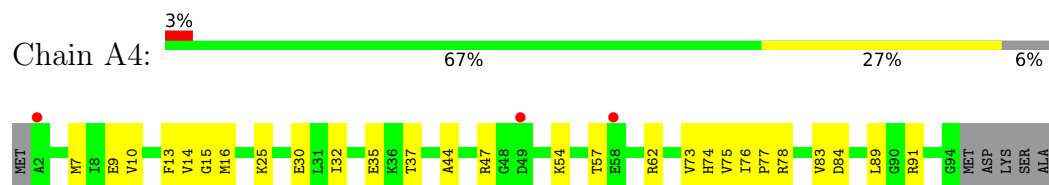
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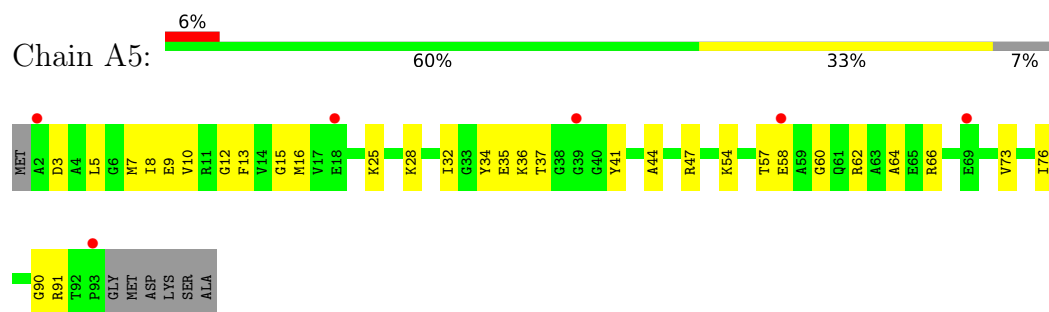
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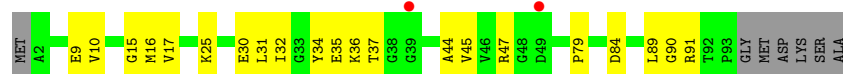
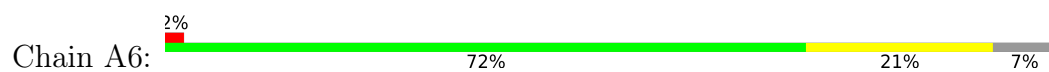
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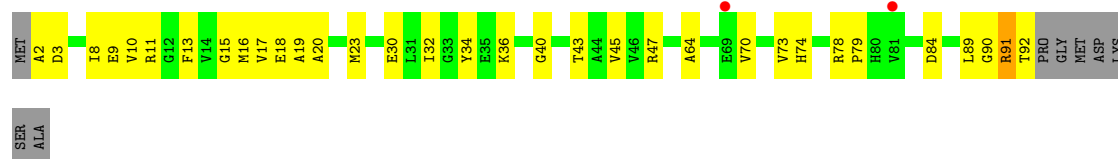
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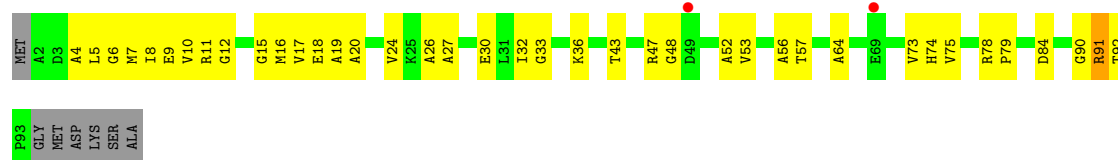
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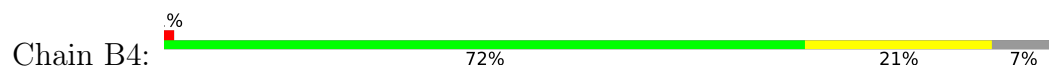
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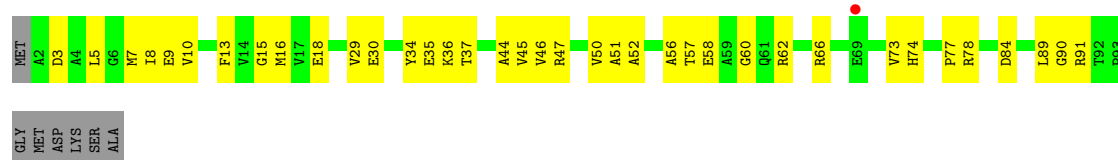
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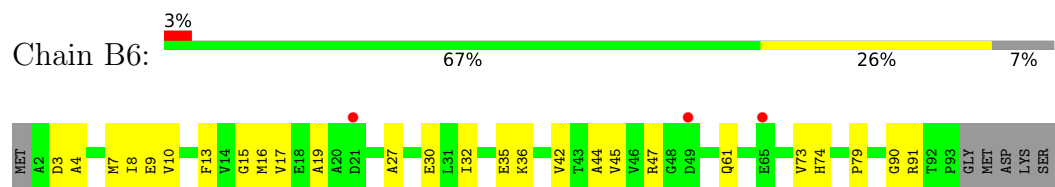
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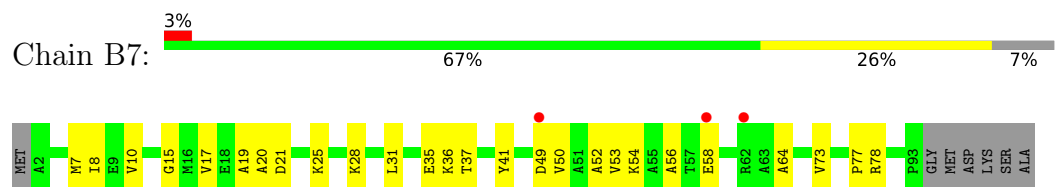
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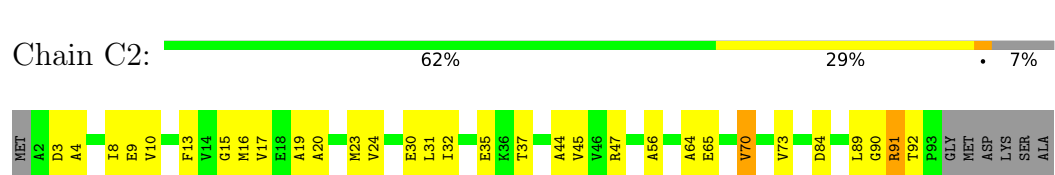
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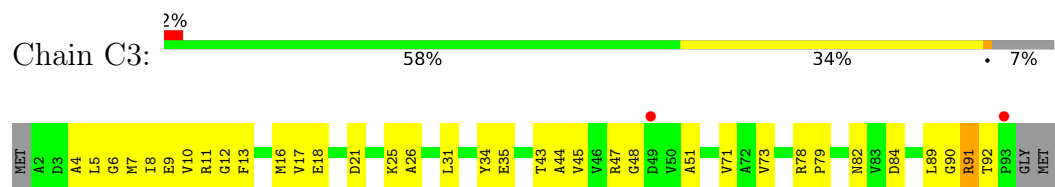
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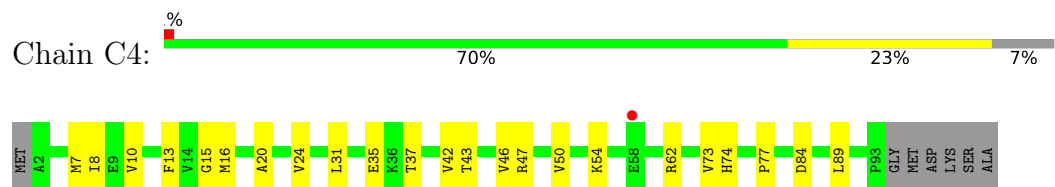
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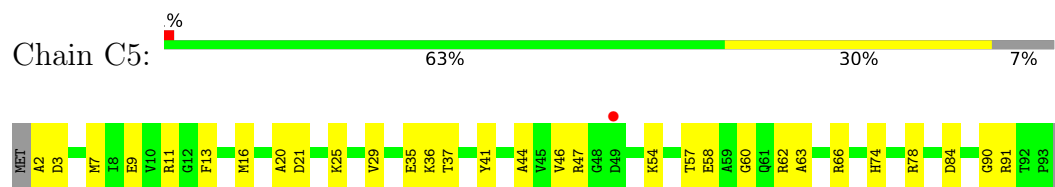
● Molecule 2: Microcompartments protein



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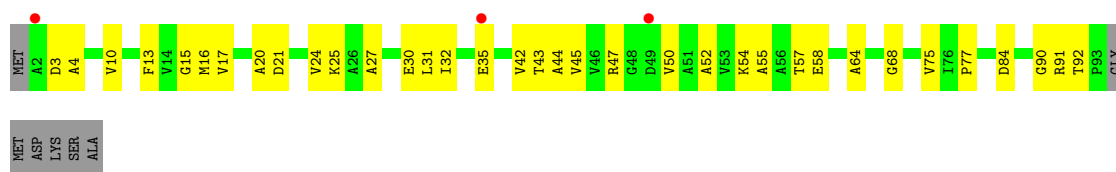


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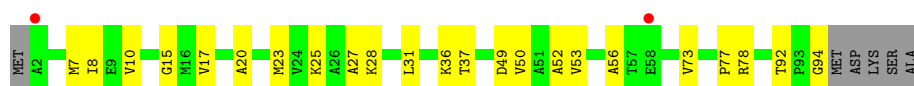


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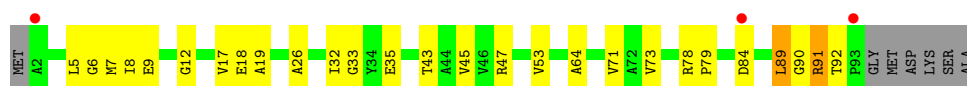
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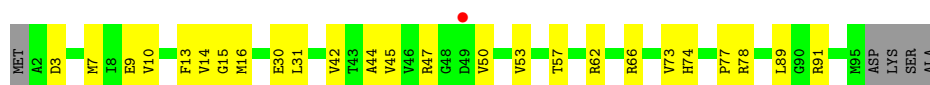
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MET
ASP
LYS
SER
ALA

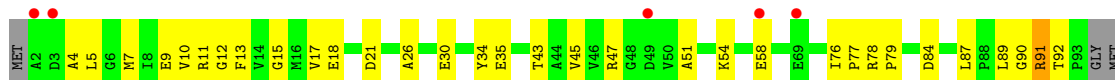
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ASP
LYS
SER
ALA

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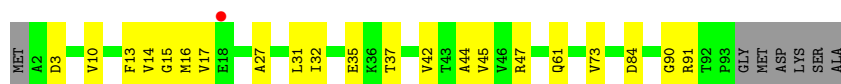
GLY
MET
ASP
LYS
SER
ALA

• Molecule 2: Microcompartments protein



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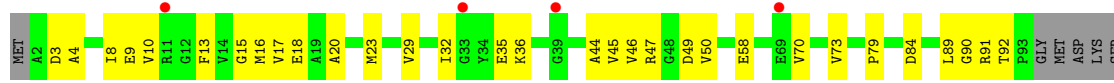




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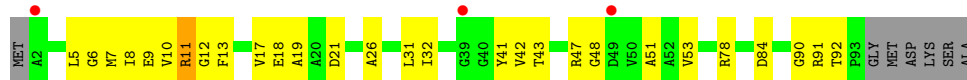


- Molecule 2: Microcompartments protein



ALA

- Molecule 2: Microcompartments protein



- Molecule 2: Microcompartments protein



LYS
SER
ALA

- Molecule 2: Microcompartments protein



ASP
LYS
SER
ALA

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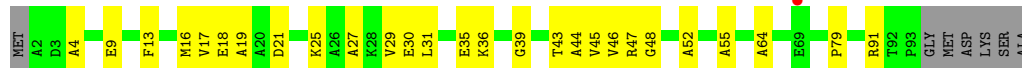
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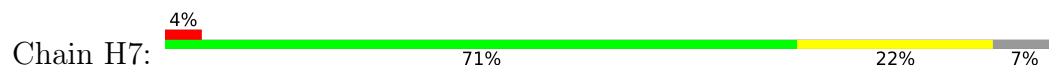
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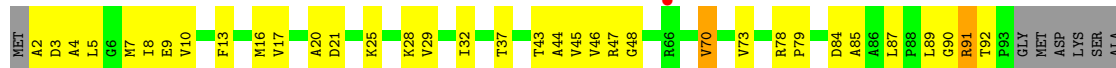
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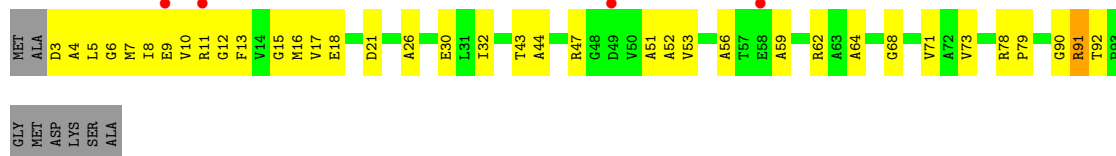
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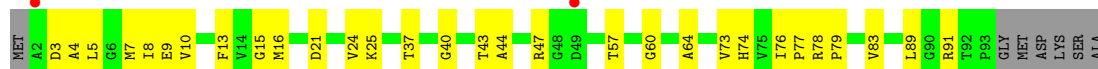
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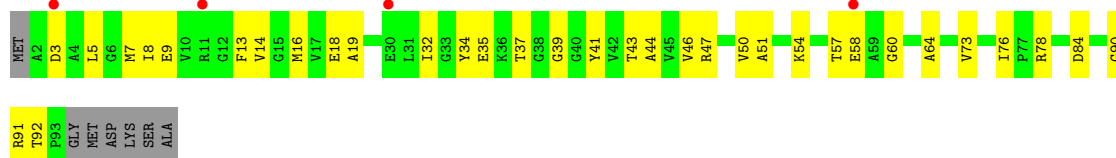
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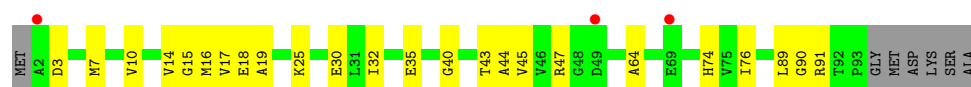
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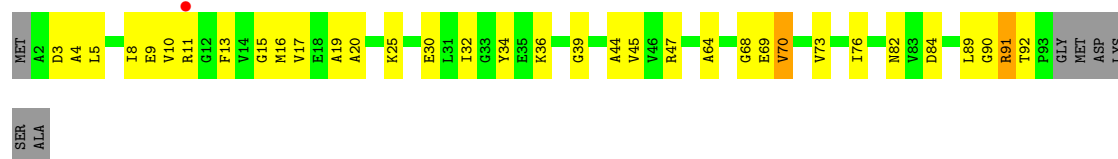
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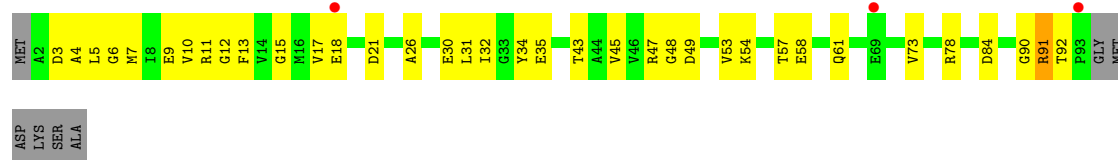
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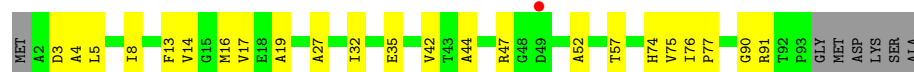
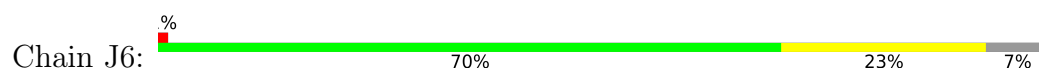
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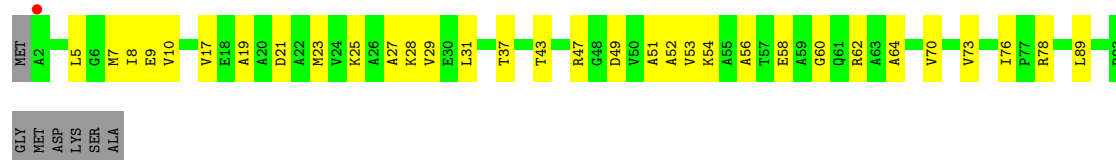
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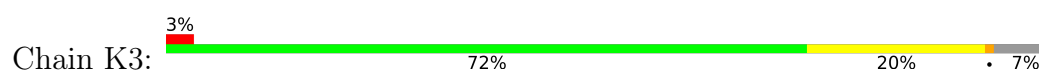
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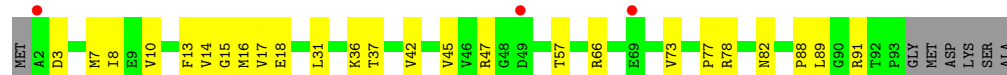
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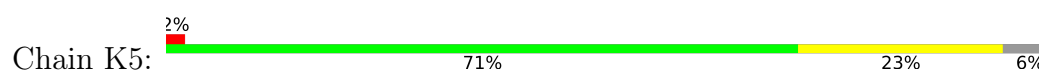
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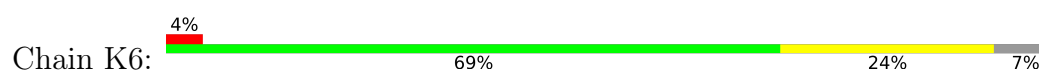
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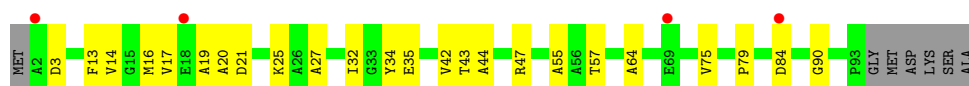


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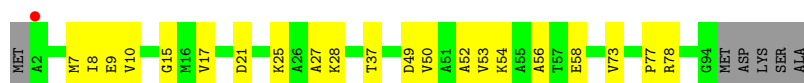
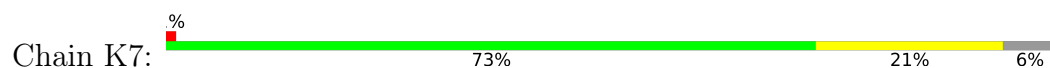


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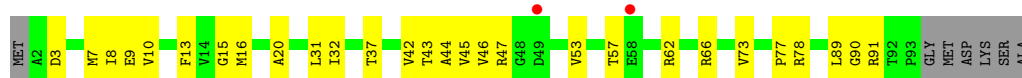
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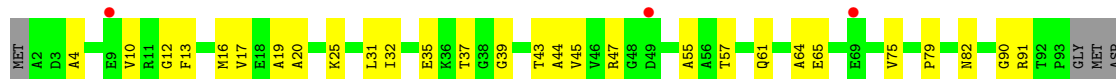
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LYS
SER
ALA

• Molecule 2: Microcompartments protein



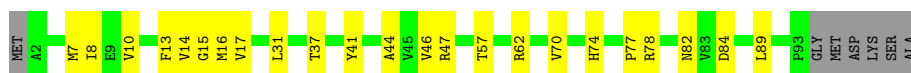
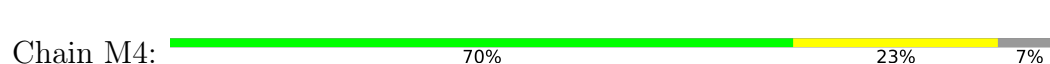
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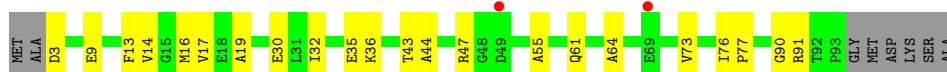
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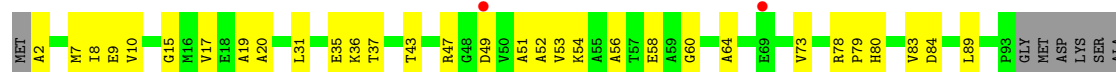
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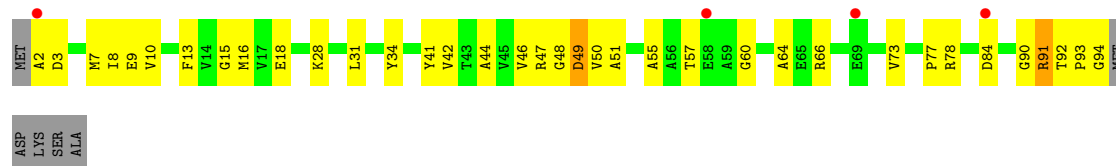
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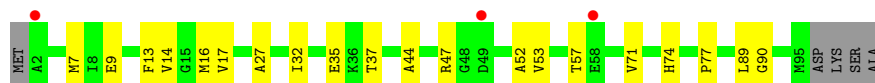
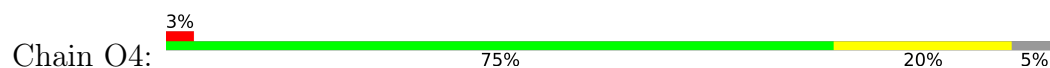
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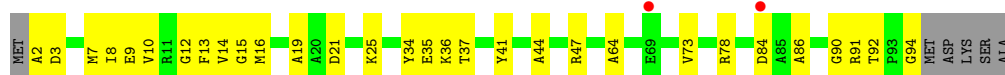
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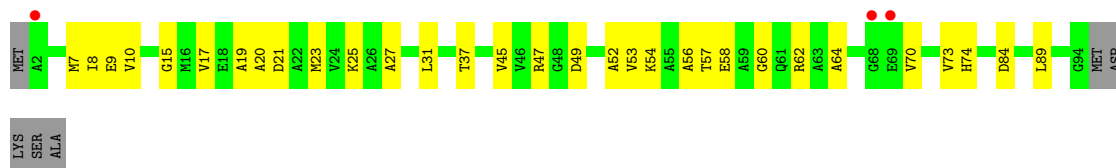
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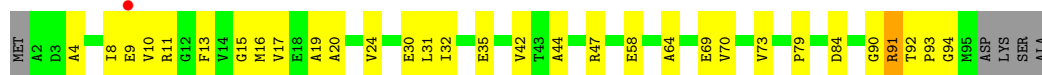
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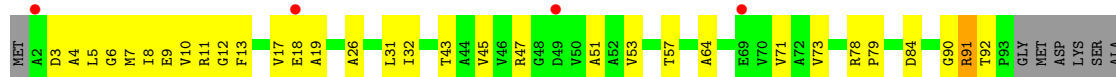
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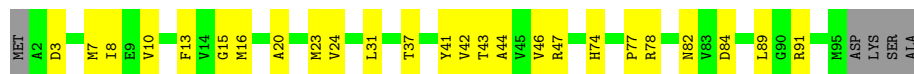
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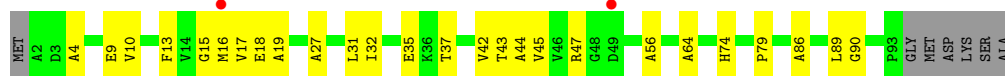
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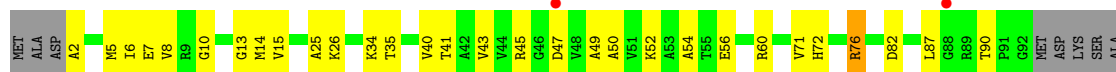
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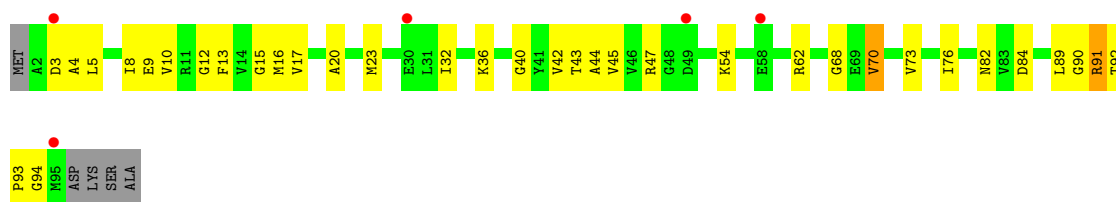


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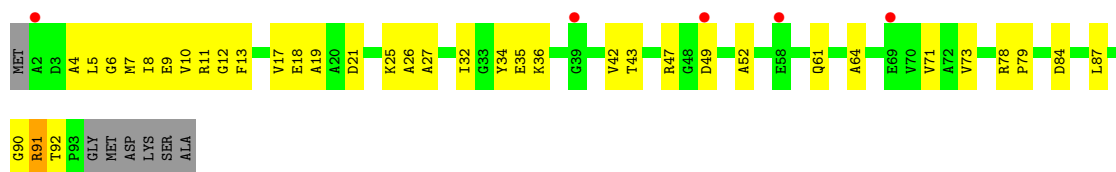


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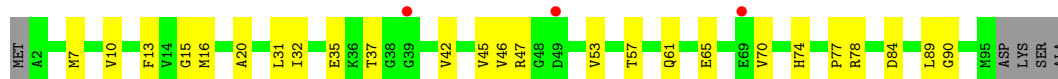
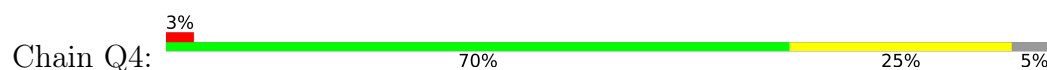




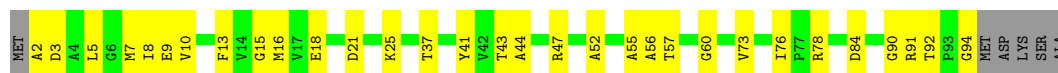
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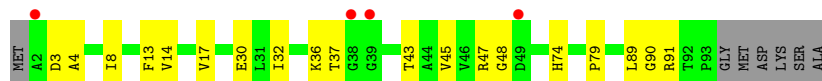
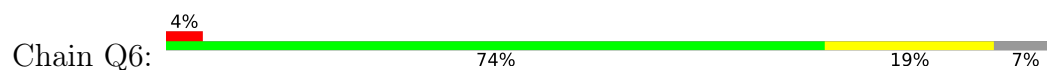
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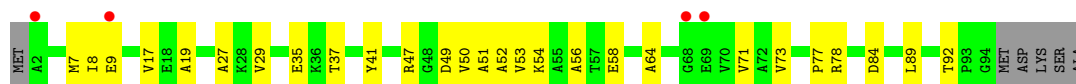
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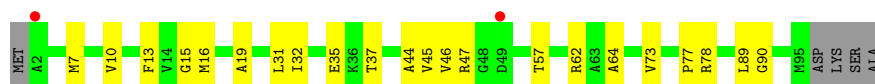
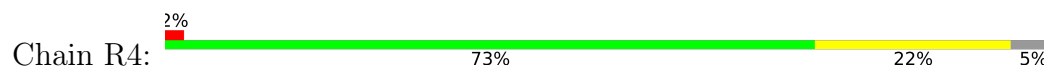




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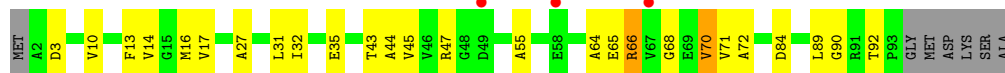
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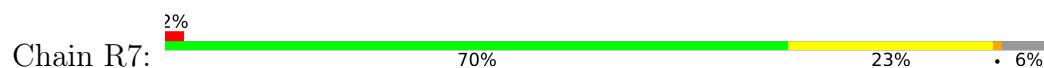
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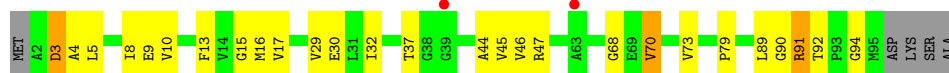
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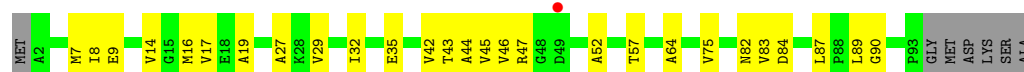
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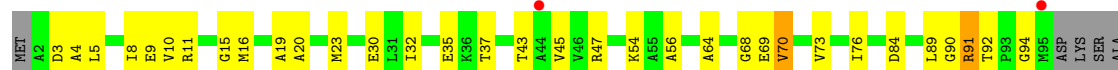
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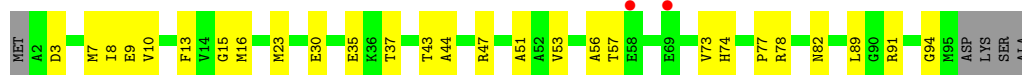
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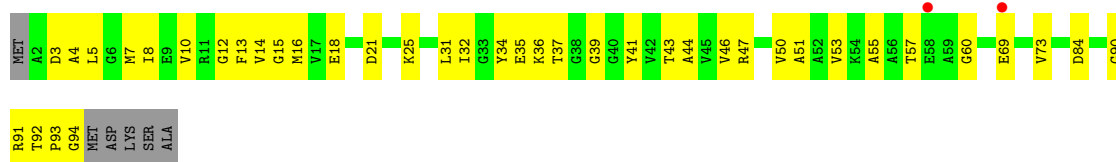
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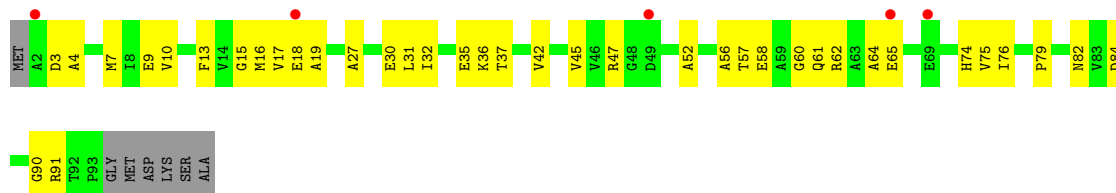
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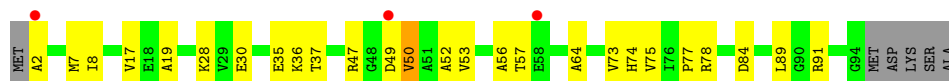
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• Molecule 2: Microcompartments protein



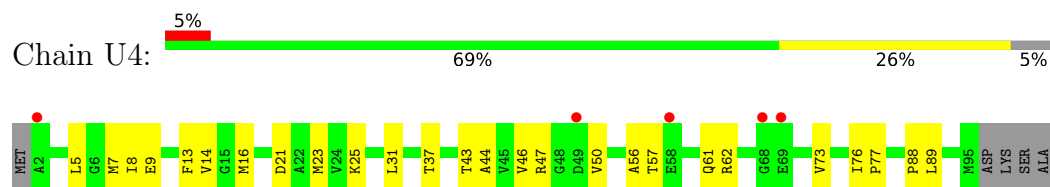
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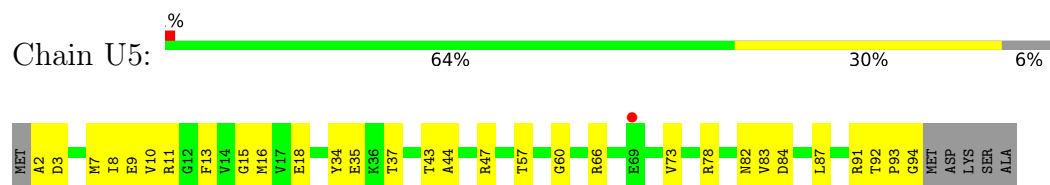
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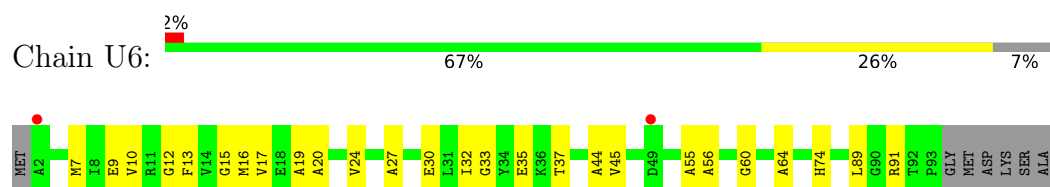
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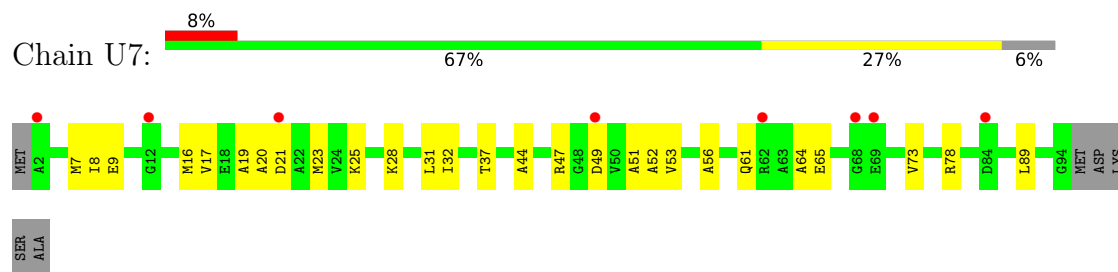
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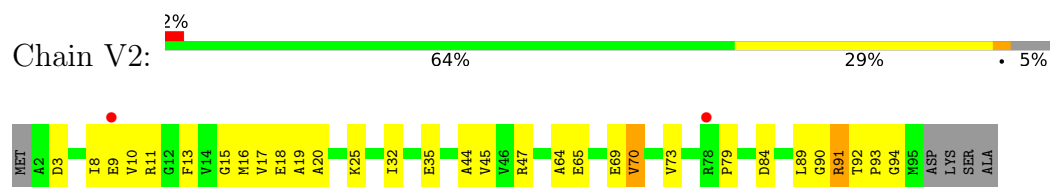
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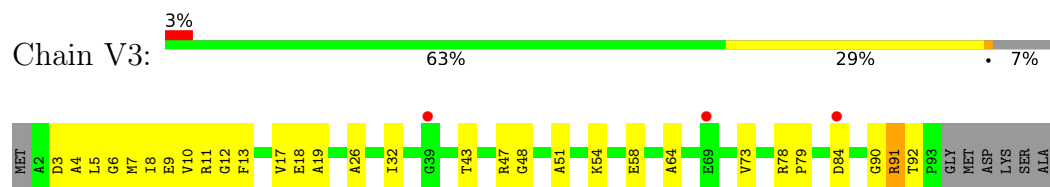
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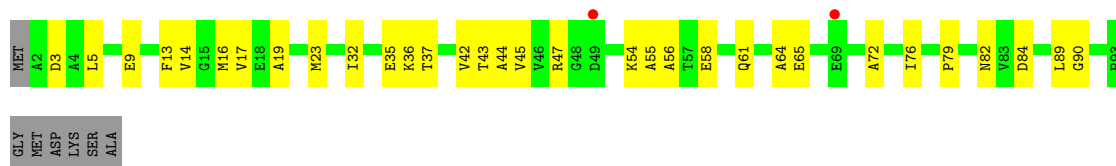




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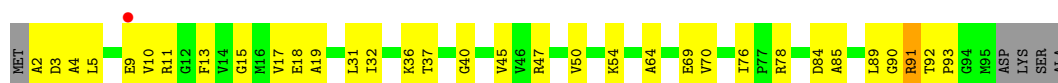
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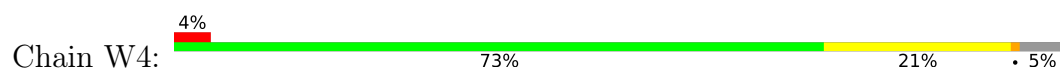
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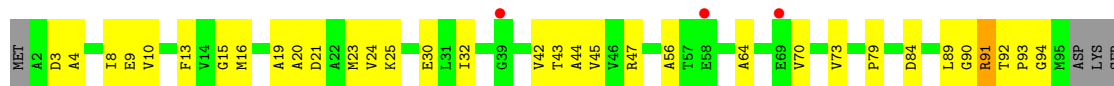
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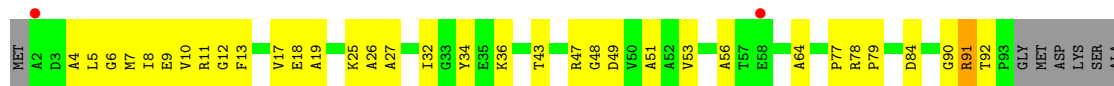
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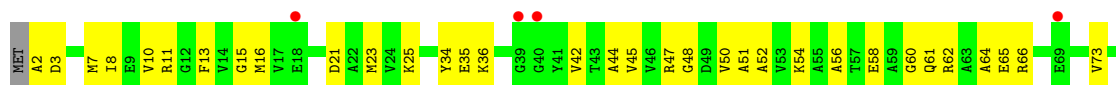


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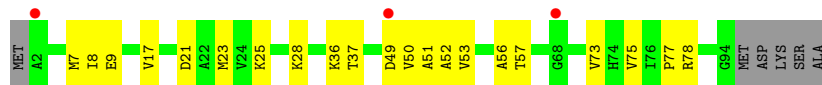
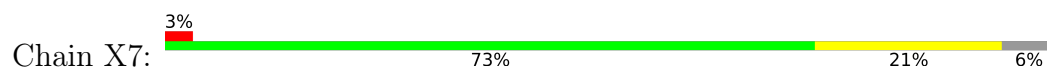
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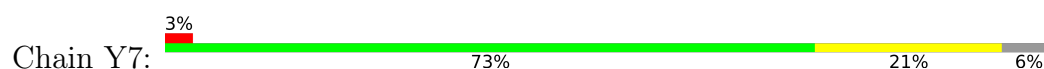
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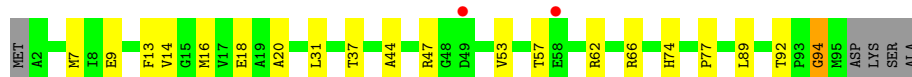
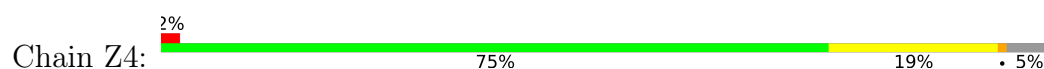
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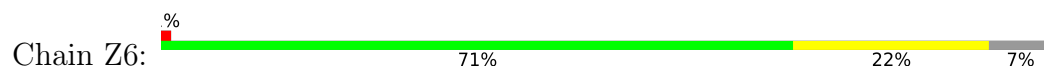
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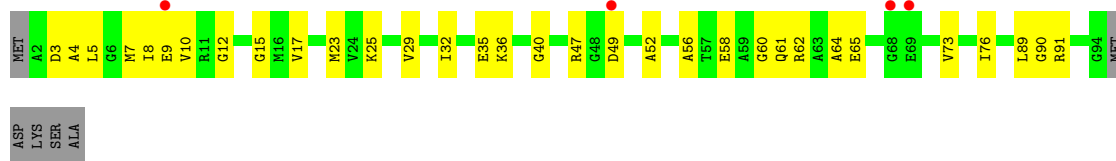
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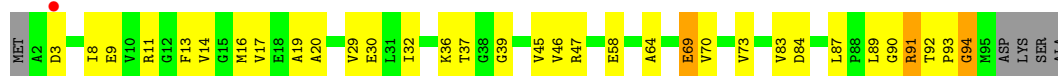
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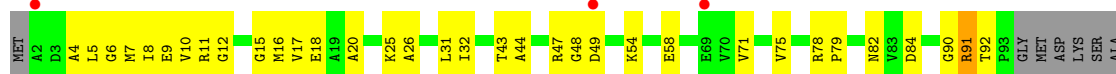
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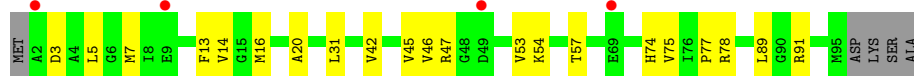
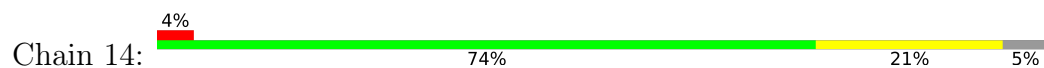
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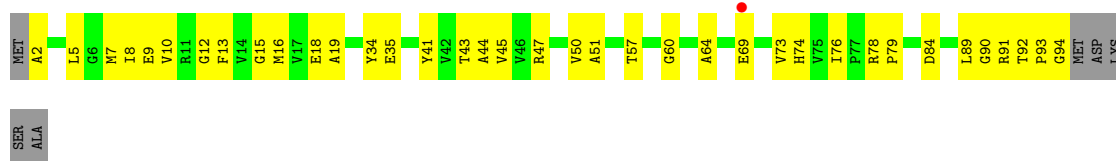


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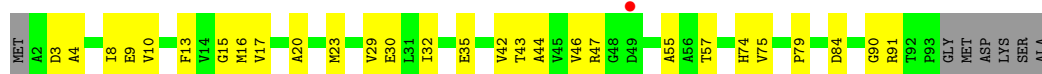


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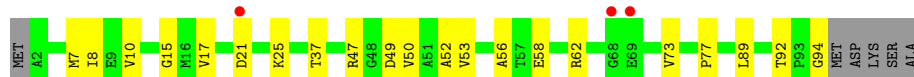
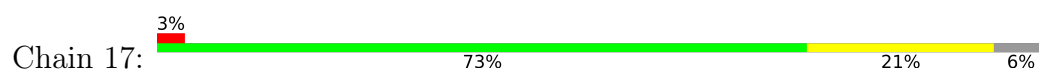




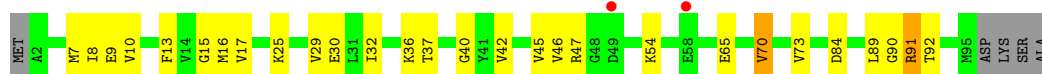
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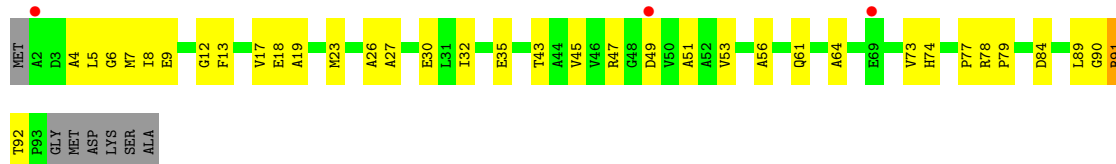
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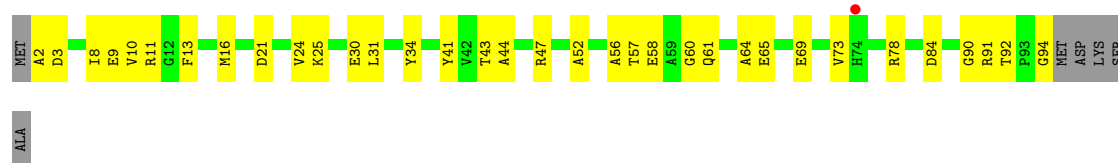


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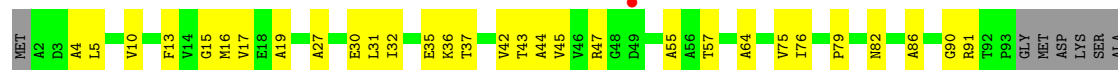


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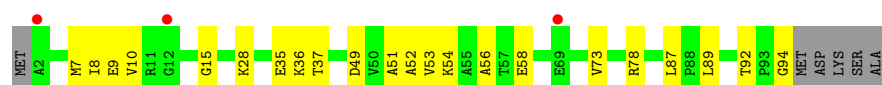
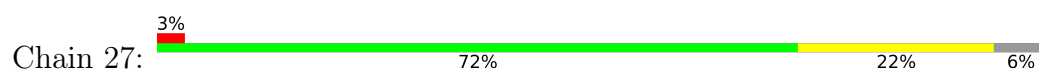




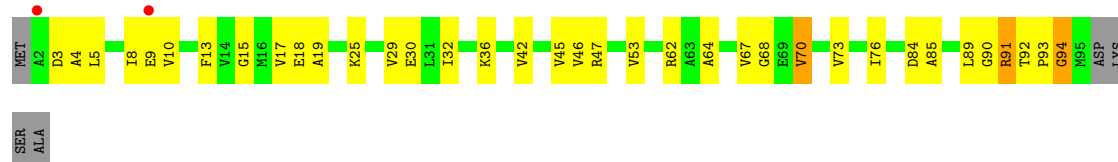
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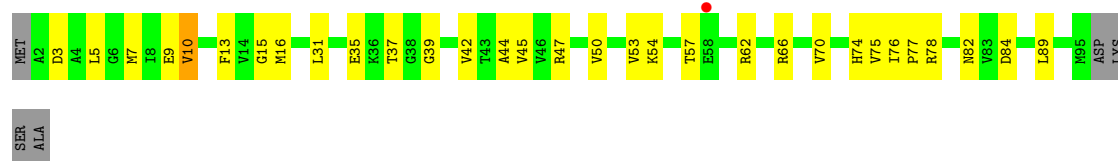
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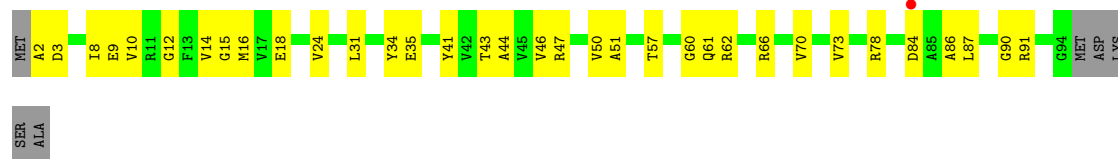
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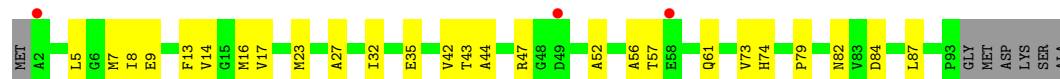
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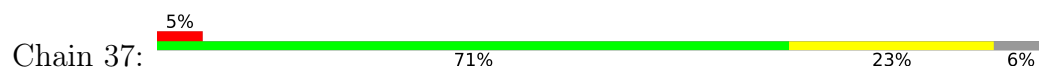
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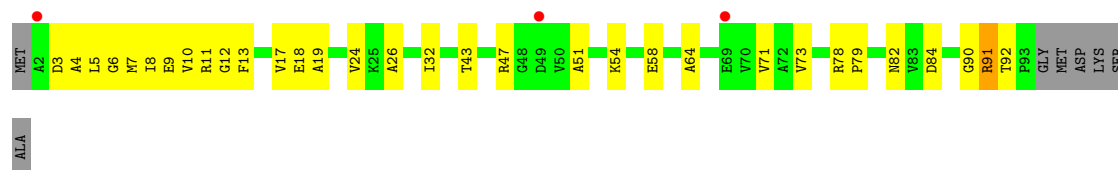
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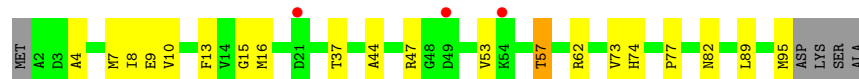
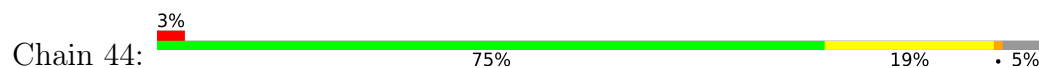
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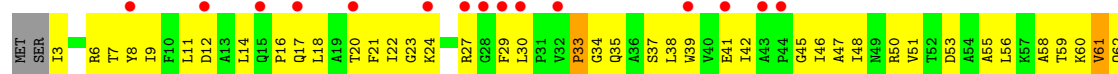
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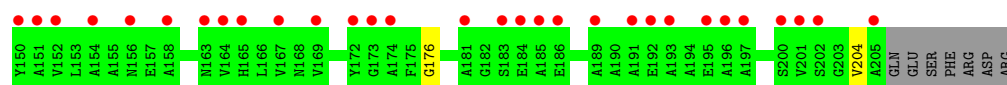
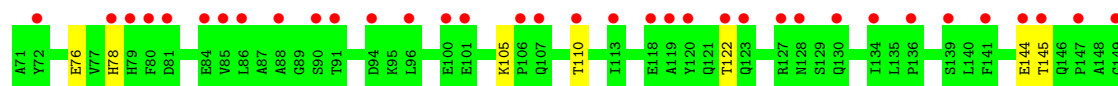
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• Molecule 3: Microcompartments protein

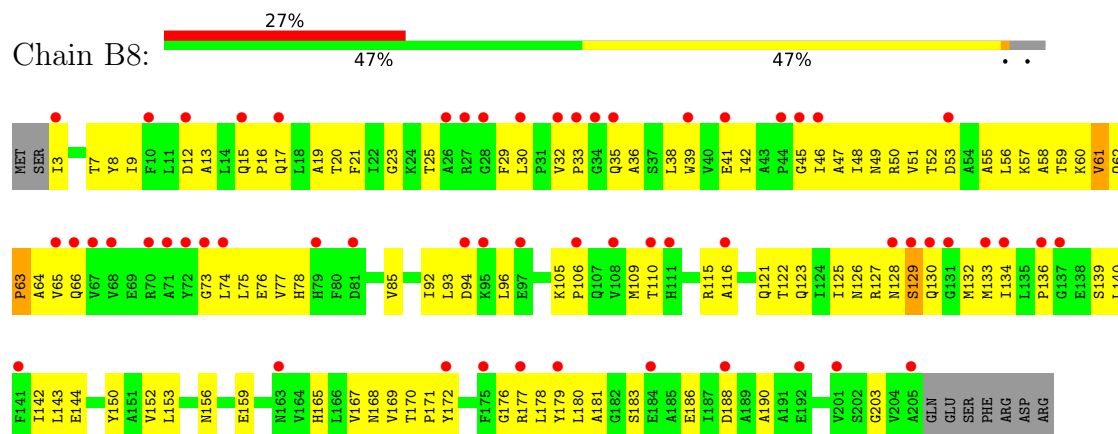


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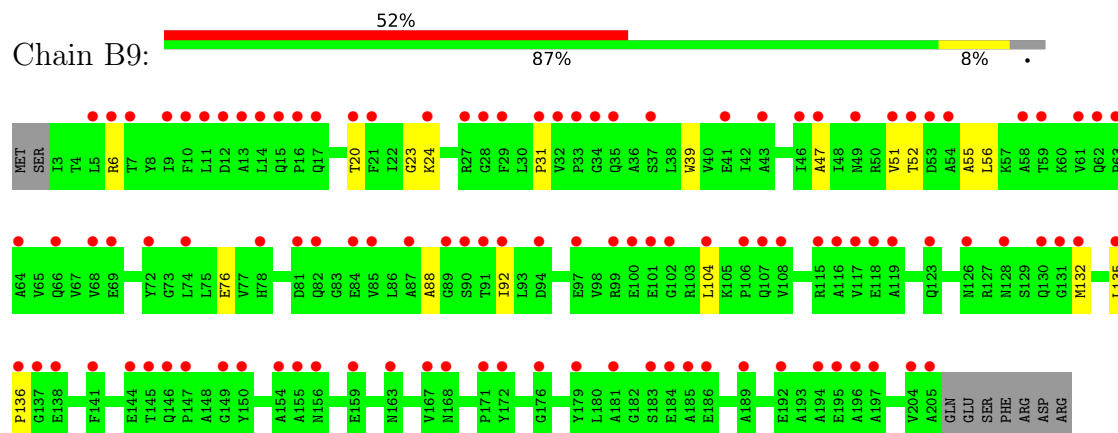
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Chain B8:



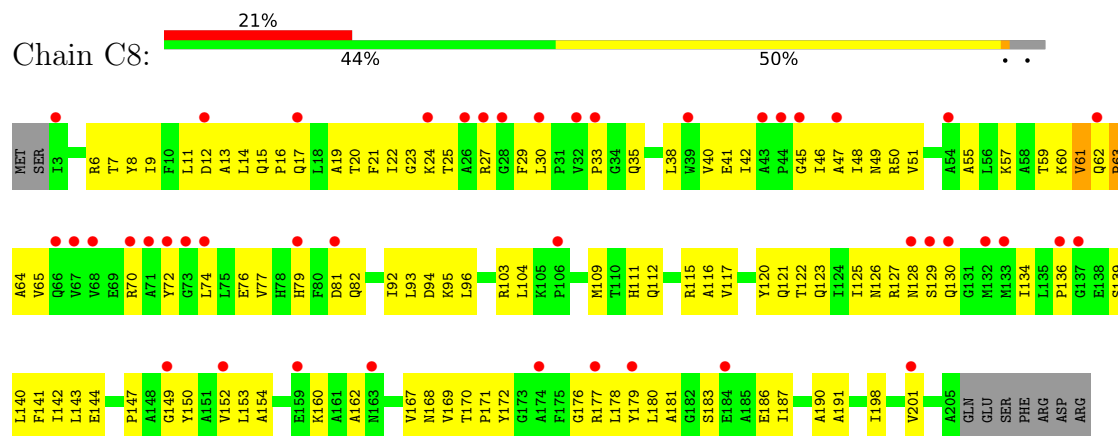
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Chain B9:



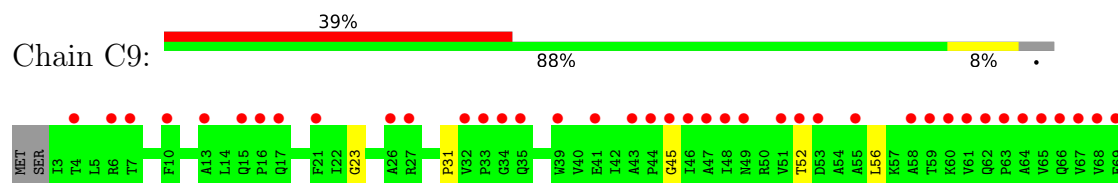
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Chain C8:



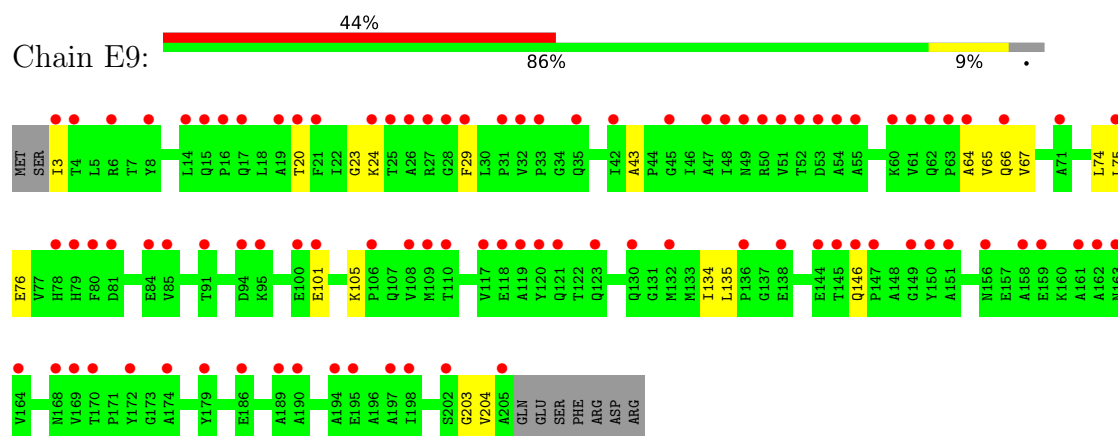
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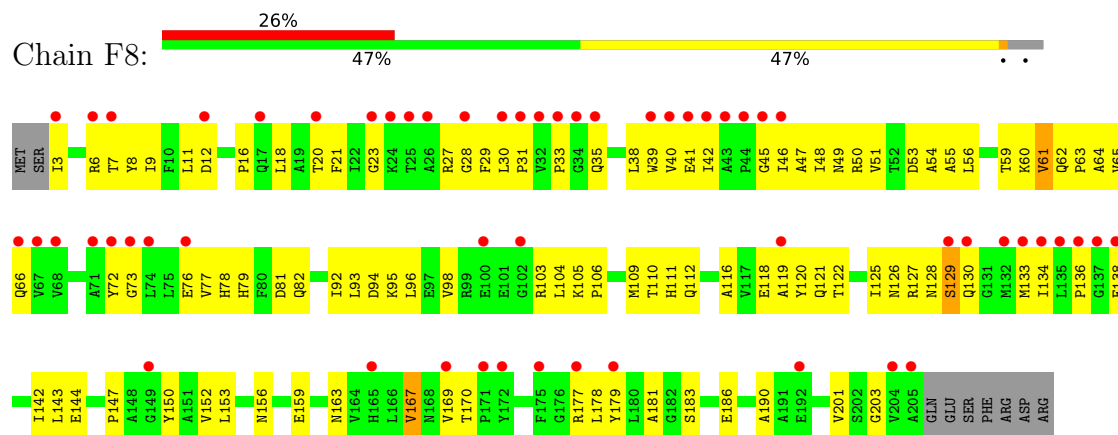
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Chain E9:



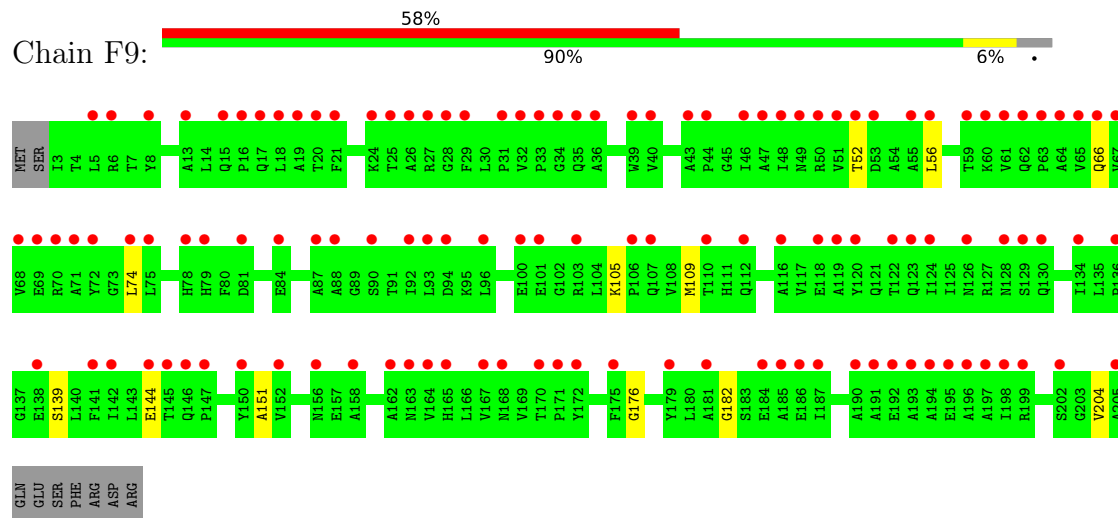
- Molecule 3: Microcompartments protein

Chain F8:



- Molecule 3: Microcompartments protein

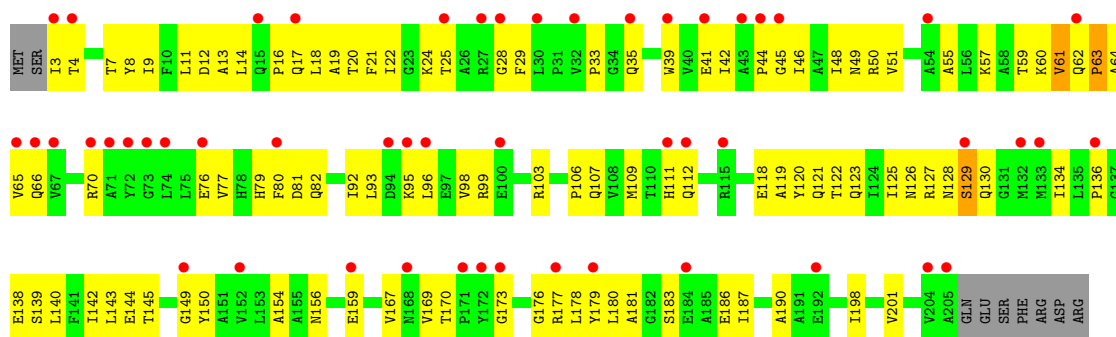
Chain F9:



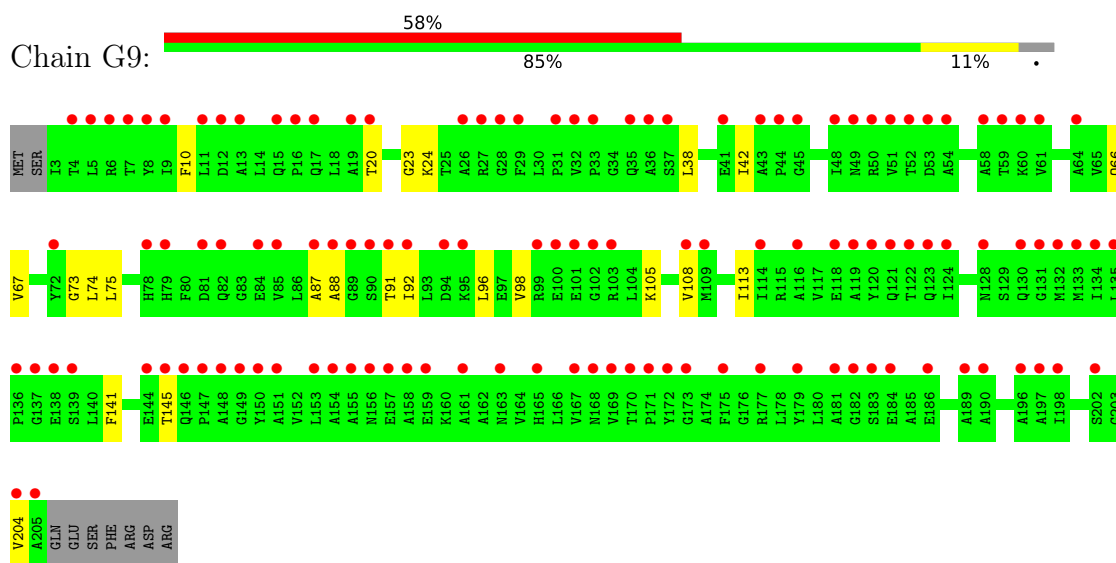
- Molecule 3: Microcompartments protein

Chain G8:

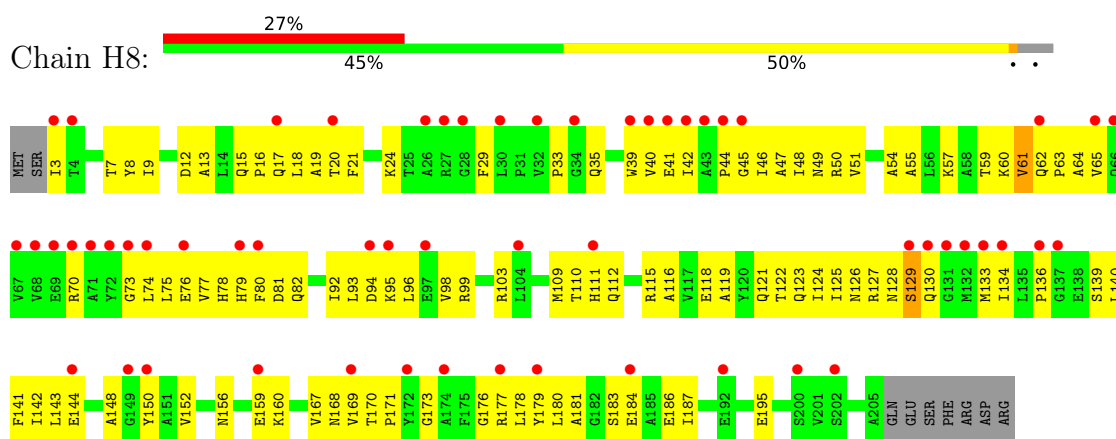




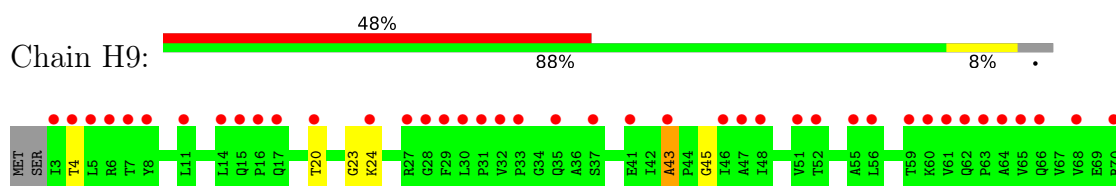
• Molecule 3: Microcompartments protein

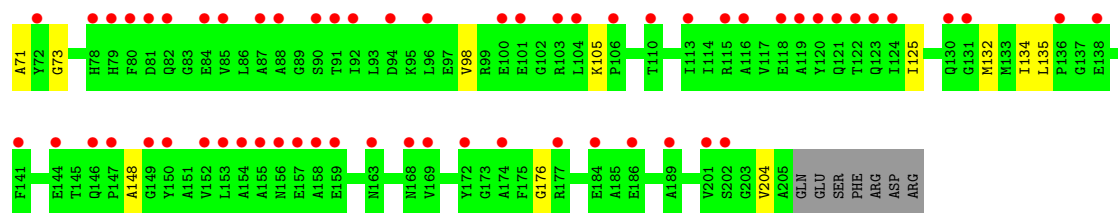


• Molecule 3: Microcompartments protein

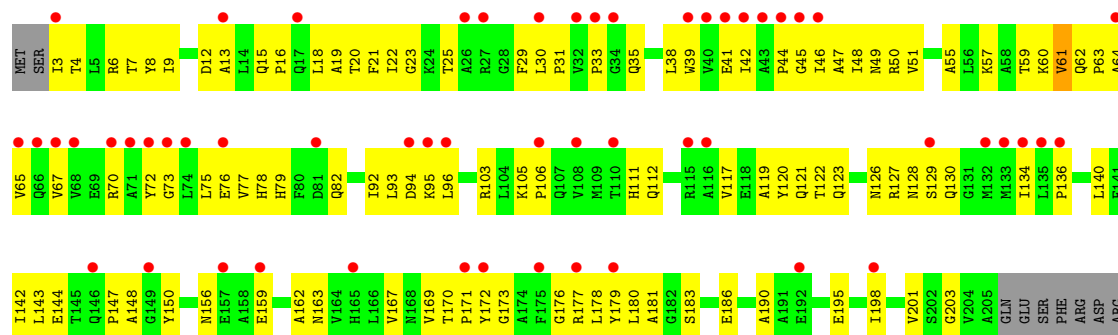


• Molecule 3: Microcompartments protein

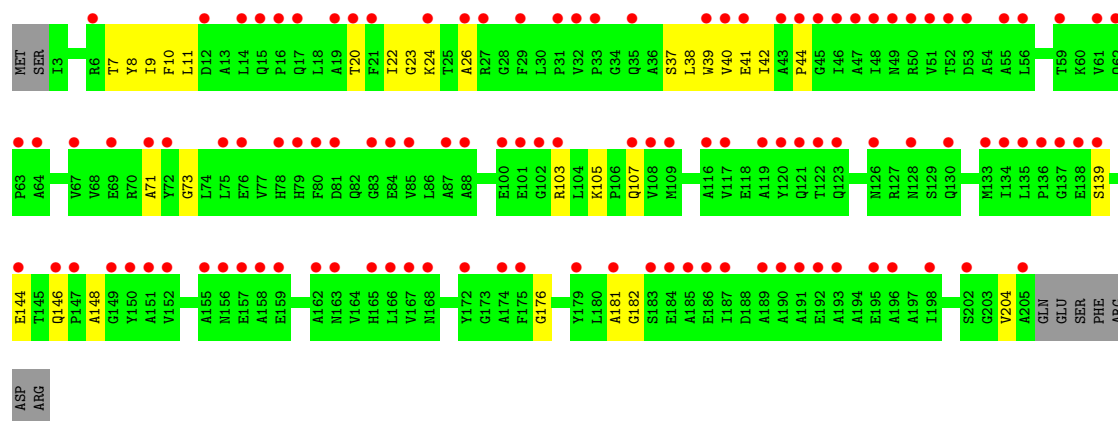
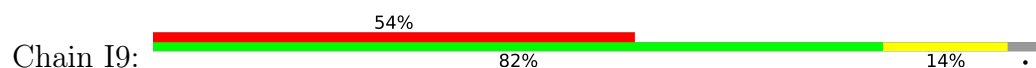




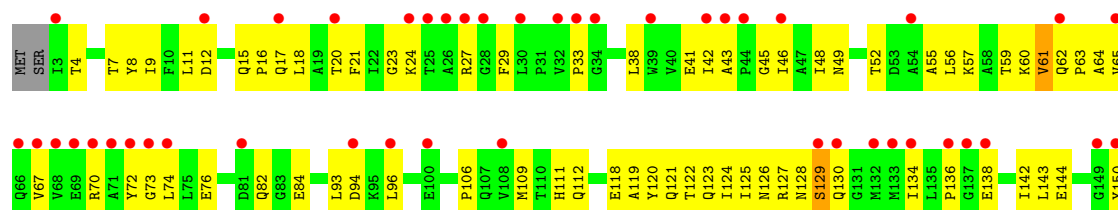
• Molecule 3: Microcompartments protein



• Molecule 3: Microcompartments protein

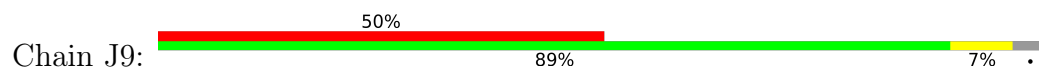


• Molecule 3: Microcompartments protein

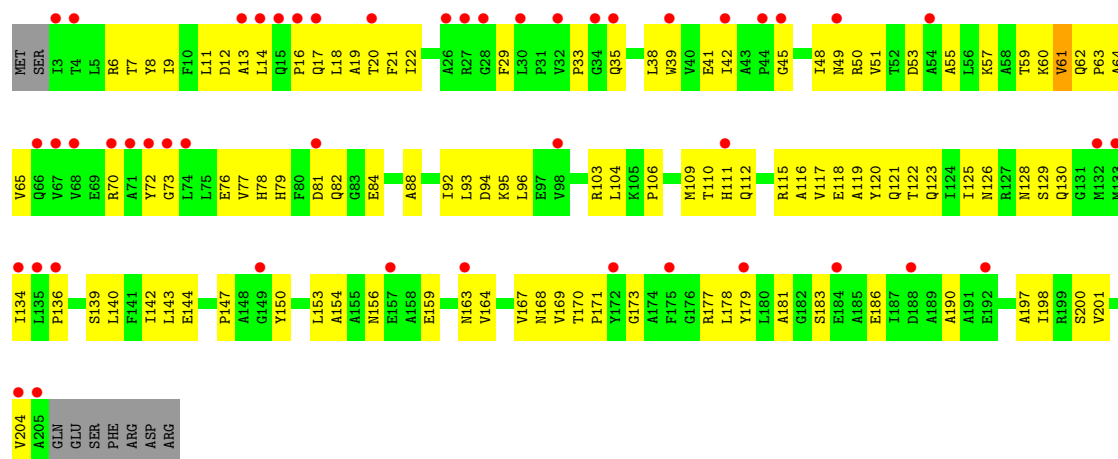




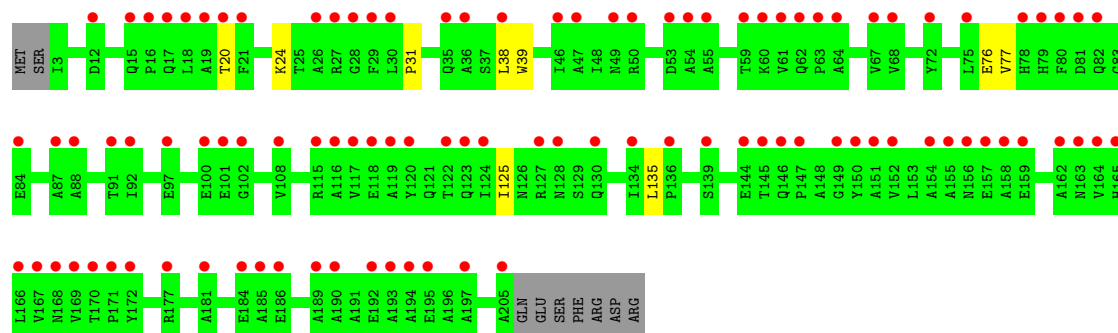
• Molecule 3: Microcompartments protein



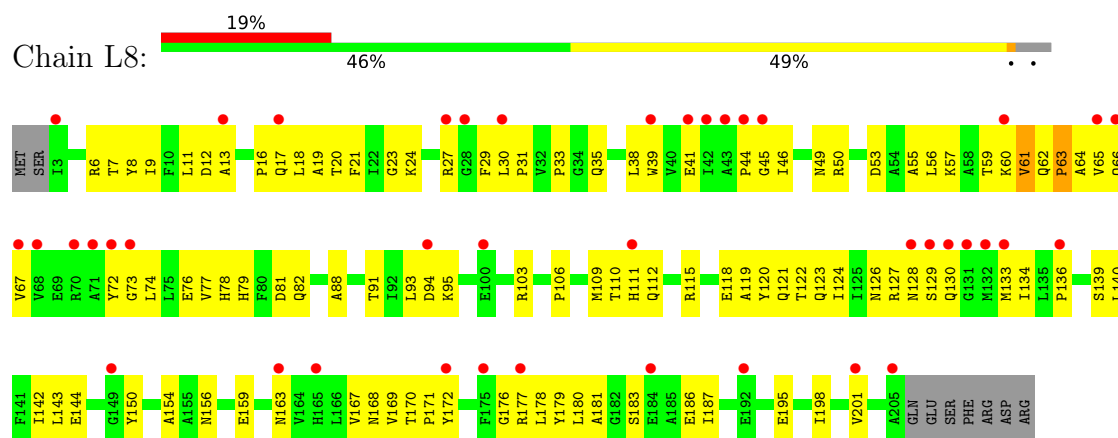
• Molecule 3: Microcompartments protein



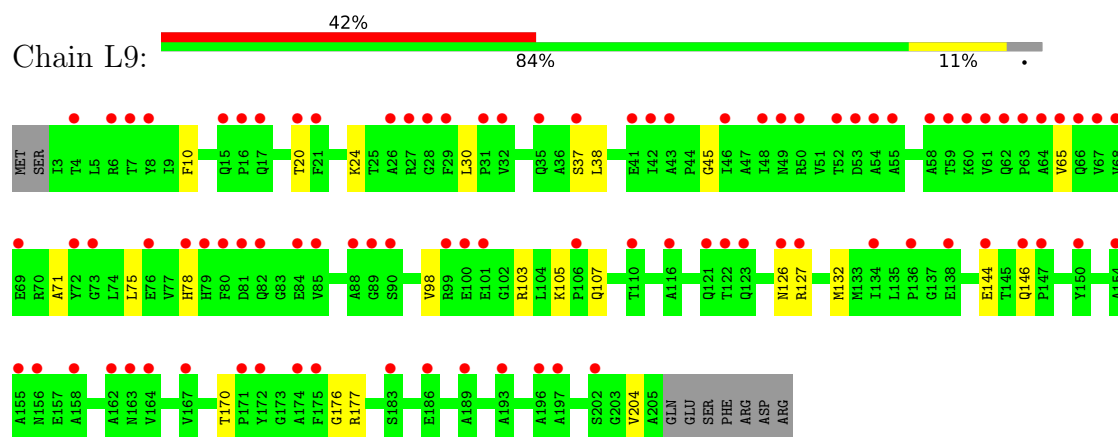
• Molecule 3: Microcompartments protein



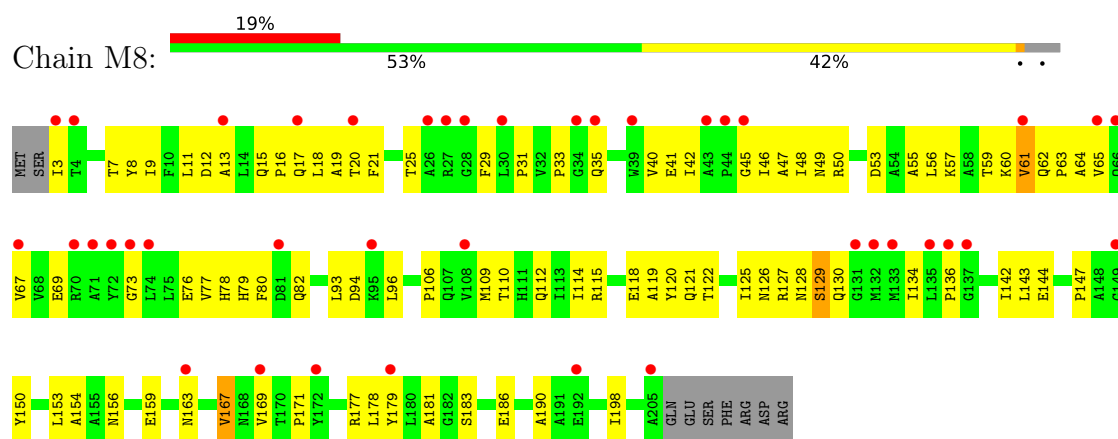
- Molecule 3: Microcompartments protein



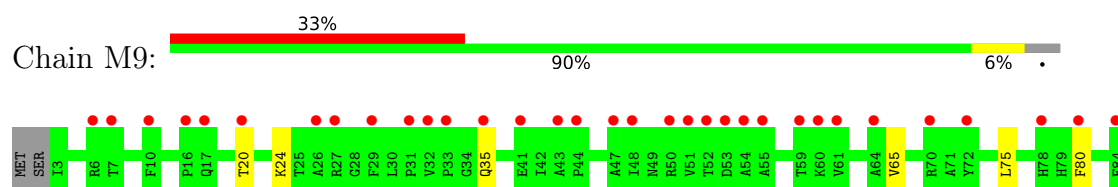
- Molecule 3: Microcompartments protein

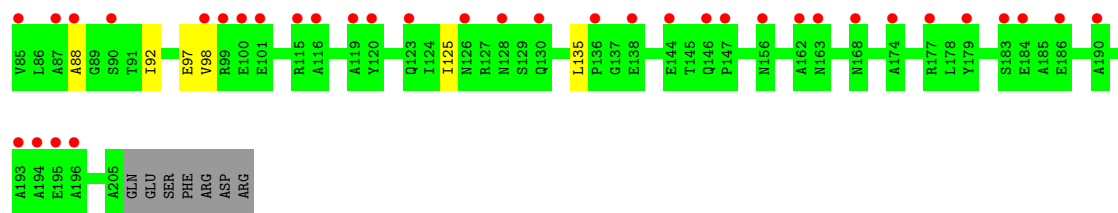


- Molecule 3: Microcompartments protein

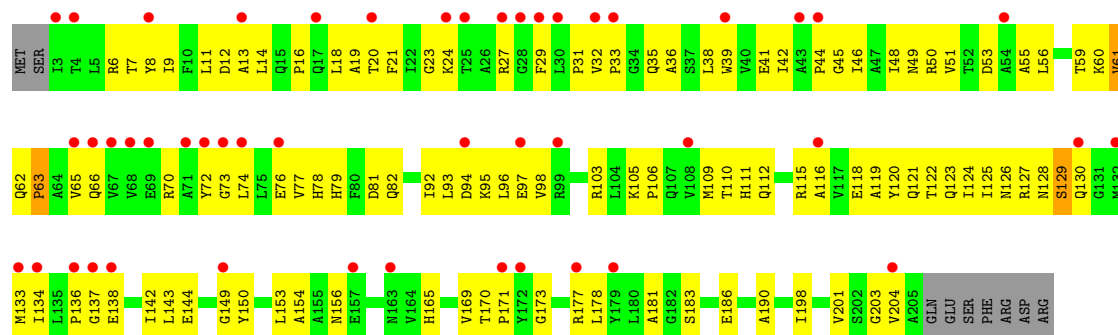


- Molecule 3: Microcompartments protein

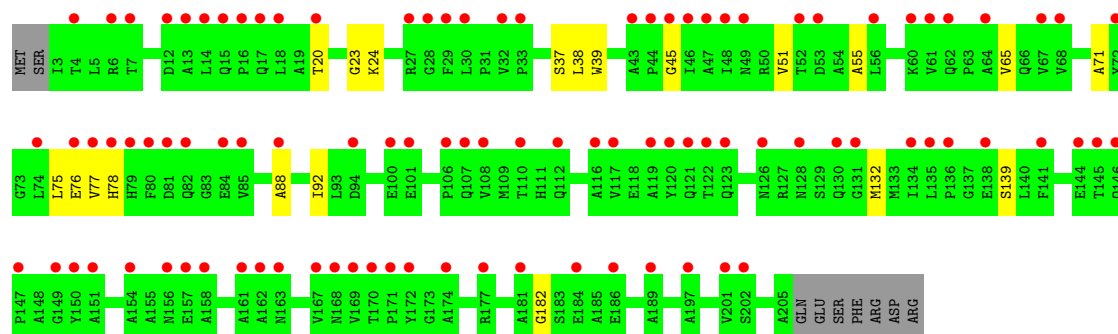
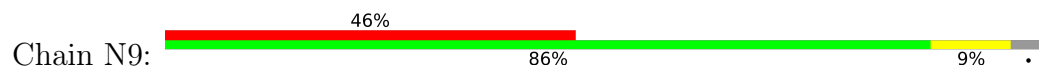




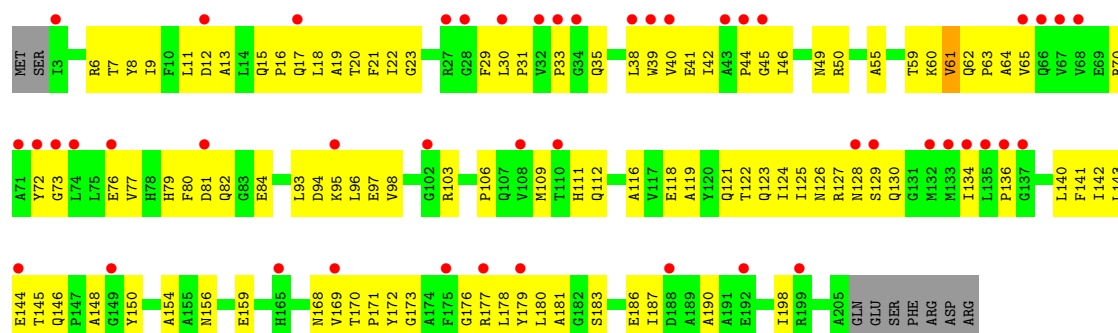
• Molecule 3: Microcompartments protein



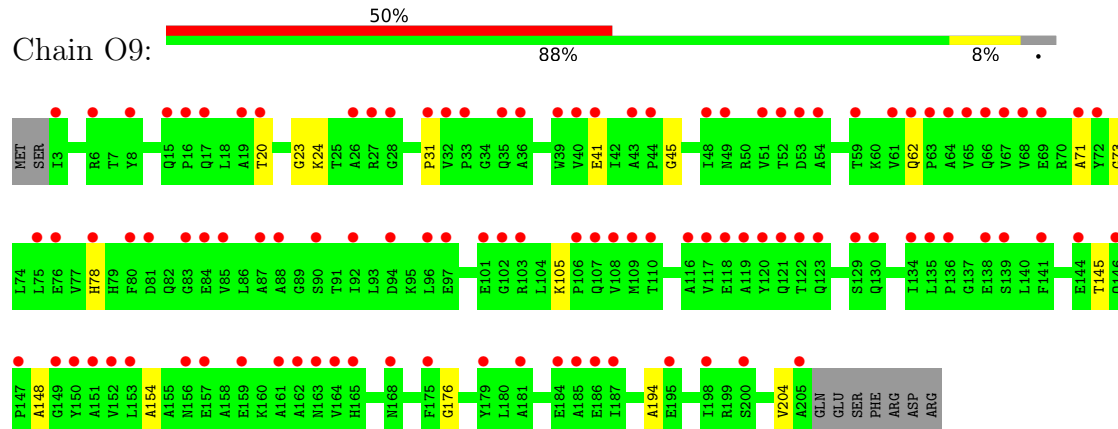
• Molecule 3: Microcompartments protein



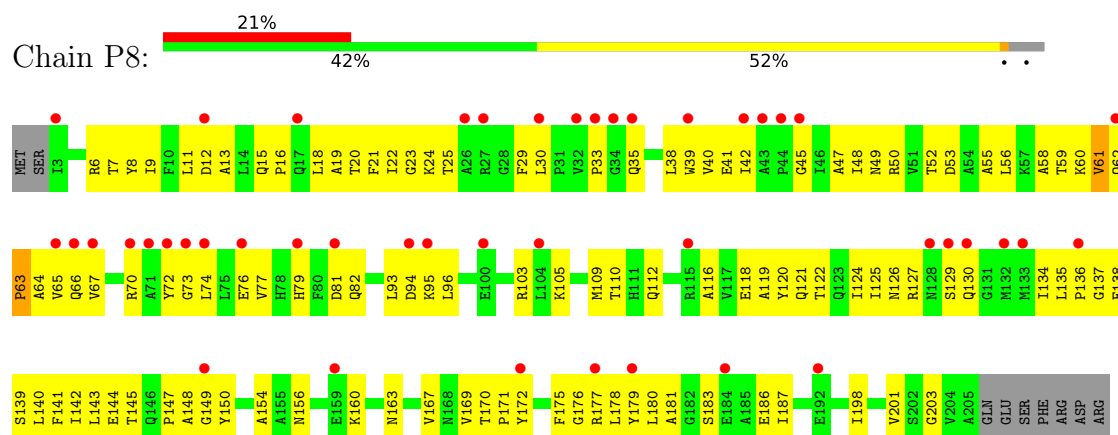
• Molecule 3: Microcompartments protein



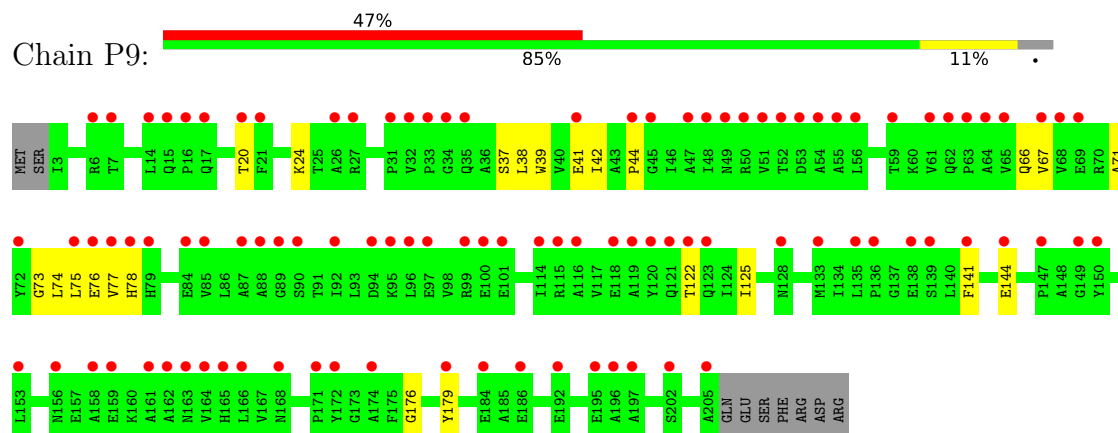
- Molecule 3: Microcompartments protein



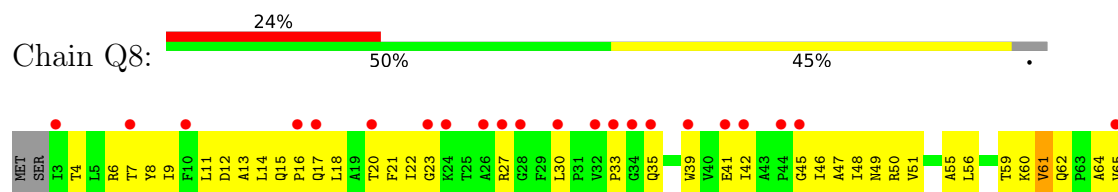
- Molecule 3: Microcompartments protein

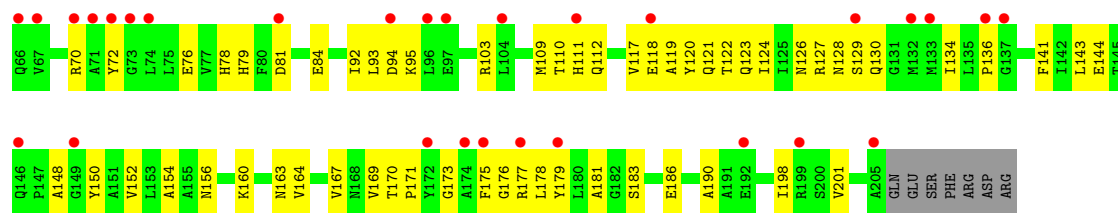


- Molecule 3: Microcompartments protein

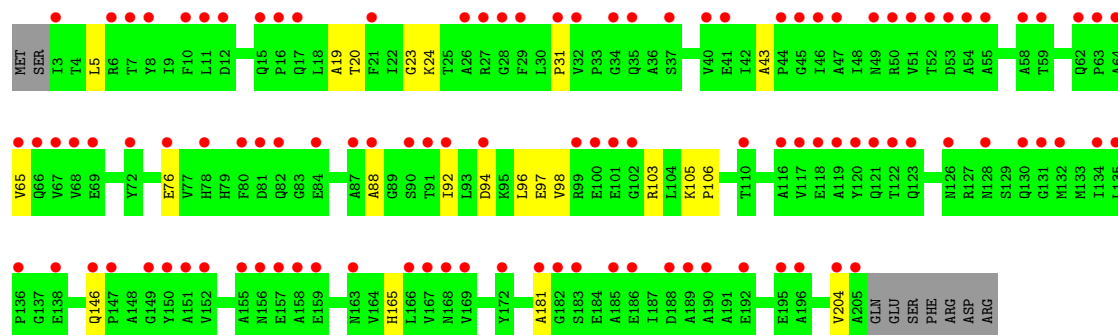
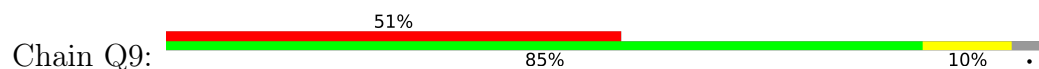


- Molecule 3: Microcompartments protein

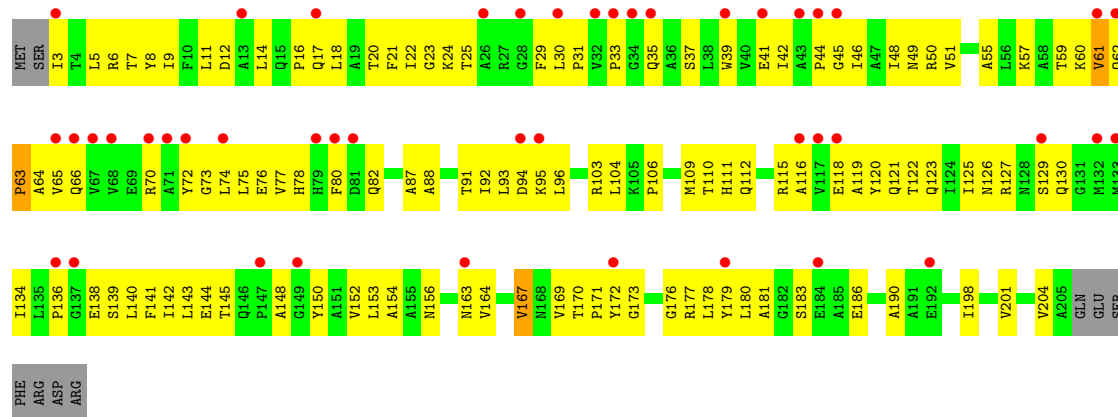
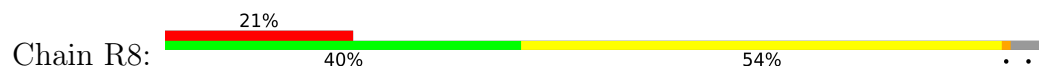




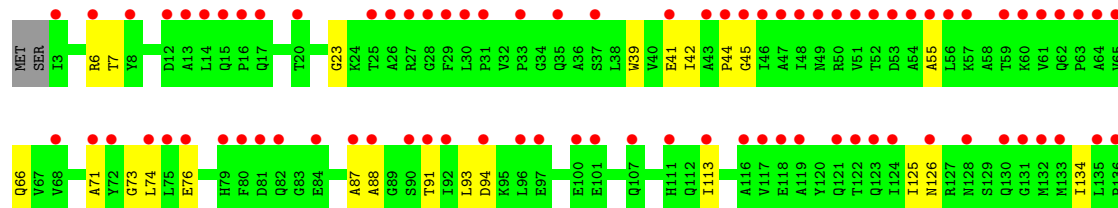
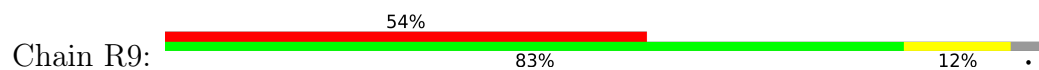
• Molecule 3: Microcompartments protein

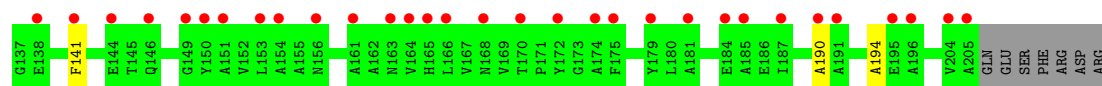


• Molecule 3: Microcompartments protein

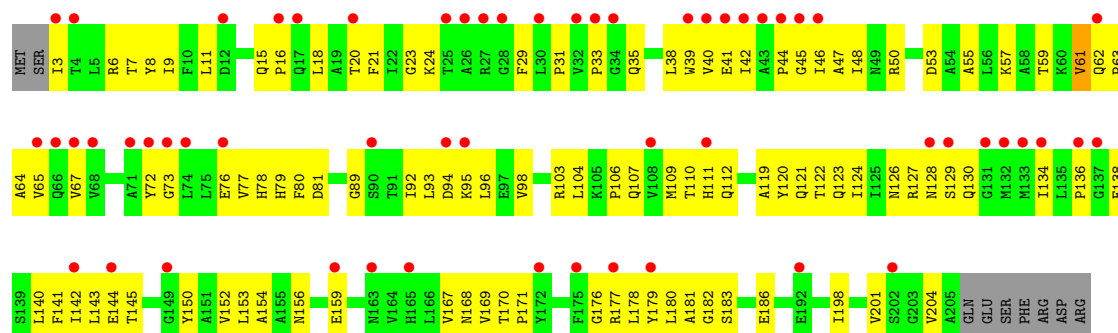


• Molecule 3: Microcompartments protein

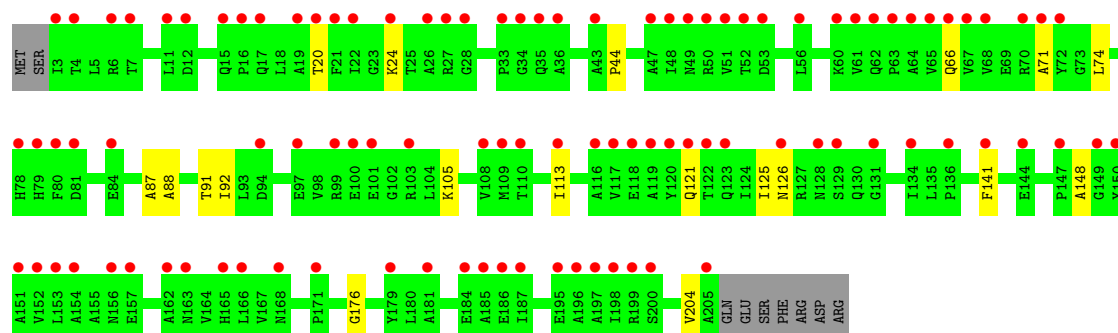




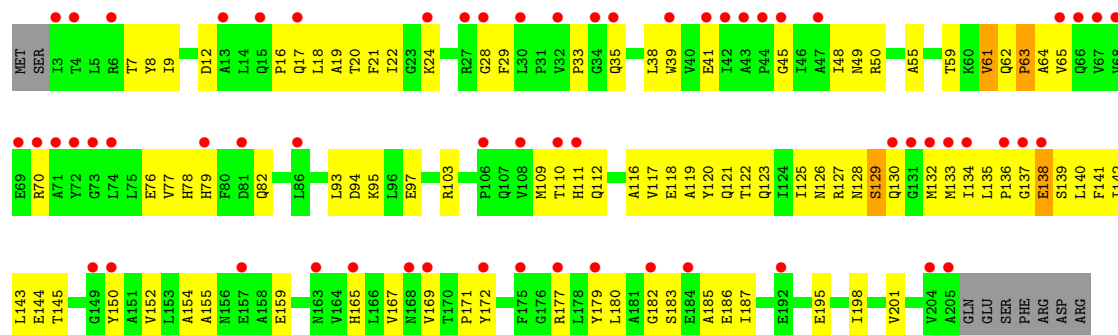
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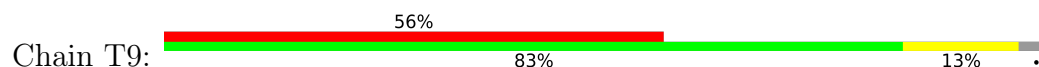
• Molecule 3: Microcompartments protein

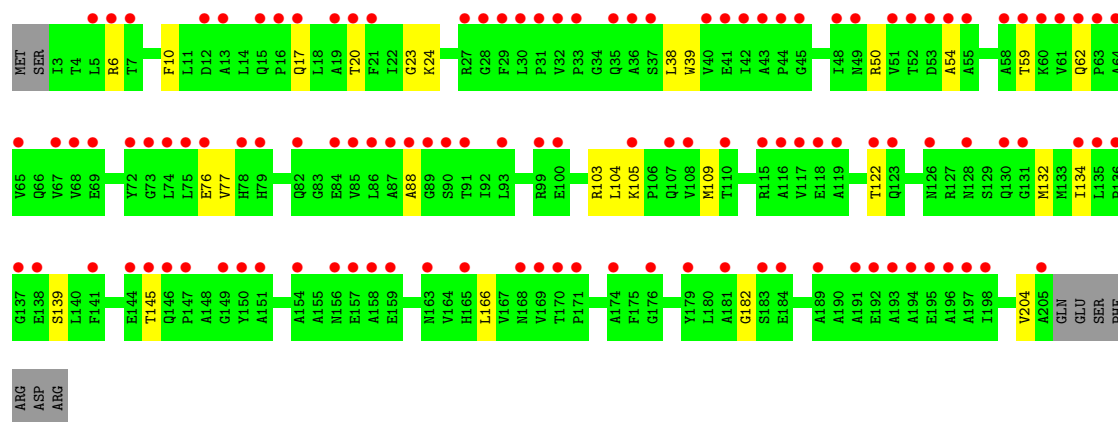


• Molecule 3: Microcompartments protein

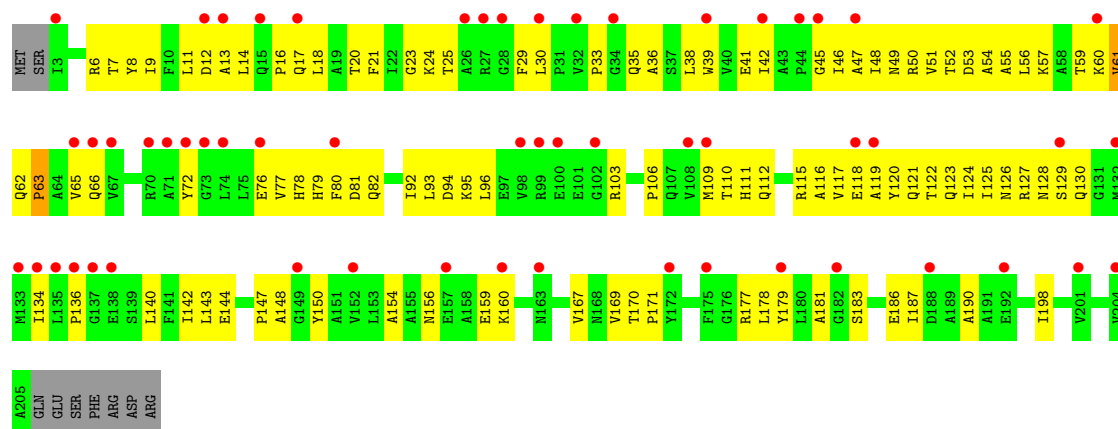


• Molecule 3: Microcompartments protein

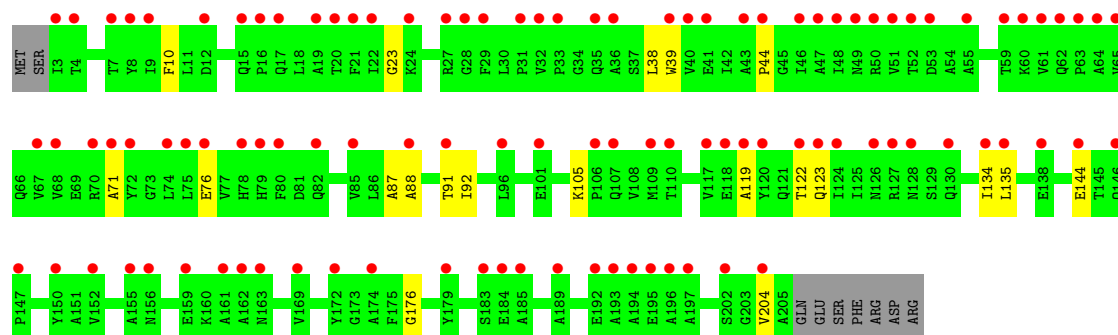
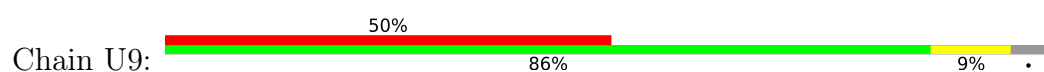




• Molecule 3: Microcompartments protein

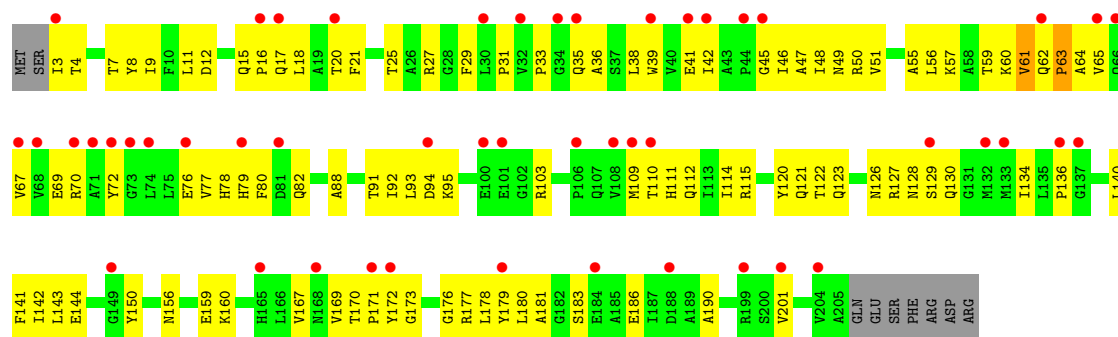


• Molecule 3: Microcompartments protein

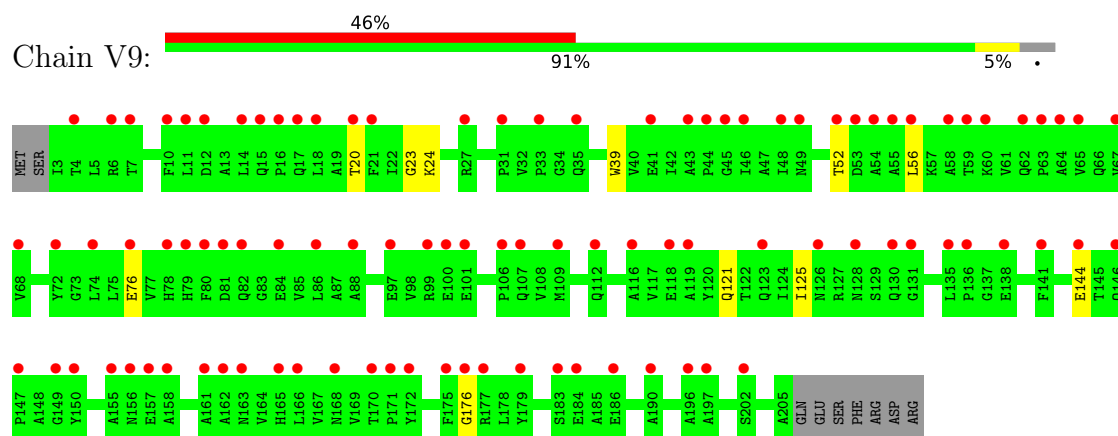


• Molecule 3: Microcompartments protein

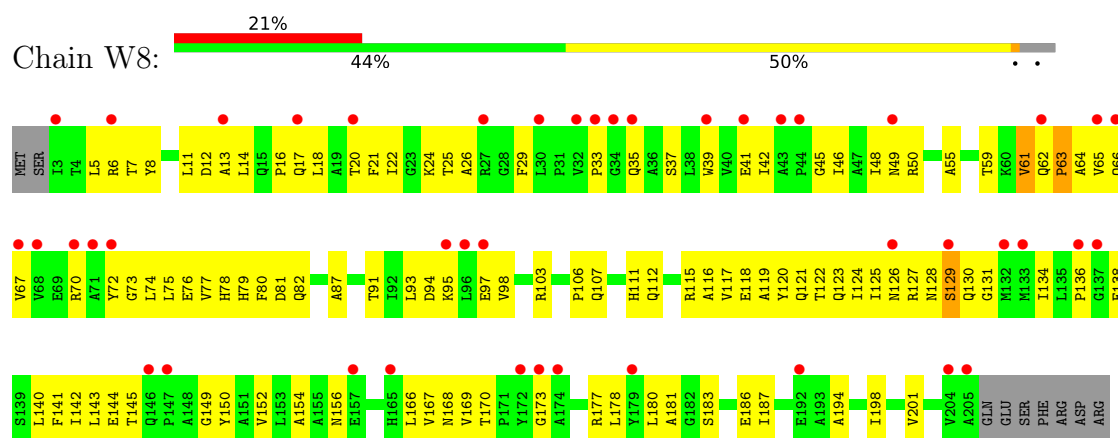




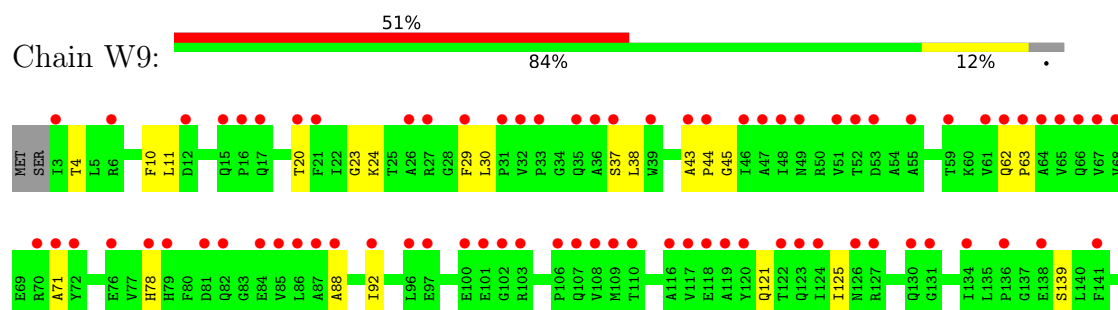
• Molecule 3: Microcompartments protein



• Molecule 3: Microcompartments protein

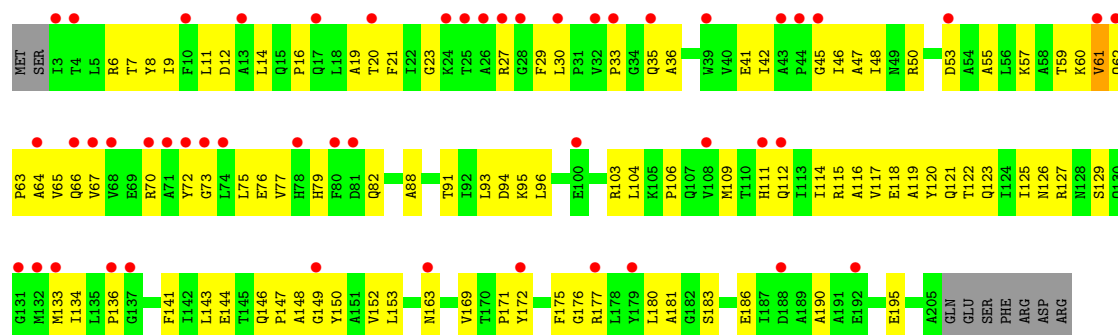


• Molecule 3: Microcompartments protein

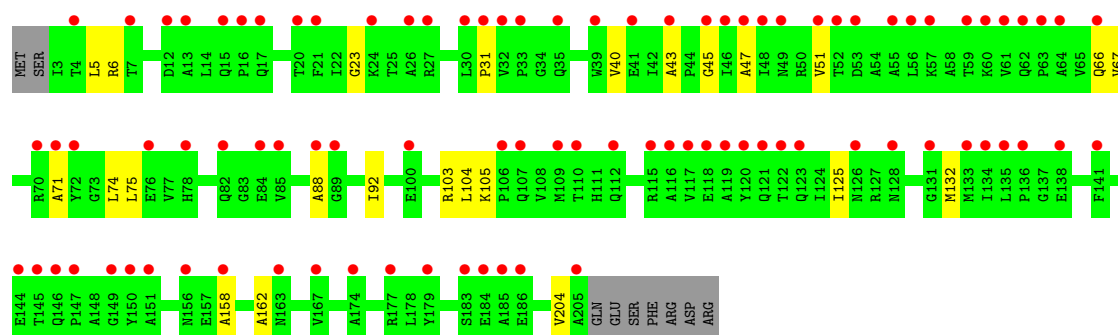
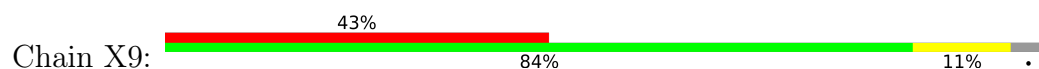




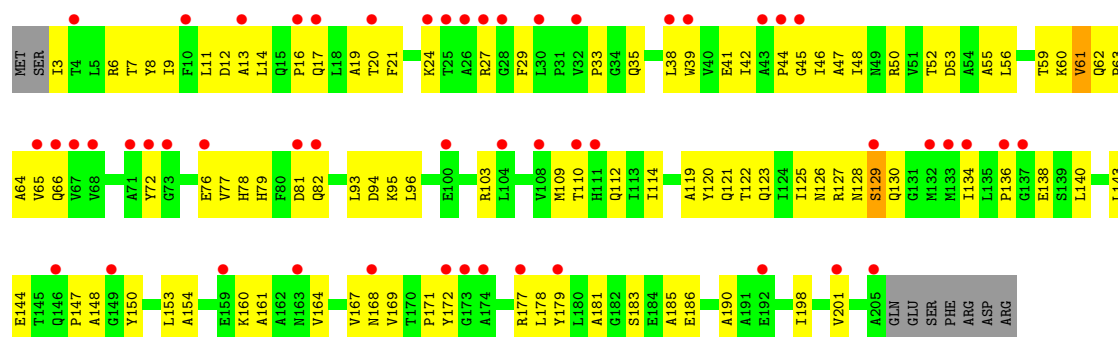
• Molecule 3: Microcompartments protein



• Molecule 3: Microcompartments protein

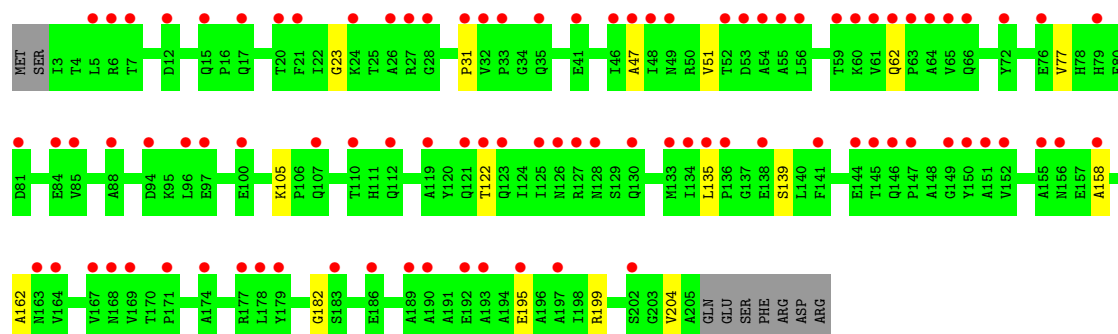


• Molecule 3: Microcompartments protein

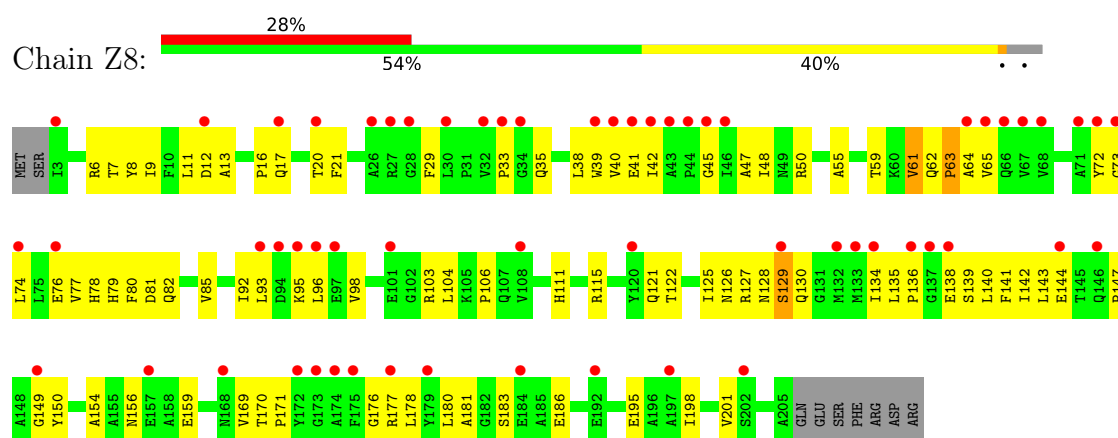


• Molecule 3: Microcompartments protein

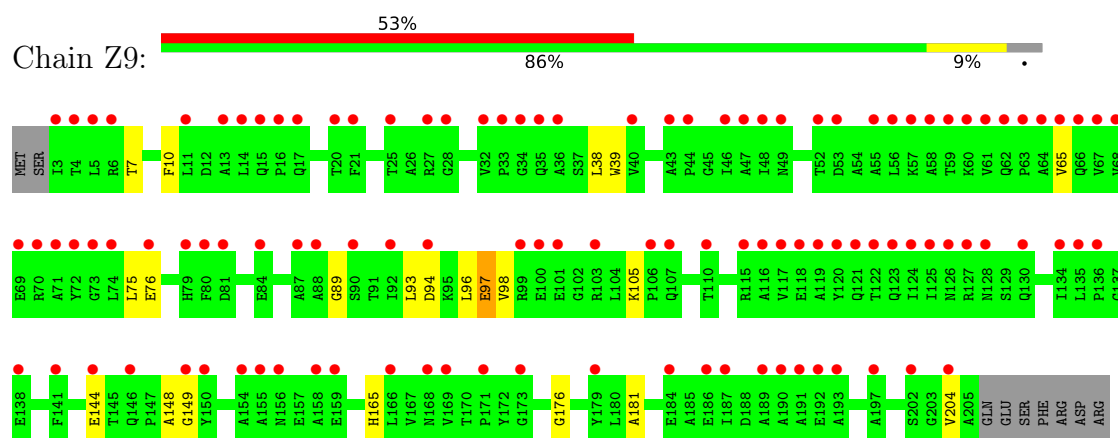




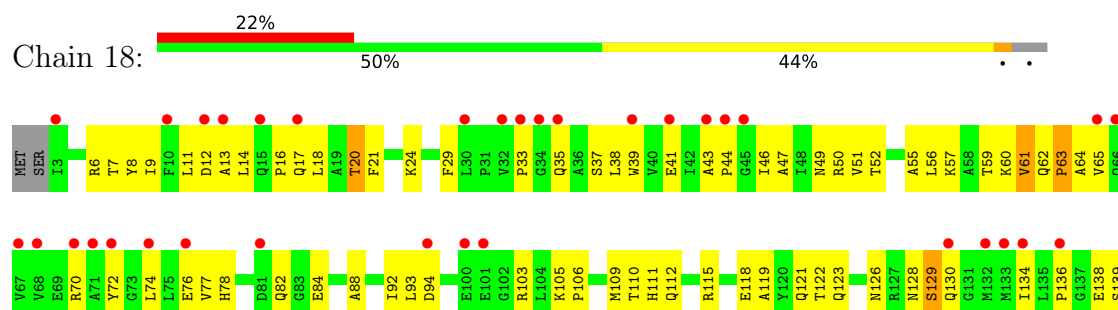
• Molecule 3: Microcompartments protein



• Molecule 3: Microcompartments protein

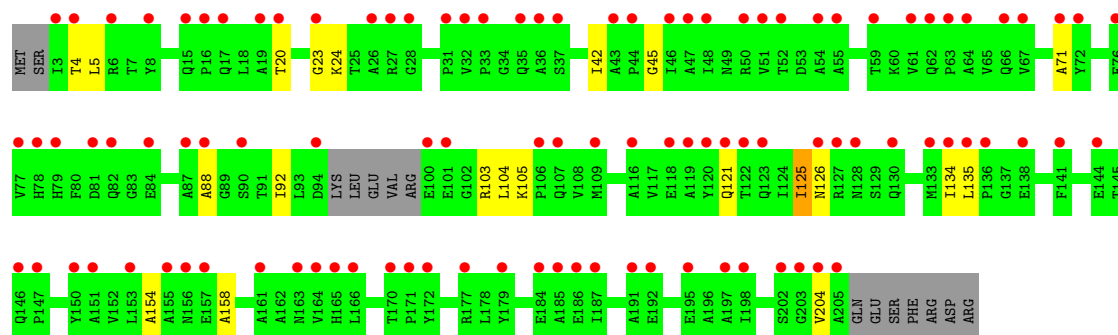
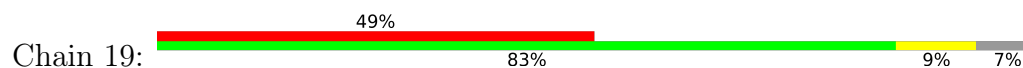


• Molecule 3: Microcompartments protein

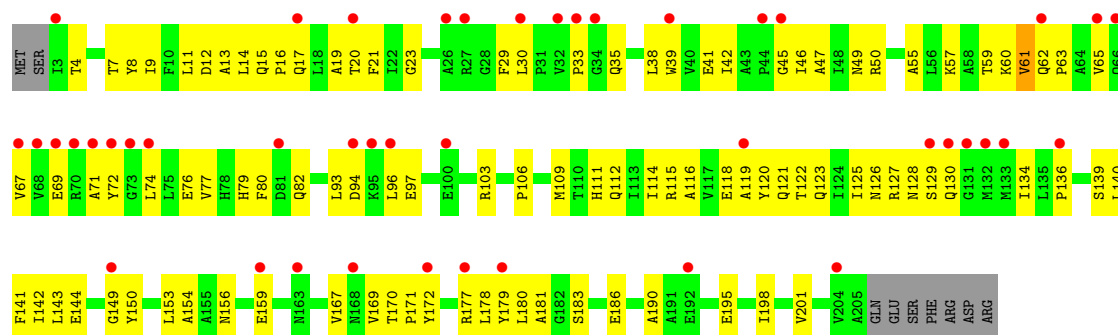




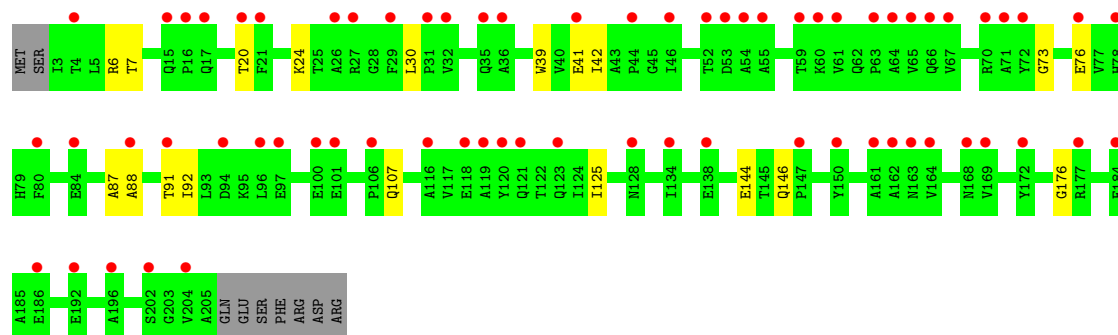
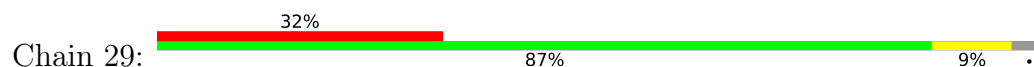
• Molecule 3: Microcompartments protein



• Molecule 3: Microcompartments protein

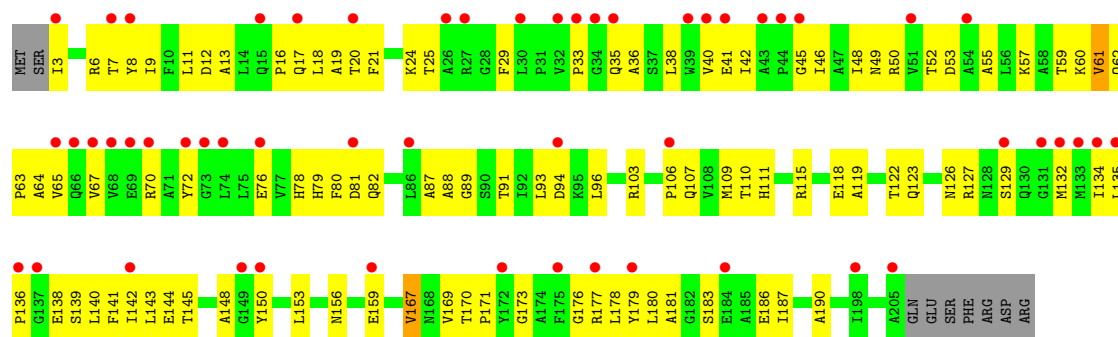


• Molecule 3: Microcompartments protein

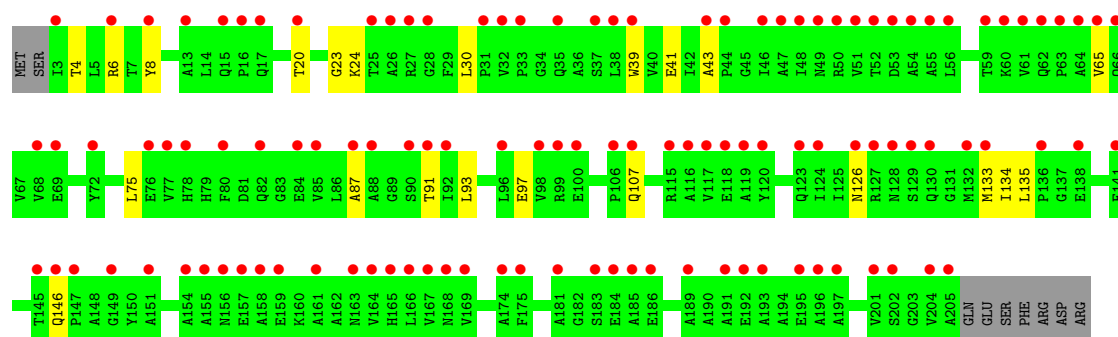
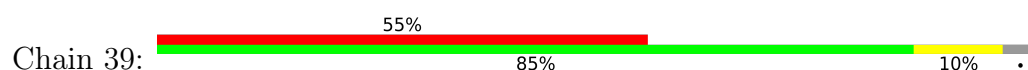


• Molecule 3: Microcompartments protein

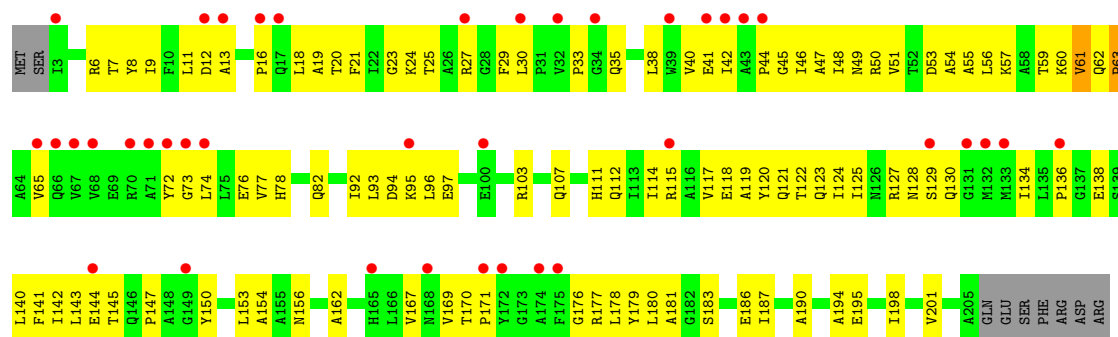




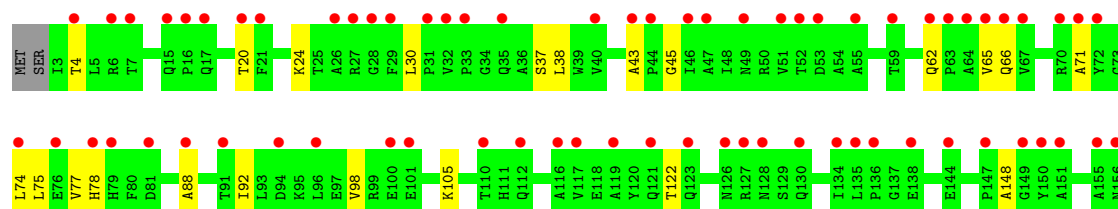
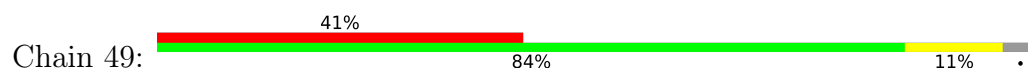
• Molecule 3: Microcompartments protein

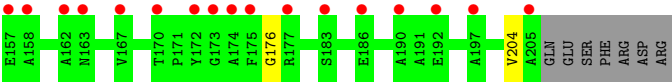


• Molecule 3: Microcompartments protein



• Molecule 3: Microcompartments protein





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	394.34Å 638.09Å 642.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.85 – 3.51 39.85 – 3.51	Depositor EDS
% Data completeness (in resolution range)	88.6 (39.85-3.51) 69.0 (39.85-3.51)	Depositor EDS
R_{merge}	0.01	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 3.48Å)	Xtriage
Refinement program	PHENIX dev_2650	Depositor
R, R_{free}	0.279 , 0.323 0.279 , 0.323	Depositor DCC
R_{free} test set	20031 reflections (2.02%)	wwPDB-VP
Wilson B-factor (Å ²)	66.9	Xtriage
Anisotropy	0.252	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 80.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	215283	wwPDB-VP
Average B, all atoms (Å ²)	101.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 45.33 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.3423e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	11	0.26	0/683	0.58	0/926
1	21	0.28	0/683	0.59	0/926
1	31	0.28	0/674	0.59	0/915
1	41	0.27	0/683	0.56	0/926
1	A1	0.24	0/683	0.55	0/926
1	B1	0.25	0/683	0.59	0/926
1	C1	0.24	0/683	0.55	0/926
1	D1	0.27	0/683	0.58	0/926
1	E1	0.24	0/683	0.56	0/926
1	F1	0.25	0/683	0.57	0/926
1	G1	0.25	0/683	0.55	0/926
1	H1	0.25	0/683	0.58	0/926
1	I1	0.27	0/683	0.57	0/926
1	J1	0.23	0/683	0.56	0/926
1	K1	0.27	0/683	0.57	0/926
1	L1	0.26	0/683	0.57	0/926
1	M1	0.28	0/683	0.60	0/926
1	N1	0.26	0/683	0.57	0/926
1	O1	0.23	0/683	0.59	0/926
1	P1	0.25	0/683	0.57	0/926
1	Q1	0.25	0/683	0.57	0/926
1	R1	0.24	0/683	0.59	0/926
1	S1	0.23	0/683	0.59	0/926
1	T1	0.27	0/683	0.61	0/926
1	U1	0.26	0/683	0.57	1/926 (0.1%)
1	V1	0.23	0/683	0.55	0/926
1	W1	0.26	0/683	0.61	0/926
1	X1	0.24	0/683	0.58	0/926
1	Y1	0.27	0/683	0.55	0/926
1	Z1	0.27	0/683	0.58	0/926
2	12	0.23	0/678	0.52	0/919
2	13	0.21	0/666	0.48	0/904
2	14	0.20	0/678	0.47	0/919
2	15	0.22	0/670	0.52	0/909

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	16	0.22	0/666	0.49	0/904
2	17	0.20	0/670	0.47	0/909
2	22	0.25	0/678	0.54	0/919
2	23	0.25	0/666	0.49	0/904
2	24	0.20	0/678	0.48	0/919
2	25	0.24	0/670	0.54	0/909
2	26	0.22	0/666	0.47	0/904
2	27	0.21	0/670	0.47	0/909
2	32	0.21	0/678	0.54	1/919 (0.1%)
2	33	0.21	0/666	0.50	0/904
2	34	0.23	0/678	0.54	0/919
2	35	0.22	0/670	0.55	0/909
2	36	0.22	0/666	0.47	0/904
2	37	0.21	0/670	0.42	0/909
2	42	0.22	0/678	0.52	0/919
2	43	0.21	0/666	0.52	0/904
2	44	0.21	0/678	0.48	0/919
2	45	0.22	0/670	0.54	0/909
2	46	0.23	0/666	0.52	0/904
2	47	0.21	0/670	0.42	0/909
2	A2	0.22	0/666	0.52	0/904
2	A3	0.22	0/666	0.52	0/904
2	A4	0.20	0/670	0.45	0/909
2	A5	0.22	0/666	0.56	0/904
2	A6	0.24	0/666	0.48	0/904
2	A7	0.21	0/666	0.47	0/904
2	B2	0.24	0/658	0.54	0/892
2	B3	0.21	0/666	0.48	0/904
2	B4	0.21	0/666	0.49	0/904
2	B5	0.22	0/666	0.54	0/904
2	B6	0.23	0/666	0.50	0/904
2	B7	0.22	0/666	0.48	0/904
2	C2	0.21	0/666	0.51	0/904
2	C3	0.21	0/666	0.48	0/904
2	C4	0.21	0/666	0.49	0/904
2	C5	0.22	0/666	0.54	0/904
2	C6	0.20	0/666	0.47	0/904
2	C7	0.21	0/670	0.46	0/909
2	D2	0.23	0/670	0.52	0/909
2	D3	0.22	0/666	0.50	0/904
2	D4	0.21	0/666	0.51	0/904
2	D5	0.21	0/666	0.50	0/904
2	D6	0.22	0/666	0.50	0/904

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	D7	0.22	0/670	0.49	0/909
2	E2	0.22	0/678	0.48	0/919
2	E3	0.21	0/666	0.46	0/904
2	E4	0.20	0/678	0.46	0/919
2	E5	0.20	0/666	0.45	0/904
2	E6	0.22	0/666	0.51	0/904
2	E7	0.21	0/666	0.44	0/904
2	F2	0.21	0/678	0.51	0/919
2	F3	0.20	0/666	0.47	0/904
2	F4	0.21	0/666	0.52	0/904
2	F5	0.20	0/666	0.48	0/904
2	F6	0.20	0/666	0.44	0/904
2	F7	0.21	0/670	0.43	0/909
2	G2	0.19	0/666	0.51	0/904
2	G3	0.21	0/666	0.50	0/904
2	G4	0.21	0/666	0.47	0/904
2	G5	0.22	0/661	0.51	0/897
2	G6	0.19	0/666	0.44	0/904
2	G7	0.21	0/666	0.43	0/904
2	H2	0.22	0/666	0.53	0/904
2	H3	0.23	0/666	0.51	0/904
2	H4	0.21	0/670	0.47	0/909
2	H5	0.22	0/661	0.52	0/897
2	H6	0.22	0/666	0.48	0/904
2	H7	0.20	0/666	0.46	0/904
2	I2	0.23	0/666	0.50	0/904
2	I3	0.21	0/661	0.46	0/897
2	I4	0.21	0/666	0.47	0/904
2	I5	0.23	0/666	0.51	0/904
2	I6	0.23	0/666	0.51	0/904
2	I7	0.20	0/666	0.46	0/904
2	J2	0.22	0/666	0.53	0/904
2	J3	0.22	0/666	0.54	0/904
2	J4	0.20	0/666	0.45	0/904
2	J5	0.25	0/661	0.55	0/897
2	J6	0.24	0/666	0.51	0/904
2	J7	0.21	0/666	0.47	0/904
2	K2	0.23	0/666	0.52	0/904
2	K3	0.21	0/666	0.48	0/904
2	K4	0.20	0/666	0.48	0/904
2	K5	0.22	0/670	0.54	0/909
2	K6	0.20	0/666	0.51	0/904
2	K7	0.20	0/670	0.45	0/909

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	L2	0.23	0/678	0.53	0/919
2	L3	0.25	0/666	0.49	0/904
2	L4	0.19	0/666	0.48	0/904
2	L5	0.22	0/666	0.50	0/904
2	L6	0.21	0/666	0.51	0/904
2	L7	0.23	0/670	0.47	0/909
2	M2	0.24	0/670	0.52	0/909
2	M3	0.22	0/666	0.49	0/904
2	M4	0.22	0/666	0.46	0/904
2	M5	0.22	0/670	0.50	0/909
2	M6	0.24	0/661	0.51	0/897
2	M7	0.23	0/666	0.50	0/904
2	N2	0.22	0/666	0.47	0/904
2	N3	0.21	0/661	0.51	0/897
2	N4	0.22	0/666	0.51	0/904
2	N5	0.24	0/670	0.55	0/909
2	N6	0.22	0/661	0.46	0/897
2	N7	0.21	0/665	0.45	0/902
2	O2	0.22	0/678	0.50	1/919 (0.1%)
2	O3	0.20	0/666	0.50	0/904
2	O4	0.21	0/678	0.47	0/919
2	O5	0.21	0/670	0.49	0/909
2	O6	0.20	0/666	0.47	0/904
2	O7	0.21	0/670	0.46	0/909
2	P2	0.23	0/678	0.49	0/919
2	P3	0.21	0/666	0.48	0/904
2	P4	0.22	0/678	0.46	0/919
2	P5	0.23	0/670	0.53	0/909
2	P6	0.21	0/666	0.48	0/904
2	P7	0.23	0/657	0.49	0/891
2	Q2	0.21	0/678	0.51	0/919
2	Q3	0.23	0/666	0.51	0/904
2	Q4	0.20	0/678	0.46	0/919
2	Q5	0.22	0/670	0.53	0/909
2	Q6	0.22	0/666	0.49	0/904
2	Q7	0.20	0/670	0.45	0/909
2	R2	0.21	0/678	0.47	0/919
2	R3	0.24	0/666	0.53	0/904
2	R4	0.20	0/678	0.48	0/919
2	R5	0.21	0/670	0.52	0/909
2	R6	0.23	0/666	0.56	0/904
2	R7	0.20	0/670	0.43	0/909
2	S2	0.25	0/678	0.52	0/919

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	S3	0.22	0/666	0.48	0/904
2	S4	0.22	0/678	0.50	0/919
2	S5	0.22	0/670	0.53	0/909
2	S6	0.21	0/666	0.49	0/904
2	S7	0.23	0/670	0.46	0/909
2	T2	0.25	0/678	0.59	0/919
2	T3	0.22	0/666	0.54	0/904
2	T4	0.22	0/678	0.53	0/919
2	T5	0.26	0/670	0.60	0/909
2	T6	0.22	0/666	0.53	0/904
2	T7	0.22	0/670	0.49	0/909
2	U2	0.24	0/678	0.55	0/919
2	U3	0.22	0/666	0.48	0/904
2	U4	0.21	0/678	0.48	0/919
2	U5	0.22	0/670	0.49	0/909
2	U6	0.22	0/666	0.49	0/904
2	U7	0.22	0/670	0.46	0/909
2	V2	0.22	0/678	0.49	0/919
2	V3	0.24	0/666	0.52	0/904
2	V4	0.24	0/678	0.52	0/919
2	V5	0.22	0/670	0.51	0/909
2	V6	0.22	0/666	0.47	0/904
2	V7	0.21	0/670	0.47	0/909
2	W2	0.23	0/678	0.52	0/919
2	W3	0.21	0/666	0.50	0/904
2	W4	0.20	0/678	0.51	0/919
2	W5	0.21	0/670	0.52	0/909
2	W6	0.21	0/666	0.49	0/904
2	W7	0.21	0/670	0.50	0/909
2	X2	0.22	0/678	0.49	0/919
2	X3	0.21	0/666	0.50	0/904
2	X4	0.20	0/678	0.46	0/919
2	X5	0.24	0/670	0.51	0/909
2	X6	0.21	0/666	0.50	0/904
2	X7	0.21	0/670	0.43	0/909
2	Y2	0.24	0/678	0.51	0/919
2	Y3	0.22	0/666	0.53	0/904
2	Y4	0.22	0/678	0.46	0/919
2	Y5	0.24	0/665	0.64	0/902
2	Y6	0.22	0/666	0.45	0/904
2	Y7	0.20	0/670	0.44	0/909
2	Z2	0.22	0/678	0.48	0/919
2	Z3	0.21	0/666	0.49	0/904

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	Z4	0.21	0/678	0.47	0/919
2	Z5	0.21	0/670	0.49	0/909
2	Z6	0.21	0/666	0.49	0/904
2	Z7	0.22	0/670	0.48	0/909
3	18	0.23	0/1559	0.57	0/2122
3	19	0.13	0/973	0.41	0/1350
3	28	0.22	0/1559	0.58	0/2122
3	29	0.13	0/999	0.38	0/1388
3	38	0.24	0/1559	0.56	0/2122
3	39	0.15	0/999	0.46	0/1388
3	48	0.23	0/1559	0.55	0/2122
3	49	0.13	0/999	0.37	0/1388
3	A8	0.25	0/1559	0.56	0/2122
3	A9	0.13	0/999	0.35	0/1388
3	B8	0.22	0/1559	0.57	0/2122
3	B9	0.13	0/999	0.42	0/1388
3	C8	0.23	0/1559	0.57	0/2122
3	C9	0.14	0/999	0.37	0/1388
3	D8	0.28	1/1559 (0.1%)	0.59	0/2122
3	D9	0.14	0/999	0.50	2/1388 (0.1%)
3	E8	0.22	0/1559	0.55	0/2122
3	E9	0.13	0/999	0.45	2/1388 (0.1%)
3	F8	0.23	0/1559	0.57	0/2122
3	F9	0.13	0/999	0.43	0/1388
3	G8	0.22	0/1559	0.55	0/2122
3	G9	0.14	0/999	0.41	0/1388
3	H8	0.23	0/1559	0.61	0/2122
3	H9	0.13	0/999	0.44	2/1388 (0.1%)
3	I8	0.23	0/1559	0.56	0/2122
3	I9	0.15	0/999	0.40	0/1388
3	J8	0.21	0/1559	0.58	0/2122
3	J9	0.13	0/999	0.36	0/1388
3	K8	0.23	0/1559	0.58	0/2122
3	K9	0.13	0/999	0.39	0/1388
3	L8	0.22	0/1559	0.55	0/2122
3	L9	0.14	0/999	0.40	0/1388
3	M8	0.22	0/1559	0.58	0/2122
3	M9	0.13	0/999	0.36	0/1388
3	N8	0.23	0/1559	0.59	0/2122
3	N9	0.13	0/999	0.39	0/1388
3	O8	0.23	0/1559	0.58	0/2122
3	O9	0.14	0/999	0.37	0/1388
3	P8	0.27	1/1559 (0.1%)	0.57	0/2122

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	P9	0.14	0/999	0.41	0/1388
3	Q8	0.28	1/1559 (0.1%)	0.57	0/2122
3	Q9	0.13	0/999	0.44	2/1388 (0.1%)
3	R8	0.24	0/1559	0.57	0/2122
3	R9	0.13	0/999	0.40	0/1388
3	S8	0.23	0/1559	0.58	0/2122
3	S9	0.12	0/999	0.40	0/1388
3	T8	0.22	0/1559	0.57	0/2122
3	T9	0.15	0/999	0.49	0/1388
3	U8	0.22	0/1559	0.54	0/2122
3	U9	0.13	0/999	0.38	0/1388
3	V8	0.22	0/1559	0.57	0/2122
3	V9	0.13	0/999	0.37	0/1388
3	W8	0.23	0/1559	0.58	0/2122
3	W9	0.14	0/999	0.40	0/1388
3	X8	0.22	0/1559	0.55	0/2122
3	X9	0.13	0/999	0.44	2/1388 (0.1%)
3	Y8	0.22	0/1559	0.56	0/2122
3	Y9	0.15	0/999	0.39	0/1388
3	Z8	0.24	0/1559	0.56	0/2122
3	Z9	0.13	0/999	0.40	0/1388
All	All	0.22	3/217621 (0.0%)	0.51	13/296423 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	P8	175	PHE	C-N	6.21	1.36	1.33
3	Q8	175	PHE	C-N	5.98	1.36	1.33
3	D8	175	PHE	C-N	5.94	1.36	1.33

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	32	67	VAL	N-CA-C	-6.81	105.95	111.81
1	U1	69	THR	CA-C-O	-6.28	111.52	120.51
3	D9	43	ALA	CA-C-N	6.27	142.06	127.00
3	D9	43	ALA	C-N-CA	6.27	142.06	127.00
3	E9	146	GLN	CA-C-N	6.09	141.62	127.00
3	E9	146	GLN	C-N-CA	6.09	141.62	127.00
3	Q9	43	ALA	CA-C-N	6.00	141.41	127.00
3	Q9	43	ALA	C-N-CA	6.00	141.41	127.00
3	X9	43	ALA	CA-C-N	5.34	139.82	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	X9	43	ALA	C-N-CA	5.34	139.82	127.00
3	H9	43	ALA	CA-C-N	5.18	139.43	127.00
3	H9	43	ALA	C-N-CA	5.18	139.43	127.00
2	O2	67	VAL	N-CA-C	-5.01	107.50	111.81

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	I1	678	0	705	40	0
1	21	678	0	705	30	1
1	31	669	0	692	43	0
1	41	678	0	705	21	1
1	A1	678	0	705	40	0
1	B1	678	0	705	39	0
1	C1	678	0	705	38	0
1	D1	678	0	705	38	0
1	E1	678	0	705	38	0
1	F1	678	0	705	46	0
1	G1	678	0	705	48	0
1	H1	678	0	705	40	0
1	I1	678	0	705	39	0
1	J1	678	0	705	49	0
1	K1	678	0	705	33	2
1	L1	678	0	705	46	0
1	M1	678	0	705	25	1
1	N1	678	0	705	37	2
1	O1	678	0	705	52	0
1	P1	678	0	705	45	0
1	Q1	678	0	705	36	0
1	R1	678	0	705	39	0
1	S1	678	0	705	43	0
1	T1	678	0	705	34	2
1	U1	678	0	705	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	V1	678	0	705	46	0
1	W1	678	0	705	40	0
1	X1	678	0	705	34	1
1	Y1	678	0	705	31	2
1	Z1	678	0	705	54	0
2	12	670	0	690	29	0
2	13	658	0	678	32	0
2	14	670	0	690	19	0
2	15	662	0	681	28	0
2	16	658	0	678	25	0
2	17	662	0	681	13	0
2	22	670	0	690	24	0
2	23	658	0	678	41	0
2	24	670	0	690	21	0
2	25	662	0	681	27	0
2	26	658	0	678	22	0
2	27	662	0	681	20	1
2	32	670	0	690	28	0
2	33	658	0	678	29	0
2	34	670	0	690	26	0
2	35	662	0	681	32	0
2	36	658	0	678	22	0
2	37	662	0	681	16	0
2	42	670	0	690	23	0
2	43	658	0	678	33	0
2	44	670	0	690	16	0
2	45	662	0	681	22	0
2	46	658	0	678	24	0
2	47	662	0	681	23	1
2	A2	658	0	678	35	0
2	A3	658	0	678	37	0
2	A4	662	0	681	23	0
2	A5	658	0	678	29	0
2	A6	658	0	678	19	0
2	A7	658	0	678	24	0
2	B2	651	0	671	30	0
2	B3	658	0	678	33	0
2	B4	658	0	678	17	0
2	B5	658	0	678	34	0
2	B6	658	0	678	23	0
2	B7	658	0	678	25	0
2	C2	658	0	678	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C3	658	0	678	32	0
2	C4	658	0	678	19	0
2	C5	658	0	678	27	0
2	C6	658	0	678	20	0
2	C7	662	0	681	26	0
2	D2	662	0	681	34	0
2	D3	658	0	678	41	0
2	D4	658	0	678	28	0
2	D5	658	0	678	27	0
2	D6	658	0	678	23	0
2	D7	662	0	681	20	0
2	E2	670	0	690	30	0
2	E3	658	0	678	24	0
2	E4	670	0	690	23	0
2	E5	658	0	678	24	0
2	E6	658	0	678	26	0
2	E7	658	0	678	26	0
2	F2	670	0	690	29	0
2	F3	658	0	678	34	0
2	F4	658	0	678	35	0
2	F5	658	0	678	23	0
2	F6	658	0	678	19	0
2	F7	662	0	681	28	0
2	G2	658	0	678	27	0
2	G3	658	0	678	32	0
2	G4	658	0	678	24	0
2	G5	653	0	673	29	0
2	G6	658	0	678	28	0
2	G7	658	0	678	32	0
2	H2	658	0	678	26	0
2	H3	658	0	678	29	0
2	H4	662	0	681	23	0
2	H5	653	0	673	28	0
2	H6	658	0	678	23	0
2	H7	658	0	678	21	0
2	I2	658	0	678	32	0
2	I3	653	0	673	31	0
2	I4	658	0	678	28	0
2	I5	658	0	678	30	0
2	I6	658	0	678	22	0
2	I7	658	0	678	22	0
2	J2	658	0	678	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	J3	658	0	678	35	0
2	J4	658	0	678	22	0
2	J5	653	0	673	21	0
2	J6	658	0	678	21	0
2	J7	658	0	678	28	0
2	K2	658	0	678	26	0
2	K3	658	0	678	16	1
2	K4	658	0	678	22	0
2	K5	662	0	681	18	0
2	K6	658	0	678	19	0
2	K7	662	0	681	19	0
2	L2	670	0	690	37	0
2	L3	658	0	678	28	0
2	L4	658	0	678	28	0
2	L5	658	0	678	36	0
2	L6	658	0	678	27	0
2	L7	662	0	681	26	0
2	M2	662	0	681	24	0
2	M3	658	0	678	23	1
2	M4	658	0	678	20	0
2	M5	662	0	681	34	0
2	M6	653	0	673	16	0
2	M7	658	0	678	28	0
2	N2	658	0	678	28	0
2	N3	653	0	673	24	0
2	N4	658	0	678	20	0
2	N5	662	0	681	31	0
2	N6	653	0	673	24	0
2	N7	657	0	676	21	0
2	O2	670	0	690	27	0
2	O3	658	0	678	26	0
2	O4	670	0	690	15	0
2	O5	662	0	681	26	0
2	O6	658	0	678	22	0
2	O7	662	0	681	25	1
2	P2	670	0	690	30	0
2	P3	658	0	678	32	0
2	P4	670	0	690	22	0
2	P5	662	0	681	24	0
2	P6	658	0	678	22	0
2	P7	649	0	672	30	0
2	Q2	670	0	690	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	Q3	658	0	678	36	0
2	Q4	670	0	690	19	0
2	Q5	662	0	681	25	0
2	Q6	658	0	678	17	0
2	Q7	662	0	681	23	0
2	R2	670	0	690	22	0
2	R3	658	0	678	31	0
2	R4	670	0	690	16	0
2	R5	662	0	681	21	0
2	R6	658	0	678	18	0
2	R7	662	0	681	21	0
2	S2	670	0	690	23	0
2	S3	658	0	678	27	0
2	S4	670	0	690	24	0
2	S5	662	0	681	26	0
2	S6	658	0	678	21	0
2	S7	662	0	681	20	0
2	T2	670	0	690	32	0
2	T3	658	0	678	28	0
2	T4	670	0	690	23	0
2	T5	662	0	681	37	0
2	T6	658	0	678	30	0
2	T7	662	0	681	20	0
2	U2	670	0	690	30	0
2	U3	658	0	678	28	0
2	U4	670	0	690	22	0
2	U5	662	0	681	23	0
2	U6	658	0	678	20	0
2	U7	662	0	681	26	0
2	V2	670	0	690	29	0
2	V3	658	0	678	32	0
2	V4	670	0	690	26	0
2	V5	662	0	681	24	0
2	V6	658	0	678	29	0
2	V7	662	0	681	29	0
2	W2	670	0	690	33	0
2	W3	658	0	678	31	0
2	W4	670	0	690	15	0
2	W5	662	0	681	37	0
2	W6	658	0	678	27	0
2	W7	662	0	681	28	0
2	X2	670	0	690	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	X3	658	0	678	33	1
2	X4	670	0	690	21	0
2	X5	662	0	681	30	0
2	X6	658	0	678	20	0
2	X7	662	0	681	21	0
2	Y2	670	0	690	25	0
2	Y3	658	0	678	34	0
2	Y4	670	0	690	19	0
2	Y5	657	0	676	20	0
2	Y6	658	0	678	23	0
2	Y7	662	0	681	16	0
2	Z2	670	0	690	21	0
2	Z3	658	0	678	27	0
2	Z4	670	0	690	19	0
2	Z5	662	0	681	21	0
2	Z6	658	0	678	17	0
2	Z7	662	0	681	22	0
3	18	1533	0	1560	94	2
3	19	975	0	499	13	0
3	28	1533	0	1560	101	0
3	29	1000	0	510	10	0
3	38	1533	0	1560	95	0
3	39	1000	0	510	14	0
3	48	1533	0	1560	97	0
3	49	1000	0	510	13	0
3	A8	1533	0	1560	95	0
3	A9	1000	0	510	13	0
3	B8	1533	0	1560	117	0
3	B9	1000	0	510	13	0
3	C8	1533	0	1560	112	0
3	C9	1000	0	510	11	0
3	D8	1533	0	1560	96	0
3	D9	1000	0	510	7	0
3	E8	1533	0	1560	95	0
3	E9	1000	0	510	11	0
3	F8	1533	0	1560	97	0
3	F9	1000	0	510	7	0
3	G8	1533	0	1560	96	0
3	G9	1000	0	510	12	0
3	H8	1533	0	1560	107	0
3	H9	1000	0	510	11	0
3	I8	1533	0	1560	104	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	I9	1000	0	510	18	0
3	J8	1533	0	1560	98	0
3	J9	1000	0	510	9	0
3	K8	1533	0	1560	102	2
3	K9	1000	0	510	5	0
3	L8	1533	0	1560	108	0
3	L9	1000	0	510	15	0
3	M8	1533	0	1560	86	0
3	M9	1000	0	510	5	0
3	N8	1533	0	1560	103	0
3	N9	1000	0	510	11	0
3	O8	1533	0	1560	84	4
3	O9	1000	0	510	10	0
3	P8	1533	0	1560	101	0
3	P9	1000	0	510	13	0
3	Q8	1533	0	1560	90	0
3	Q9	1000	0	510	13	0
3	R8	1533	0	1560	110	0
3	R9	1000	0	510	17	0
3	S8	1533	0	1560	93	0
3	S9	1000	0	510	10	0
3	T8	1533	0	1560	77	1
3	T9	1000	0	510	18	0
3	U8	1533	0	1560	102	0
3	U9	1000	0	510	12	0
3	V8	1533	0	1560	89	0
3	V9	1000	0	510	6	0
3	W8	1533	0	1560	89	0
3	W9	1000	0	510	14	0
3	X8	1533	0	1560	89	0
3	X9	1000	0	510	13	0
3	Y8	1533	0	1560	94	0
3	Y9	1000	0	510	11	0
3	Z8	1533	0	1560	77	1
3	Z9	1000	0	510	12	0
All	All	215283	0	205772	7422	14

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 18.

All (7422) 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)
2:C3:35:GLU:OE2	2:D7:36:LYS:NZ	1.66	1.28
2:A7:36:LYS:NZ	2:E3:35:GLU:OE2	1.73	1.20
2:G7:36:LYS:NZ	2:W3:35:GLU:OE2	1.79	1.14
2:P5:3:ASP:OD2	2:P5:91:ARG:NH1	1.82	1.12
2:K7:54:LYS:NZ	2:K7:58:GLU:OE2	1.84	1.09
2:V2:35:GLU:OE2	2:V4:36:LYS:NZ	1.85	1.08
3:V8:9:ILE:HD11	3:V8:150:TYR:HA	1.36	1.07
2:K4:47:ARG:NH1	2:K4:89:LEU:O	1.88	1.07
3:M8:67:VAL:HG12	3:28:127:ARG:HH12	1.11	1.06
2:E4:47:ARG:NH1	2:E4:89:LEU:O	1.88	1.06
1:T1:53:GLU:OE2	1:T1:95:LYS:NZ	1.89	1.06
2:L7:36:LYS:NZ	2:23:35:GLU:OE2	1.89	1.05
2:O5:2:ALA:O	2:O5:78:ARG:NH1	1.91	1.02
2:T4:47:ARG:NH1	2:T4:89:LEU:O	1.91	1.02
3:Z8:9:ILE:HD11	3:Z8:150:TYR:HA	1.40	1.01
3:E8:9:ILE:HD11	3:E8:150:TYR:HA	1.43	1.00
2:S5:35:GLU:OE2	2:32:36:LYS:NZ	1.93	1.00
2:B2:74:HIS:NE2	2:B4:18:GLU:OE2	1.96	0.99
3:38:16:PRO:HA	3:38:33:PRO:HB3	1.45	0.98
2:I7:36:LYS:NZ	2:J3:35:GLU:OE2	1.96	0.98
2:B2:36:LYS:NZ	2:C5:35:GLU:OE2	1.95	0.98
2:43:47:ARG:HH11	2:43:91:ARG:HB2	1.24	0.97
2:M7:36:LYS:NZ	2:N3:35:GLU:OE2	1.97	0.97
2:Q3:47:ARG:HH11	2:Q3:91:ARG:HB2	1.25	0.97
2:T5:35:GLU:OE2	2:U2:36:LYS:NZ	1.97	0.97
2:Y3:32:ILE:HD13	2:Y3:90:GLY:HA3	1.46	0.97
2:S5:3:ASP:O	2:S5:47:ARG:NH1	1.98	0.97
2:J5:47:ARG:NH1	2:J5:84:ASP:OD1	1.99	0.96
3:L8:9:ILE:HD11	3:L8:150:TYR:HA	1.44	0.96
3:R8:60:LYS:HG2	2:U7:78:ARG:HD3	1.47	0.95
2:S7:36:LYS:NZ	2:33:35:GLU:OE2	1.99	0.95
2:J3:47:ARG:NH1	2:J3:84:ASP:OD1	2.00	0.95
1:K1:13:SER:OG	1:L1:83:ASP:OD2	1.85	0.95
2:L4:47:ARG:NH1	2:L4:89:LEU:O	2.00	0.95
2:H5:3:ASP:O	2:H5:47:ARG:NH1	1.97	0.95
2:B7:54:LYS:NZ	2:B7:58:GLU:OE1	2.00	0.94
3:P8:9:ILE:HD11	3:P8:150:TYR:HA	1.48	0.94
3:K8:9:ILE:HD11	3:K8:150:TYR:HA	1.48	0.94
2:E2:9:GLU:OE2	2:E4:13:PHE:N	2.01	0.94
1:Z1:45:ASP:OD2	1:Z1:49:ALA:N	1.98	0.94
2:I4:47:ARG:NH1	2:I4:89:LEU:O	1.99	0.94
2:K7:17:VAL:HG11	2:L3:7:MET:HE1	1.47	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O8:16:PRO:HA	3:O8:33:PRO:HB3	1.45	0.94
1:U1:68:VAL:O	1:U1:72:ARG:NH1	2.00	0.94
2:23:47:ARG:HH11	2:23:91:ARG:HB2	1.33	0.94
3:A8:9:ILE:HD11	3:A8:150:TYR:HA	1.47	0.94
2:B4:47:ARG:NH1	2:B4:89:LEU:O	2.00	0.94
2:A6:25:LYS:NZ	3:G8:57:LYS:O	2.00	0.93
2:K3:47:ARG:HH11	2:K3:91:ARG:HB2	1.33	0.93
2:15:2:ALA:O	2:15:78:ARG:NH1	2.01	0.93
1:W1:45:ASP:OD2	1:W1:49:ALA:N	2.00	0.93
1:G1:94:ARG:NH1	2:G2:49:ASP:OD2	2.00	0.93
2:N5:47:ARG:NH1	2:N5:84:ASP:OD1	2.00	0.93
1:T1:75:ASP:OD2	1:U1:59:SER:N	2.01	0.93
2:M5:34:TYR:OH	2:M6:35:GLU:OE2	1.85	0.93
1:R1:45:ASP:OD2	1:R1:49:ALA:N	2.01	0.93
3:Y8:9:ILE:HD11	3:Y8:150:TYR:HA	1.49	0.93
2:14:47:ARG:NH1	2:14:89:LEU:O	2.01	0.92
2:H5:34:TYR:OH	2:H6:35:GLU:OE2	1.87	0.92
3:H8:60:LYS:HG2	2:Y7:78:ARG:HD3	1.51	0.92
1:A1:28:ARG:HD2	1:A1:36:PRO:HB2	1.48	0.92
2:L3:47:ARG:HH11	2:L3:91:ARG:HB2	1.31	0.92
2:S4:47:ARG:NH1	2:S4:89:LEU:O	2.03	0.92
2:Z4:47:ARG:NH1	2:Z4:89:LEU:O	2.02	0.92
2:D5:3:ASP:OD2	2:D5:91:ARG:NH2	2.02	0.92
1:U1:13:SER:OG	1:41:83:ASP:OD2	1.86	0.92
2:13:32:ILE:HD13	2:13:90:GLY:HA3	1.49	0.92
3:G8:9:ILE:HD11	3:G8:150:TYR:HA	1.51	0.91
2:D4:47:ARG:NH1	2:D4:89:LEU:O	2.02	0.91
3:N8:16:PRO:HA	3:N8:33:PRO:HB3	1.52	0.91
2:G7:54:LYS:NZ	2:G7:58:GLU:OE1	2.04	0.91
3:X8:60:LYS:HG2	2:47:78:ARG:HD3	1.52	0.91
3:18:9:ILE:HD11	3:18:150:TYR:HA	1.50	0.91
2:B5:3:ASP:OD2	2:B5:91:ARG:NE	2.02	0.91
3:I8:9:ILE:HD11	3:I8:150:TYR:HA	1.53	0.91
2:Z2:9:GLU:OE2	2:Z4:13:PHE:N	2.03	0.91
2:E3:47:ARG:HH11	2:E3:91:ARG:HB2	1.35	0.91
1:F1:45:ASP:OD2	1:F1:49:ALA:N	2.02	0.91
2:F2:25:LYS:NZ	1:R1:48:GLY:O	2.03	0.91
3:Q8:9:ILE:HD11	3:Q8:150:TYR:HA	1.53	0.91
2:G5:35:GLU:OE2	2:W2:36:LYS:NZ	2.03	0.90
3:T8:9:ILE:HD11	3:T8:150:TYR:HA	1.54	0.90
2:Z2:3:ASP:O	2:Z2:47:ARG:NH1	2.03	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D7:78:ARG:HD3	3:N8:60:LYS:HG2	1.50	0.90
2:K2:9:GLU:OE2	2:K4:13:PHE:N	2.04	0.90
3:K8:9:ILE:HB	3:K8:39:TRP:HB2	1.53	0.90
3:X8:16:PRO:HA	3:X8:33:PRO:HB3	1.53	0.90
2:43:32:ILE:HD13	2:43:90:GLY:HA3	1.51	0.90
2:M6:17:VAL:HG21	2:M7:7:MET:HE1	1.54	0.90
2:W7:78:ARG:HD3	3:Y8:60:LYS:HG2	1.53	0.90
1:41:45:ASP:OD2	1:41:49:ALA:N	2.04	0.90
2:A3:36:LYS:O	2:B7:36:LYS:NZ	2.05	0.90
2:V6:36:LYS:NZ	2:V7:35:GLU:OE1	2.03	0.90
2:Y4:47:ARG:NH1	2:Y4:89:LEU:O	2.04	0.90
2:34:47:ARG:NH1	2:34:89:LEU:O	2.04	0.90
2:X6:17:VAL:HG21	2:X7:7:MET:HE1	1.54	0.90
2:E7:78:ARG:HD3	3:Q8:60:LYS:HG2	1.54	0.90
2:N4:47:ARG:NH1	2:N4:89:LEU:O	2.05	0.90
2:B7:28:LYS:HA	2:J3:78:ARG:NH1	1.87	0.89
1:S1:45:ASP:OD2	1:S1:49:ALA:N	2.04	0.89
2:B7:78:ARG:HD3	3:J8:60:LYS:HG2	1.52	0.89
3:G8:16:PRO:HA	3:G8:33:PRO:HB3	1.52	0.89
2:N6:17:VAL:HG21	2:N7:7:MET:HE1	1.55	0.89
3:U8:16:PRO:HA	3:U8:33:PRO:HB3	1.54	0.89
1:B1:12:ALA:O	1:B1:15:LYS:NZ	2.05	0.89
1:G1:28:ARG:HH11	1:G1:36:PRO:HB2	1.36	0.89
3:18:16:PRO:HA	3:18:33:PRO:HB3	1.54	0.89
3:R8:16:PRO:HA	3:R8:33:PRO:HB3	1.52	0.89
2:A7:78:ARG:HD3	3:G8:60:LYS:HG2	1.54	0.89
3:M8:16:PRO:HA	3:M8:33:PRO:HB3	1.53	0.89
2:26:17:VAL:HG21	2:27:7:MET:HE1	1.54	0.89
3:J8:16:PRO:HA	3:J8:33:PRO:HB3	1.52	0.89
2:Q5:2:ALA:O	2:Q5:78:ARG:NH1	2.05	0.89
1:T1:13:SER:OG	1:U1:83:ASP:OD2	1.91	0.89
2:U5:34:TYR:OH	2:U6:35:GLU:OE2	1.91	0.89
2:M5:2:ALA:O	2:M5:78:ARG:NH1	2.05	0.88
1:D1:45:ASP:OD2	1:D1:49:ALA:N	2.06	0.88
2:X4:47:ARG:NH1	2:X4:89:LEU:O	2.06	0.88
3:Q8:16:PRO:HA	3:Q8:33:PRO:HB3	1.55	0.88
2:12:30:GLU:OE1	2:12:91:ARG:NH1	2.06	0.88
2:T5:3:ASP:OD2	2:T5:91:ARG:NH2	2.06	0.88
2:36:17:VAL:HG21	2:37:7:MET:HE1	1.54	0.88
2:F4:47:ARG:NH1	2:F4:89:LEU:O	2.07	0.88
2:I2:9:GLU:OE2	2:I4:13:PHE:N	2.07	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I6:17:VAL:HG21	2:I7:7:MET:HE1	1.56	0.88
2:S2:9:GLU:OE2	2:S4:13:PHE:N	2.05	0.88
1:X1:18:ARG:NH1	1:Y1:65:GLN:O	2.06	0.88
2:X6:3:ASP:OD2	2:X6:91:ARG:NE	2.04	0.88
3:Y8:9:ILE:HB	3:Y8:39:TRP:HB2	1.54	0.88
3:H8:16:PRO:HA	3:H8:33:PRO:HB3	1.54	0.88
2:S5:34:TYR:OH	2:S6:35:GLU:OE2	1.90	0.88
2:U4:47:ARG:NH1	2:U4:89:LEU:O	2.07	0.88
2:Y6:17:VAL:HG21	2:Y7:7:MET:HE1	1.53	0.88
1:C1:59:SER:N	1:D1:75:ASP:OD2	2.05	0.88
2:U3:47:ARG:HH11	2:U3:91:ARG:HB2	1.39	0.88
3:E8:67:VAL:HG12	3:F8:127:ARG:HH21	1.36	0.88
1:F1:13:SER:OG	1:G1:83:ASP:OD2	1.91	0.88
1:K1:45:ASP:OD2	1:K1:49:ALA:N	2.06	0.88
2:P5:34:TYR:OH	2:P6:35:GLU:OE2	1.91	0.88
2:S4:3:ASP:OD2	2:S4:91:ARG:NE	2.07	0.88
2:J2:9:GLU:OE2	2:J4:13:PHE:N	2.07	0.87
2:O6:17:VAL:HG21	2:O7:7:MET:HE1	1.54	0.87
2:T2:30:GLU:OE1	2:T2:91:ARG:NH1	2.05	0.87
2:X3:25:LYS:NZ	2:X4:78:ARG:O	2.06	0.87
3:A8:35:GLN:HB3	3:A8:80:PHE:HA	1.55	0.87
2:L2:9:GLU:OE2	2:L4:13:PHE:N	2.07	0.87
2:M7:54:LYS:NZ	2:M7:58:GLU:OE1	2.07	0.87
2:Z6:17:VAL:HG21	2:Z7:7:MET:HE1	1.56	0.87
2:B3:47:ARG:HH11	2:B3:91:ARG:HB2	1.36	0.87
2:P6:17:VAL:HG21	2:P7:5:MET:HE1	1.56	0.87
3:48:16:PRO:HA	3:48:33:PRO:HB3	1.55	0.87
2:F3:7:MET:HE1	2:R7:17:VAL:HG11	1.56	0.87
2:J6:17:VAL:HG21	2:J7:7:MET:HE1	1.54	0.87
2:K2:36:LYS:O	2:K4:36:LYS:NZ	2.07	0.87
1:L1:13:SER:OG	1:21:83:ASP:OD2	1.90	0.87
3:M8:67:VAL:HG12	3:28:127:ARG:NH1	1.89	0.87
2:E3:78:ARG:NH1	2:F7:24:VAL:O	2.07	0.87
1:S1:68:VAL:HA	1:S1:72:ARG:HH12	1.40	0.87
2:V4:47:ARG:NH1	2:V4:89:LEU:O	2.08	0.87
2:W3:17:VAL:HG21	2:W4:7:MET:HE1	1.57	0.87
2:C5:2:ALA:O	2:C5:78:ARG:NH1	2.07	0.87
2:R4:47:ARG:NH1	2:R4:89:LEU:O	2.08	0.87
2:V2:3:ASP:O	2:V2:47:ARG:NH1	2.06	0.87
2:X2:9:GLU:OE2	2:X4:13:PHE:N	2.08	0.87
2:A3:8:ILE:HG22	2:A3:73:VAL:HG22	1.56	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M5:10:VAL:HG11	2:M5:15:GLY:HA3	1.55	0.86
2:P7:52:LYS:NZ	2:P7:56:GLU:OE1	2.08	0.86
2:R2:9:GLU:OE2	2:R4:13:PHE:N	2.07	0.86
2:R3:34:TYR:OH	2:R4:35:GLU:OE2	1.93	0.86
3:Z8:122:THR:HG21	3:Z8:136:PRO:HA	1.57	0.86
2:F2:9:GLU:OE2	2:F4:13:PHE:N	2.06	0.86
1:Y1:45:ASP:OD2	1:Y1:49:ALA:N	2.08	0.86
2:I2:90:GLY:O	2:I2:92:THR:N	2.08	0.86
2:V3:7:MET:HE1	2:W7:17:VAL:HG11	1.57	0.86
3:R8:50:ARG:NE	3:U8:112:GLN:OE1	2.08	0.86
2:K6:17:VAL:HG21	2:K7:7:MET:HE1	1.56	0.86
2:P3:47:ARG:HH11	2:P3:91:ARG:HB2	1.39	0.86
2:A6:17:VAL:HG21	2:A7:7:MET:HE1	1.58	0.86
2:Y3:47:ARG:HH11	2:Y3:91:ARG:HB2	1.40	0.86
2:37:54:LYS:NZ	2:37:58:GLU:OE1	2.08	0.86
2:S6:17:VAL:HG21	2:S7:7:MET:HE1	1.56	0.86
2:C2:3:ASP:OD2	2:C2:91:ARG:NE	2.09	0.85
3:H8:9:ILE:HD11	3:H8:150:TYR:HA	1.57	0.85
1:I1:45:ASP:OD2	1:I1:49:ALA:N	2.09	0.85
2:Q6:17:VAL:HG21	2:Q7:7:MET:HE1	1.58	0.85
2:46:17:VAL:HG21	2:47:7:MET:HE1	1.57	0.85
2:B5:34:TYR:OH	2:B6:35:GLU:OE2	1.93	0.85
1:D1:83:ASP:OD2	1:E1:13:SER:OG	1.93	0.85
2:Q4:47:ARG:NH1	2:Q4:89:LEU:O	2.09	0.85
3:Q8:122:THR:HG21	3:Q8:136:PRO:HA	1.58	0.85
2:B2:9:GLU:OE2	2:B4:13:PHE:N	2.10	0.85
2:V5:34:TYR:OH	2:V6:35:GLU:OE2	1.94	0.85
2:H2:10:VAL:HG11	2:H2:15:GLY:HA3	1.59	0.85
2:W2:90:GLY:O	2:W2:92:THR:N	2.10	0.85
2:D6:17:VAL:HG21	2:D7:7:MET:HE1	1.57	0.85
2:F7:54:LYS:NZ	2:F7:58:GLU:OE1	2.09	0.85
2:D3:3:ALA:O	2:P7:26:LYS:NZ	2.08	0.85
2:K2:30:GLU:OE1	2:K2:91:ARG:NH1	2.08	0.85
2:K3:17:VAL:HG21	2:K4:7:MET:HE1	1.59	0.85
2:B6:17:VAL:HG21	2:B7:7:MET:HE1	1.59	0.85
3:D8:60:LYS:HG2	2:P7:76:ARG:HD3	1.58	0.85
3:T8:154:ALA:HB2	3:T8:198:ILE:HD11	1.58	0.85
1:M1:53:GLU:OE2	2:M5:78:ARG:HB3	1.77	0.85
2:Z2:32:ILE:HD13	2:Z2:90:GLY:HA3	1.57	0.85
2:C4:47:ARG:NH1	2:C4:89:LEU:O	2.09	0.85
2:R5:34:TYR:OH	2:R6:35:GLU:OE2	1.95	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:V3:32:ILE:HD13	2:V3:90:GLY:HA3	1.58	0.85
1:31:45:ASP:OD2	1:31:49:ALA:N	2.10	0.85
2:35:8:ILE:HG12	2:35:73:VAL:HG22	1.56	0.85
2:I3:47:ARG:HH11	2:I3:91:ARG:HB2	1.39	0.84
2:35:34:TYR:OH	2:36:35:GLU:OE2	1.93	0.84
3:H8:121:GLN:NE2	3:W8:49:ASN:OD1	2.10	0.84
3:I8:9:ILE:HB	3:I8:39:TRP:HB2	1.60	0.84
1:Q1:13:SER:OG	1:S1:83:ASP:OD2	1.95	0.84
2:W3:32:ILE:HD13	2:W3:90:GLY:HA3	1.58	0.84
3:C8:16:PRO:HA	3:C8:33:PRO:HB3	1.58	0.84
2:V6:17:VAL:HG21	2:V7:7:MET:HE1	1.60	0.84
2:C3:47:ARG:NH1	2:C3:84:ASP:OD1	2.11	0.84
2:H3:35:GLU:OE2	2:Z7:36:LYS:NZ	2.10	0.84
2:R3:47:ARG:NH1	2:R3:84:ASP:OD1	2.11	0.84
3:Y8:16:PRO:HA	3:Y8:33:PRO:HB3	1.60	0.84
2:43:47:ARG:HH12	2:43:84:ASP:CG	1.85	0.84
2:A3:47:ARG:NH1	2:A3:84:ASP:OD1	2.09	0.84
3:J8:121:GLN:NE2	3:L8:49:ASN:OD1	2.11	0.84
1:O1:16:GLU:CD	1:O1:17:PRO:HD2	2.02	0.84
2:O2:90:GLY:O	2:O2:92:THR:N	2.09	0.84
3:B8:16:PRO:HA	3:B8:33:PRO:HB3	1.59	0.84
2:P2:9:GLU:OE2	2:P4:13:PHE:N	2.09	0.84
2:15:10:VAL:HG11	2:15:15:GLY:HA3	1.60	0.84
2:F5:35:GLU:OE2	2:G2:36:LYS:NZ	2.11	0.84
2:R6:17:VAL:HG21	2:R7:7:MET:HE1	1.58	0.84
3:R8:121:GLN:NE2	3:S8:53:ASP:OD1	2.11	0.84
2:27:54:LYS:NZ	2:27:58:GLU:OE1	2.11	0.84
2:45:36:LYS:NZ	2:46:35:GLU:OE2	2.10	0.84
3:P8:16:PRO:HA	3:P8:33:PRO:HB3	1.59	0.83
3:B8:65:VAL:HG12	3:B8:76:GLU:HB3	1.60	0.83
3:E8:16:PRO:HA	3:E8:33:PRO:HB3	1.61	0.83
2:M2:9:GLU:OE2	2:M4:13:PHE:N	2.10	0.83
3:R8:112:GLN:OE1	3:S8:50:ARG:NE	2.12	0.83
3:D8:122:THR:HG21	3:D8:136:PRO:HA	1.59	0.83
2:K2:90:GLY:O	2:K2:92:THR:N	2.11	0.83
3:U8:154:ALA:HB2	3:U8:198:ILE:HD11	1.61	0.83
1:M1:45:ASP:OD2	1:M1:49:ALA:N	2.10	0.83
3:P8:154:ALA:HB2	3:P8:198:ILE:HD11	1.60	0.83
2:35:2:ALA:O	2:35:78:ARG:NH1	2.11	0.83
3:K8:112:GLN:OE1	3:18:50:ARG:NE	2.12	0.83
2:R3:78:ARG:NH1	2:U7:28:LYS:HA	1.93	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R2:90:GLY:O	2:R2:92:THR:N	2.12	0.83
2:W2:11:ARG:HB3	2:W2:69:GLU:HG2	1.58	0.83
2:47:54:LYS:NZ	2:47:58:GLU:OE1	2.11	0.83
2:F6:17:VAL:HG21	2:F7:7:MET:HE1	1.61	0.83
2:M4:47:ARG:NH1	2:M4:89:LEU:O	2.11	0.83
2:42:90:GLY:O	2:42:92:THR:N	2.10	0.83
2:L6:17:VAL:HG21	2:L7:7:MET:HE1	1.60	0.83
2:C5:58:GLU:O	2:C5:62:ARG:NH2	2.11	0.83
2:U5:2:ALA:O	2:U5:78:ARG:NH1	2.12	0.83
2:E2:10:VAL:HG11	2:E2:15:GLY:HA3	1.59	0.83
1:C1:83:ASP:OD2	1:D1:13:SER:OG	1.96	0.82
2:L7:8:ILE:HG12	2:L7:73:VAL:HG22	1.61	0.82
2:E2:8:ILE:HG12	2:E2:73:VAL:HG22	1.59	0.82
2:F3:47:ARG:HH22	2:F3:79:PRO:HG2	1.43	0.82
1:G1:13:SER:OG	1:W1:83:ASP:OD2	1.96	0.82
2:I5:35:GLU:OE2	2:J2:36:LYS:NZ	2.11	0.82
2:Q2:90:GLY:O	2:Q2:92:THR:N	2.11	0.82
2:V2:90:GLY:O	2:V2:92:THR:N	2.12	0.82
2:V3:47:ARG:HH11	2:V3:91:ARG:HB2	1.44	0.82
1:Z1:83:ASP:OD2	1:11:13:SER:OG	1.96	0.82
2:Z2:30:GLU:OE1	2:Z2:91:ARG:NH1	2.11	0.82
3:18:9:ILE:HB	3:18:39:TRP:HB2	1.59	0.82
2:J5:34:TYR:OH	2:J6:35:GLU:OE2	1.95	0.82
2:T3:3:ASP:OD2	2:T3:91:ARG:NE	2.12	0.82
2:U6:30:GLU:OE1	2:U6:91:ARG:NH2	2.12	0.82
2:A2:90:GLY:O	2:A2:92:THR:N	2.11	0.82
1:R1:28:ARG:HH11	1:R1:36:PRO:HB2	1.44	0.82
3:Z8:16:PRO:HA	3:Z8:33:PRO:HB3	1.60	0.82
2:J2:11:ARG:HB3	2:J2:69:GLU:HG2	1.61	0.82
3:K8:122:THR:HG21	3:K8:136:PRO:HA	1.61	0.82
1:M1:13:SER:OG	1:N1:83:ASP:OD2	1.96	0.82
3:M8:18:LEU:HD11	3:M8:156:ASN:HA	1.61	0.82
1:O1:45:ASP:OD2	1:O1:49:ALA:N	2.11	0.82
2:Q4:10:VAL:HG11	2:Q4:15:GLY:HA3	1.59	0.82
2:T3:32:ILE:HD13	2:T3:90:GLY:HA3	1.62	0.82
3:Q8:9:ILE:HB	3:Q8:39:TRP:HB2	1.61	0.82
3:W8:16:PRO:HA	3:W8:33:PRO:HB3	1.60	0.82
2:X2:90:GLY:O	2:X2:92:THR:N	2.13	0.82
2:17:47:ARG:NH1	2:17:89:LEU:O	2.12	0.82
1:P1:53:GLU:OE2	2:P5:78:ARG:HB3	1.79	0.82
2:U6:17:VAL:HG21	2:U7:7:MET:HE1	1.59	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P5:35:GLU:OE2	2:Q2:36:LYS:NZ	2.13	0.82
2:12:9:GLU:OE2	2:14:13:PHE:N	2.11	0.82
1:A1:45:ASP:OD2	1:A1:49:ALA:N	2.12	0.81
2:M5:8:ILE:HG12	2:M5:73:VAL:HG22	1.62	0.81
2:C6:17:VAL:HG21	2:C7:7:MET:HE1	1.61	0.81
3:D8:50:ARG:NE	3:P8:112:GLN:OE1	2.13	0.81
3:F8:49:ASN:OD1	3:Q8:121:GLN:NE2	2.13	0.81
2:M6:30:GLU:OE1	2:M6:91:ARG:NH1	2.10	0.81
2:S7:17:VAL:HG21	2:33:7:MET:HE1	1.62	0.81
2:V7:28:LYS:HA	2:43:78:ARG:NH1	1.94	0.81
2:X2:3:ASP:O	2:X2:47:ARG:NH1	2.12	0.81
2:Y6:25:LYS:NZ	2:Y7:78:ARG:O	2.10	0.81
2:26:36:LYS:NZ	2:27:35:GLU:OE1	2.13	0.81
2:N2:9:GLU:OE2	2:N4:13:PHE:N	2.13	0.81
2:O3:47:ARG:HH12	2:O3:79:PRO:HG2	1.46	0.81
1:V1:45:ASP:OD2	1:V1:49:ALA:N	2.12	0.81
2:M2:78:ARG:NH1	2:M5:28:LYS:HD3	1.95	0.81
3:A8:121:GLN:NE2	3:G8:49:ASN:OD1	2.13	0.81
2:B2:10:VAL:HG11	2:B2:15:GLY:HA3	1.63	0.81
1:C1:45:ASP:OD2	1:C1:49:ALA:N	2.13	0.81
2:F3:17:VAL:HG21	2:F4:7:MET:HE1	1.63	0.81
3:R8:122:THR:HG21	3:R8:136:PRO:HA	1.63	0.81
2:T3:18:GLU:OE1	2:T4:74:HIS:NE2	2.13	0.81
2:Y5:2:ASP:O	2:Y5:46:ARG:NH2	2.14	0.81
2:12:90:GLY:O	2:12:92:THR:N	2.14	0.81
2:24:47:ARG:NH1	2:24:89:LEU:O	2.14	0.81
2:B6:32:ILE:HD11	2:B6:47:ARG:HD2	1.63	0.81
2:X7:17:VAL:HG21	2:Y3:7:MET:HE1	1.63	0.81
1:H1:13:SER:OG	1:I1:83:ASP:OD2	1.99	0.81
1:N1:28:ARG:NH1	1:N1:36:PRO:HB2	1.96	0.81
3:N8:121:GLN:NE2	3:P8:49:ASN:OD1	2.13	0.81
2:H5:7:MET:HE1	2:I2:17:VAL:HG21	1.62	0.81
2:K7:78:ARG:HD3	3:18:60:LYS:HG2	1.63	0.81
2:L3:32:ILE:HD13	2:L3:90:GLY:HA3	1.60	0.81
2:N2:10:VAL:HG11	2:N2:15:GLY:HA3	1.63	0.81
1:Q1:53:GLU:OE2	2:Q5:78:ARG:HB3	1.80	0.81
2:U2:9:GLU:OE2	2:U4:13:PHE:N	2.12	0.81
2:16:17:VAL:HG21	2:17:7:MET:HE1	1.62	0.81
3:V8:109:MET:HB2	3:V8:144:GLU:HB3	1.61	0.81
3:N8:112:GLN:OE1	3:P8:50:ARG:NE	2.10	0.80
3:18:122:THR:HG21	3:18:136:PRO:HA	1.62	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:22:9:GLU:OE2	2:24:13:PHE:N	2.14	0.80
3:O8:154:ALA:HB2	3:O8:198:ILE:HD11	1.62	0.80
2:R3:3:ASP:OD2	2:R3:91:ARG:NE	2.12	0.80
2:W6:17:VAL:HG21	2:W7:7:MET:HE1	1.62	0.80
1:R1:53:GLU:OE2	2:R5:78:ARG:HB3	1.80	0.80
3:W8:45:GLY:HA3	3:W8:73:GLY:H	1.45	0.80
2:Y3:17:VAL:HG21	2:Y4:7:MET:HE1	1.64	0.80
2:Z7:8:ILE:HG12	2:Z7:73:VAL:HG22	1.64	0.80
2:32:8:ILE:HG12	2:32:73:VAL:HG22	1.63	0.80
3:F8:122:THR:HG21	3:F8:136:PRO:HA	1.63	0.80
2:L2:3:ASP:OD2	2:L2:91:ARG:NE	2.13	0.80
2:M6:36:LYS:NZ	2:M7:35:GLU:OE1	2.14	0.80
2:Q3:32:ILE:HD13	2:Q3:90:GLY:HA3	1.62	0.80
3:N8:65:VAL:HG12	3:N8:76:GLU:HB3	1.64	0.80
3:S8:112:GLN:OE1	3:U8:50:ARG:NE	2.14	0.80
2:13:25:LYS:NZ	2:14:78:ARG:O	2.12	0.80
3:38:122:THR:HG21	3:38:136:PRO:HA	1.64	0.80
2:E3:47:ARG:NH1	2:E3:84:ASP:OD1	2.14	0.80
1:G1:45:ASP:OD2	1:G1:49:ALA:N	2.14	0.80
2:I5:7:MET:HE1	2:J2:17:VAL:HG21	1.63	0.80
3:L8:154:ALA:HB2	3:L8:198:ILE:HD11	1.64	0.80
2:T6:17:VAL:HG21	2:T7:7:MET:HE1	1.62	0.80
3:B8:121:GLN:NE2	3:J8:49:ASN:OD1	2.13	0.80
2:O2:36:LYS:NZ	2:35:35:GLU:OE2	2.13	0.80
2:D2:90:GLY:O	2:D2:92:THR:N	2.14	0.80
3:S8:8:TYR:HE2	3:S8:93:LEU:HB3	1.47	0.80
2:E2:3:ASP:OD2	2:E2:91:ARG:NE	2.10	0.80
3:E8:60:LYS:HG2	2:F7:78:ARG:HD3	1.64	0.80
1:W1:28:ARG:HH11	1:W1:36:PRO:HB2	1.46	0.80
1:L1:45:ASP:OD2	1:L1:49:ALA:N	2.15	0.79
3:S8:16:PRO:HA	3:S8:33:PRO:HB3	1.63	0.79
1:21:53:GLU:OE2	2:25:78:ARG:HB3	1.82	0.79
2:35:47:ARG:NH1	2:35:84:ASP:OD1	2.13	0.79
2:B2:19:ALA:HB2	2:B2:64:ALA:HB2	1.65	0.79
2:T6:36:LYS:NZ	2:T7:35:GLU:OE1	2.15	0.79
2:Y2:9:GLU:OE2	2:Y4:13:PHE:N	2.14	0.79
2:Q7:54:LYS:NZ	2:Q7:58:GLU:OE1	2.15	0.79
2:S2:3:ASP:O	2:S2:47:ARG:NH1	2.14	0.79
2:S3:47:ARG:HH12	2:S3:79:PRO:HG2	1.46	0.79
1:X1:53:GLU:OE2	2:X5:78:ARG:HB3	1.82	0.79
1:E1:28:ARG:NH1	1:E1:36:PRO:HB2	1.97	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K5:8:ILE:HG12	2:K5:73:VAL:HG22	1.62	0.79
3:K8:45:GLY:HA3	3:K8:73:GLY:H	1.46	0.79
2:P3:8:ILE:HG12	2:P3:73:VAL:HG22	1.64	0.79
3:E8:122:THR:HG21	3:E8:136:PRO:HA	1.64	0.79
2:Q7:8:ILE:HG12	2:Q7:73:VAL:HG22	1.64	0.79
1:R1:65:GLN:O	1:V1:18:ARG:NH1	2.15	0.79
2:L5:36:LYS:NZ	2:L6:35:GLU:OE2	2.14	0.79
2:22:47:ARG:HD3	2:22:91:ARG:HG2	1.63	0.79
3:R8:45:GLY:HA3	3:R8:73:GLY:H	1.47	0.79
2:A3:78:ARG:NH1	2:I7:28:LYS:HA	1.98	0.79
2:I5:3:ASP:OD2	2:I5:91:ARG:NH2	2.15	0.79
2:M3:47:ARG:HH11	2:M3:91:ARG:HB2	1.46	0.79
1:B1:53:GLU:OE2	2:B5:78:ARG:HB3	1.82	0.79
2:P5:3:ASP:CG	2:P5:91:ARG:HH11	1.90	0.79
2:R7:47:ARG:NH1	2:R7:89:LEU:O	2.16	0.79
2:C2:9:GLU:OE2	2:C4:13:PHE:N	2.14	0.79
1:J1:45:ASP:OD2	1:J1:49:ALA:N	2.15	0.79
2:K5:7:MET:HE1	2:L2:17:VAL:HG21	1.65	0.79
2:T2:8:ILE:HG12	2:T2:73:VAL:HG22	1.64	0.79
2:T3:5:LEU:HD11	2:T3:7:MET:HE3	1.65	0.79
3:U8:122:THR:HG21	3:U8:136:PRO:HA	1.65	0.79
1:21:45:ASP:OD2	1:21:49:ALA:N	2.15	0.79
3:H8:9:ILE:HB	3:H8:39:TRP:HB2	1.64	0.78
3:T8:9:ILE:HB	3:T8:39:TRP:HB2	1.64	0.78
2:W5:10:VAL:HG11	2:W5:15:GLY:HA3	1.65	0.78
2:H2:8:ILE:HG12	2:H2:73:VAL:HG22	1.64	0.78
2:P3:47:ARG:HH12	2:P3:84:ASP:CG	1.90	0.78
1:V1:53:GLU:OE2	2:V5:78:ARG:HB3	1.83	0.78
2:Z3:45:VAL:HG11	2:Z3:89:LEU:HD12	1.65	0.78
2:13:47:ARG:HH21	2:13:91:ARG:HB2	1.47	0.78
3:C8:112:GLN:OE1	3:28:50:ARG:NE	2.16	0.78
1:G1:28:ARG:NH1	1:G1:36:PRO:HB2	1.98	0.78
2:H4:47:ARG:NH1	2:H4:89:LEU:O	2.17	0.78
2:I4:5:LEU:HB3	2:I4:76:ILE:HB	1.64	0.78
2:L5:35:GLU:OE2	2:22:36:LYS:NZ	2.14	0.78
2:M2:30:GLU:OE1	2:M2:91:ARG:NH1	2.17	0.78
2:Q5:3:ASP:O	2:Q5:47:ARG:NH2	2.15	0.78
3:W8:112:GLN:OE1	3:Y8:50:ARG:NE	2.15	0.78
2:X7:8:ILE:HG12	2:X7:73:VAL:HG22	1.65	0.78
1:11:45:ASP:OD2	1:11:49:ALA:N	2.16	0.78
2:27:8:ILE:HG12	2:27:73:VAL:HG22	1.66	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A1:53:GLU:OE2	2:A5:78:ARG:HB3	1.83	0.78
3:A8:50:ARG:NE	3:I8:112:GLN:OE1	2.16	0.78
2:N4:19:ALA:O	2:N4:23:MET:HG3	1.84	0.78
3:T9:6:ARG:O	3:T9:104:LEU:N	2.12	0.78
2:Y5:9:VAL:HG11	2:Y5:14:GLY:HA3	1.64	0.78
2:33:34:TYR:OH	2:34:35:GLU:OE2	2.02	0.78
2:F7:8:ILE:HG12	2:F7:73:VAL:HG22	1.65	0.78
2:Y2:30:GLU:OE1	2:Y2:91:ARG:NH1	2.15	0.78
2:D2:17:VAL:HG21	2:E5:7:MET:HE1	1.65	0.78
2:F2:90:GLY:O	2:F2:92:THR:N	2.16	0.78
2:R7:8:ILE:HG12	2:R7:73:VAL:HG22	1.65	0.78
2:T2:90:GLY:O	2:T2:92:THR:N	2.14	0.78
2:23:47:ARG:HH12	2:23:84:ASP:CG	1.91	0.78
3:A8:38:LEU:HB2	3:A8:85:VAL:HG13	1.64	0.78
2:Q2:9:GLU:OE2	2:Q4:13:PHE:N	2.16	0.78
2:B2:8:ILE:HG12	2:B2:73:VAL:HG22	1.66	0.78
2:B5:30:GLU:OE1	2:B5:91:ARG:NH2	2.16	0.78
2:C6:3:ASP:OD2	2:C6:91:ARG:NE	2.13	0.78
1:U1:45:ASP:OD2	1:U1:49:ALA:N	2.16	0.78
2:D5:2:ALA:O	2:D5:78:ARG:NH1	2.16	0.78
1:G1:53:GLU:OE2	2:G5:78:ARG:HB3	1.84	0.78
3:K8:134:ILE:HD11	3:K8:140:LEU:HD13	1.66	0.78
3:T8:121:GLN:NE2	3:38:49:ASN:OD1	2.17	0.78
2:D3:18:VAL:HG21	2:D4:7:MET:HE1	1.66	0.78
2:G6:17:VAL:HG21	2:G7:7:MET:HE1	1.66	0.78
3:W8:12:ASP:O	3:W8:82:GLN:NE2	2.17	0.78
3:F8:16:PRO:HA	3:F8:33:PRO:HB3	1.65	0.77
2:I2:8:ILE:HG12	2:I2:73:VAL:HG22	1.65	0.77
1:X1:45:ASP:OD2	1:X1:49:ALA:N	2.16	0.77
2:E5:34:TYR:OH	2:E6:35:GLU:OE2	2.02	0.77
1:L1:86:GLU:HG2	2:L2:28:LYS:HB2	1.65	0.77
2:Z7:3:ASP:OD2	2:Z7:91:ARG:NH2	2.15	0.77
2:E2:90:GLY:O	2:E2:92:THR:N	2.17	0.77
2:J6:5:LEU:HB3	2:J6:76:ILE:HG23	1.67	0.77
2:K2:8:ILE:HG12	2:K2:73:VAL:HG22	1.65	0.77
3:O8:128:ASN:O	3:O8:168:ASN:ND2	2.17	0.77
2:R5:8:ILE:HG12	2:R5:73:VAL:HG22	1.66	0.77
2:B3:17:VAL:HG21	2:B4:7:MET:HE1	1.67	0.77
3:48:45:GLY:HA3	3:48:73:GLY:H	1.49	0.77
2:A2:10:VAL:HG11	2:A2:15:GLY:HA3	1.65	0.77
2:N7:28:LYS:HA	2:P3:78:ARG:NH1	1.99	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:22:90:GLY:O	2:22:92:THR:N	2.18	0.77
2:B2:30:GLU:OE1	2:B2:91:ARG:NH1	2.15	0.77
3:J8:20:THR:HB	3:J8:24:LYS:HZ1	1.50	0.77
2:M7:8:ILE:HG12	2:M7:73:VAL:HG22	1.66	0.77
2:N5:3:ASP:HB3	2:N5:49:ASP:H	1.49	0.77
3:W8:122:THR:HG21	3:W8:136:PRO:HA	1.66	0.77
3:C8:122:THR:HG21	3:C8:136:PRO:HA	1.64	0.77
2:F2:10:VAL:HG11	2:F2:15:GLY:HA3	1.65	0.77
1:W1:28:ARG:NH1	1:W1:36:PRO:HB2	2.00	0.77
2:A5:3:ASP:O	2:A5:47:ARG:NH2	2.18	0.77
3:G8:127:ARG:HH12	3:I8:67:VAL:HG12	1.48	0.77
2:R7:78:ARG:NH2	3:S8:57:LYS:O	2.18	0.77
2:S3:32:ILE:HD11	2:S3:47:ARG:HG3	1.67	0.77
2:13:17:VAL:HG21	2:14:7:MET:HE1	1.66	0.77
2:V2:8:ILE:HG12	2:V2:73:VAL:HG22	1.67	0.77
2:Y2:8:ILE:HG12	2:Y2:73:VAL:HG22	1.66	0.77
2:Z2:13:PHE:HE2	2:15:35:GLU:HG2	1.50	0.77
2:Z2:90:GLY:O	2:Z2:92:THR:N	2.16	0.77
2:23:47:ARG:NH1	2:23:84:ASP:OD1	2.16	0.77
3:28:16:PRO:HA	3:28:33:PRO:HB3	1.65	0.77
3:28:45:GLY:HA3	3:28:72:TYR:HB2	1.67	0.77
2:A2:8:ILE:HG12	2:A2:73:VAL:HG22	1.66	0.77
2:G3:13:PHE:HB2	2:G4:37:THR:HG21	1.66	0.77
2:H6:17:VAL:HG21	2:H7:7:MET:HE1	1.67	0.77
2:E4:10:VAL:HG11	2:E4:15:GLY:HA3	1.66	0.76
2:J6:32:ILE:HD13	2:J6:90:GLY:HA3	1.68	0.76
1:A1:13:SER:OG	1:E1:83:ASP:OD2	2.00	0.76
1:H1:28:ARG:NH1	1:H1:36:PRO:HB2	2.01	0.76
2:J3:17:VAL:HG21	2:J4:7:MET:HE1	1.65	0.76
2:L2:30:GLU:OE1	2:L2:91:ARG:NH1	2.17	0.76
2:M5:35:GLU:OE2	2:N2:36:LYS:NZ	2.17	0.76
3:A8:60:LYS:HG2	2:I7:78:ARG:HD3	1.67	0.76
2:D3:35:TYR:OH	2:D4:35:GLU:OE2	2.03	0.76
2:D3:48:ARG:HH11	2:D3:92:ARG:HB2	1.50	0.76
2:K2:84:ASP:O	2:K2:92:THR:OG1	2.03	0.76
2:W2:45:VAL:HG11	2:W2:89:LEU:HD12	1.66	0.76
1:X1:13:SER:OG	1:Y1:83:ASP:OD2	2.00	0.76
3:X8:141:PHE:HB3	3:X8:180:LEU:HB2	1.66	0.76
2:E6:17:VAL:HG21	2:E7:7:MET:HE1	1.67	0.76
3:I8:45:GLY:HA2	3:I8:48:ILE:HD13	1.67	0.76
2:O4:47:ARG:NH1	2:O4:89:LEU:O	2.19	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P8:109:MET:HB2	3:P8:144:GLU:HB3	1.67	0.76
2:S2:10:VAL:HG11	2:S2:15:GLY:HA3	1.67	0.76
3:Y8:123:GLN:NE2	3:Y9:31:PRO:O	2.18	0.76
3:A8:58:ALA:HA	2:I6:25:LYS:NZ	2.01	0.76
2:E6:32:ILE:HG12	2:E6:90:GLY:HA3	1.66	0.76
2:M3:47:ARG:HH22	2:M3:79:PRO:HG2	1.51	0.76
2:O3:34:TYR:OH	2:O4:35:GLU:OE2	2.01	0.76
2:V2:25:LYS:NZ	1:W1:48:GLY:O	2.18	0.76
3:X8:126:ASN:HA	3:X8:129:SER:HB3	1.68	0.76
3:Z8:134:ILE:HG12	3:Z8:181:ALA:HB2	1.67	0.76
3:C8:127:ARG:HH12	3:28:67:VAL:HG12	1.50	0.76
3:E8:12:ASP:O	3:E8:82:GLN:NE2	2.18	0.76
1:H1:45:ASP:OD2	1:H1:49:ALA:N	2.18	0.76
2:L3:5:LEU:HD13	2:L3:47:ARG:HD3	1.67	0.76
2:Q5:8:ILE:HG12	2:Q5:73:VAL:HG22	1.67	0.76
1:R1:83:ASP:OD2	1:V1:13:SER:OG	2.02	0.76
2:S7:78:ARG:HD3	3:U8:60:LYS:HG2	1.67	0.76
1:V1:28:ARG:HH11	1:V1:36:PRO:HB2	1.51	0.76
2:X3:17:VAL:HG21	2:X4:7:MET:HE1	1.67	0.76
2:D7:10:VAL:HG11	2:D7:15:GLY:HA3	1.68	0.76
3:M8:69:GLU:CD	3:28:127:ARG:HH22	1.93	0.76
2:O3:5:LEU:HD13	2:O3:47:ARG:HD3	1.68	0.76
3:I8:122:THR:HG21	3:I8:136:PRO:HA	1.68	0.76
2:P4:47:ARG:NH1	2:P4:89:LEU:O	2.18	0.76
3:R8:21:PHE:O	3:R8:25:THR:OG1	2.02	0.76
3:S8:109:MET:HB2	3:S8:144:GLU:HB3	1.66	0.76
2:W4:47:ARG:NH1	2:W4:89:LEU:O	2.18	0.76
3:B8:122:THR:HG21	3:B8:136:PRO:HA	1.67	0.76
2:G5:7:MET:HE1	2:W2:17:VAL:HG21	1.67	0.76
3:H8:18:LEU:HD11	3:H8:156:ASN:HA	1.68	0.76
1:J1:13:SER:OG	1:11:83:ASP:OD2	2.02	0.76
3:N8:45:GLY:HA2	3:N8:48:ILE:HD13	1.67	0.76
2:12:8:ILE:HG12	2:12:73:VAL:HG22	1.65	0.76
3:38:55:ALA:O	3:38:59:THR:OG1	2.04	0.76
2:C6:13:PHE:HB2	2:C7:37:THR:HG21	1.68	0.76
3:D8:49:ASN:OD1	3:P8:121:GLN:NE2	2.18	0.76
1:F1:18:ARG:NH1	1:G1:65:GLN:O	2.19	0.76
3:P8:21:PHE:O	3:P8:25:THR:OG1	2.04	0.76
2:A7:17:VAL:HG11	2:E3:7:MET:HE1	1.66	0.75
3:B8:49:ASN:OD1	3:L8:121:GLN:NE2	2.18	0.75
2:G7:28:LYS:HA	2:I3:78:ARG:NH1	2.00	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P2:90:GLY:O	2:P2:92:THR:N	2.15	0.75
2:R3:13:PHE:HB2	2:R4:37:THR:HG21	1.68	0.75
2:R5:3:ASP:O	2:R5:47:ARG:NH2	2.19	0.75
1:31:53:GLU:OE2	2:35:78:ARG:HB3	1.86	0.75
2:A6:32:ILE:HG21	2:A6:90:GLY:HA3	1.68	0.75
2:H5:8:ILE:HG12	2:H5:73:VAL:HG22	1.67	0.75
2:15:47:ARG:NH1	2:15:84:ASP:OD1	2.17	0.75
2:37:8:ILE:HG12	2:37:73:VAL:HG22	1.68	0.75
2:P3:19:ALA:HB2	2:P3:64:ALA:HB2	1.68	0.75
3:S8:121:GLN:NE2	3:U8:49:ASN:OD1	2.19	0.75
3:18:170:THR:HG1	3:18:177:ARG:H	1.34	0.75
2:E3:17:VAL:HG21	2:E4:7:MET:HE1	1.68	0.75
3:G8:121:GLN:NE2	3:I8:49:ASN:OD1	2.18	0.75
2:H2:90:GLY:O	2:H2:92:THR:N	2.19	0.75
2:X2:8:ILE:HG12	2:X2:73:VAL:HG22	1.69	0.75
2:26:32:ILE:HD13	2:26:90:GLY:HA3	1.67	0.75
2:G2:90:GLY:O	2:G2:92:THR:N	2.16	0.75
3:H8:49:ASN:O	3:Y8:121:GLN:NE2	2.18	0.75
3:J8:55:ALA:O	3:J8:59:THR:OG1	2.04	0.75
2:O3:17:VAL:HG21	2:O4:7:MET:HE1	1.67	0.75
2:T7:28:LYS:HA	2:33:78:ARG:NH1	2.02	0.75
2:X3:47:ARG:HH22	2:X3:79:PRO:HG2	1.50	0.75
1:J1:53:GLU:OE2	2:J5:78:ARG:HB3	1.87	0.75
2:M2:19:ALA:HB2	2:M2:64:ALA:HB2	1.68	0.75
2:C3:18:GLU:OE1	2:C4:74:HIS:NE2	2.17	0.75
2:E5:8:ILE:HG12	2:E5:73:VAL:HG22	1.68	0.75
1:J1:28:ARG:NH1	1:J1:36:PRO:HB2	2.02	0.75
2:W5:2:ALA:O	2:W5:78:ARG:NH1	2.19	0.75
3:38:12:ASP:O	3:38:82:GLN:NE2	2.19	0.75
2:C2:17:VAL:HG21	2:D5:7:MET:HE1	1.67	0.75
2:D5:34:TYR:OH	2:D6:35:GLU:OE2	2.05	0.75
2:E4:3:ASP:OD2	2:E4:91:ARG:NE	2.20	0.75
2:H7:25:LYS:NZ	2:I3:78:ARG:O	2.16	0.75
3:K8:16:PRO:HA	3:K8:33:PRO:HB3	1.67	0.75
3:N8:55:ALA:O	3:N8:59:THR:OG1	2.03	0.75
2:T2:45:VAL:HG11	2:T2:89:LEU:HD12	1.68	0.75
2:W2:9:GLU:OE2	2:W4:13:PHE:N	2.18	0.75
3:D8:16:PRO:HA	3:D8:33:PRO:HB3	1.66	0.75
2:22:8:ILE:HG12	2:22:73:VAL:HG22	1.69	0.75
3:I8:106:PRO:HB2	3:I8:198:ILE:HG23	1.68	0.74
3:I9:10:PHE:HA	3:I9:38:LEU:HA	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J2:10:VAL:HG11	2:J2:15:GLY:HA3	1.69	0.74
2:U5:8:ILE:HG12	2:U5:73:VAL:HG22	1.70	0.74
3:28:65:VAL:HG12	3:28:76:GLU:HB3	1.69	0.74
1:A1:75:ASP:OD2	1:E1:59:SER:N	2.19	0.74
3:E8:49:ASN:O	3:F8:121:GLN:NE2	2.17	0.74
1:N1:53:GLU:OE2	2:N5:78:ARG:HB3	1.87	0.74
1:D1:53:GLU:OE2	2:D5:78:ARG:HB3	1.87	0.74
3:E8:65:VAL:HG12	3:E8:76:GLU:HB3	1.69	0.74
2:L5:7:MET:HE1	2:22:17:VAL:HG21	1.68	0.74
3:O8:61:VAL:HG12	3:O8:62:GLN:H	1.52	0.74
3:28:61:VAL:HG12	3:28:62:GLN:H	1.51	0.74
2:A2:9:GLU:OE2	2:A4:13:PHE:N	2.19	0.74
1:O1:53:GLU:OE2	2:O5:78:ARG:HB3	1.87	0.74
2:P6:13:PHE:HB3	2:P7:41:THR:HG21	1.68	0.74
2:B5:3:ASP:O	2:B5:47:ARG:NH2	2.17	0.74
2:C3:8:ILE:HG12	2:C3:73:VAL:HG22	1.68	0.74
2:C3:17:VAL:HG21	2:C4:7:MET:HE1	1.67	0.74
2:X2:30:GLU:OE1	2:X2:91:ARG:NH1	2.19	0.74
2:Z6:36:LYS:NZ	2:Z7:35:GLU:OE1	2.19	0.74
2:I5:8:ILE:HG12	2:I5:73:VAL:HG22	1.69	0.74
3:J8:24:LYS:HG2	3:J9:127:ARG:HA	1.70	0.74
1:T1:45:ASP:OD2	1:T1:49:ALA:N	2.19	0.74
2:45:34:TYR:OH	2:46:35:GLU:OE2	2.04	0.74
2:K6:19:ALA:HB2	2:K6:64:ALA:HB2	1.70	0.74
2:N5:10:VAL:HG11	2:N5:15:GLY:HA3	1.70	0.74
2:22:54:LYS:NZ	2:25:58:GLU:OE2	2.20	0.74
2:A5:8:ILE:HG12	2:A5:73:VAL:HG22	1.69	0.74
1:Z1:53:GLU:OE2	2:Z5:78:ARG:HB3	1.87	0.74
2:42:3:ASP:O	2:42:47:ARG:NH1	2.19	0.74
2:42:8:ILE:HG12	2:42:73:VAL:HG22	1.69	0.74
3:A8:134:ILE:O	3:A8:135:LEU:HG	1.86	0.74
2:S2:90:GLY:O	2:S2:92:THR:N	2.20	0.74
2:T5:8:ILE:HG12	2:T5:73:VAL:HG22	1.70	0.74
3:48:122:THR:HG21	3:48:136:PRO:HA	1.69	0.74
2:J3:32:ILE:HD12	2:J3:90:GLY:HA3	1.70	0.74
2:L4:10:VAL:HG11	2:L4:15:GLY:HA3	1.70	0.74
3:M8:69:GLU:OE2	3:28:127:ARG:NH2	2.21	0.74
2:Y2:90:GLY:O	2:Y2:92:THR:N	2.20	0.74
2:43:5:LEU:HD13	2:43:47:ARG:HD3	1.69	0.74
2:D3:31:GLU:OE1	2:D3:92:ARG:NH2	2.20	0.73
2:O2:84:ASP:O	2:O2:92:THR:OG1	2.06	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:X8:123:GLN:NE2	3:X9:31:PRO:O	2.21	0.73
2:F3:13:PHE:HB2	2:F4:37:THR:HG21	1.67	0.73
2:O3:47:ARG:HH21	2:O3:91:ARG:HB2	1.54	0.73
2:X3:34:TYR:OH	2:X4:35:GLU:OE2	2.05	0.73
3:E8:45:GLY:HA3	3:E8:73:GLY:H	1.52	0.73
3:E8:112:GLN:OE1	3:Q8:50:ARG:NE	2.20	0.73
2:H3:47:ARG:HH22	2:H3:79:PRO:HG2	1.52	0.73
1:S1:13:SER:OG	1:31:83:ASP:OD2	2.03	0.73
3:S8:45:GLY:HA2	3:S8:48:ILE:HD13	1.71	0.73
2:I7:8:ILE:HG12	2:I7:73:VAL:HG22	1.67	0.73
2:M5:7:MET:HE1	2:N2:17:VAL:HG21	1.70	0.73
2:44:10:VAL:HG11	2:44:15:GLY:HA3	1.69	0.73
3:A8:61:VAL:HG12	3:A8:62:GLN:H	1.53	0.73
3:E8:50:ARG:NE	3:F8:112:GLN:OE1	2.20	0.73
3:H8:12:ASP:O	3:H8:82:GLN:NE2	2.21	0.73
3:J8:154:ALA:HB2	3:J8:198:ILE:HD11	1.70	0.73
1:P1:45:ASP:OD2	1:P1:49:ALA:N	2.20	0.73
3:18:55:ALA:O	3:18:59:THR:OG1	2.06	0.73
3:48:42:ILE:HD11	3:48:96:LEU:HD11	1.71	0.73
2:C3:5:LEU:HD13	2:C3:47:ARG:HD3	1.71	0.73
3:I8:16:PRO:HA	3:I8:33:PRO:HB3	1.70	0.73
2:J4:10:VAL:HG11	2:J4:15:GLY:HA3	1.69	0.73
1:O1:75:ASP:OD2	1:P1:59:SER:N	2.15	0.73
1:Z1:1:MET:N	1:11:75:ASP:OD1	2.20	0.73
2:43:17:VAL:HG21	2:44:7:MET:HE1	1.69	0.73
3:L8:8:TYR:CE2	3:L8:93:LEU:HD23	2.24	0.73
1:P1:86:GLU:O	1:P1:87:MET:SD	2.47	0.73
1:Q1:75:ASP:OD1	1:S1:1:MET:N	2.19	0.73
3:R8:12:ASP:O	3:R8:82:GLN:NE2	2.21	0.73
3:R8:154:ALA:HB2	3:R8:198:ILE:HD11	1.70	0.73
3:D8:45:GLY:HA2	3:D8:48:ILE:HD13	1.69	0.73
2:F6:32:ILE:HD13	2:F6:90:GLY:HA3	1.69	0.73
2:G5:8:ILE:HG12	2:G5:73:VAL:HG22	1.69	0.73
2:H3:9:GLU:HB3	2:H3:43:THR:HG23	1.71	0.73
2:M3:8:ILE:HG12	2:M3:73:VAL:HG22	1.70	0.73
2:M3:78:ARG:NH1	2:27:28:LYS:HA	2.04	0.73
3:P9:66:GLN:HA	3:P9:75:LEU:HA	1.70	0.73
2:X5:8:ILE:HG12	2:X5:73:VAL:HG22	1.71	0.73
2:I7:17:VAL:HG21	2:J3:7:MET:HE1	1.69	0.73
3:P8:116:ALA:HA	3:P8:137:GLY:HA2	1.68	0.73
2:Q3:34:TYR:OH	2:Q4:35:GLU:OE2	2.04	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:U5:16:MET:HG2	2:U5:44:ALA:HB2	1.71	0.73
2:X3:47:ARG:HH11	2:X3:91:ARG:HB2	1.52	0.73
3:F8:50:ARG:NE	3:Q8:112:GLN:OE1	2.16	0.73
3:N8:12:ASP:O	3:N8:82:GLN:NE2	2.22	0.73
3:P8:45:GLY:HA3	3:P8:73:GLY:H	1.51	0.73
2:A3:18:GLU:OE1	2:A4:74:HIS:NE2	2.22	0.72
2:B2:18:GLU:OE1	2:C5:74:HIS:NE2	2.21	0.72
3:H9:45:GLY:N	3:H9:71:ALA:O	2.19	0.72
3:J8:127:ARG:HH11	3:L8:27:ARG:HD2	1.54	0.72
2:K7:8:ILE:HG12	2:K7:73:VAL:HG22	1.69	0.72
3:K8:45:GLY:HA2	3:K8:48:ILE:HD13	1.69	0.72
2:R3:47:ARG:HH12	2:R3:84:ASP:CG	1.98	0.72
2:S7:28:LYS:HA	2:U3:78:ARG:NH1	2.04	0.72
2:T5:10:VAL:HG11	2:T5:15:GLY:HA3	1.69	0.72
2:T6:32:ILE:HG21	2:T6:90:GLY:HA3	1.71	0.72
2:U5:13:PHE:HB2	2:U6:37:THR:HG21	1.69	0.72
2:32:19:ALA:HB2	2:32:64:ALA:HB2	1.71	0.72
3:48:65:VAL:HG12	3:48:76:GLU:HB3	1.71	0.72
2:I3:17:VAL:HG21	2:I4:7:MET:HE1	1.69	0.72
3:J8:122:THR:HG21	3:J8:136:PRO:HA	1.72	0.72
2:R2:84:ASP:O	2:R2:92:THR:OG1	2.06	0.72
2:Y6:47:ARG:HH22	2:Y6:79:PRO:HG3	1.54	0.72
2:Y7:25:LYS:O	2:Z7:25:LYS:NZ	2.22	0.72
2:A2:29:VAL:CG1	2:A2:46:VAL:HG22	2.19	0.72
2:B7:8:ILE:HG12	2:B7:73:VAL:HG22	1.69	0.72
2:G2:9:GLU:OE2	2:G4:13:PHE:N	2.21	0.72
3:K8:154:ALA:HB2	3:K8:198:ILE:HD11	1.69	0.72
3:U8:9:ILE:HD11	3:U8:150:TYR:HA	1.70	0.72
2:V5:10:VAL:HG11	2:V5:15:GLY:HA3	1.71	0.72
3:C8:130:GLN:NE2	3:C8:172:TYR:OH	2.19	0.72
2:D3:14:PHE:HB2	2:D4:37:THR:HG21	1.71	0.72
2:J4:47:ARG:NH1	2:J4:89:LEU:O	2.23	0.72
2:P4:3:ASP:OD2	2:P4:91:ARG:NE	2.21	0.72
2:15:8:ILE:HG12	2:15:73:VAL:HG22	1.71	0.72
2:W5:8:ILE:HG12	2:W5:73:VAL:HG22	1.69	0.72
2:32:9:GLU:OE2	2:34:13:PHE:N	2.22	0.72
2:E3:8:ILE:HG22	2:E3:73:VAL:HG22	1.72	0.72
1:O1:79:MET:HE1	1:31:73:PRO:HB2	1.71	0.72
2:42:84:ASP:O	2:42:92:THR:OG1	2.05	0.72
2:B2:11:ARG:NH2	2:C5:41:TYR:OH	2.21	0.72
3:F8:60:LYS:HG2	2:Q7:78:ARG:HD3	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K5:34:TYR:OH	2:K6:35:GLU:OE2	2.07	0.72
2:Q6:13:PHE:HB2	2:Q7:37:THR:HG21	1.72	0.72
3:W8:7:THR:HG21	3:W8:149:GLY:HA3	1.69	0.72
3:Y8:154:ALA:HB2	3:Y8:198:ILE:HD11	1.72	0.72
2:A5:7:MET:HE1	2:E2:17:VAL:HG21	1.71	0.72
2:C2:10:VAL:HG11	2:C2:15:GLY:HA3	1.70	0.72
3:G8:177:ARG:HG2	3:I8:46:ILE:HD11	1.70	0.72
2:J2:90:GLY:O	2:J2:92:THR:N	2.16	0.72
3:K8:55:ALA:O	3:K8:59:THR:OG1	2.08	0.72
3:L8:12:ASP:O	3:L8:82:GLN:NE2	2.22	0.72
1:T1:75:ASP:OD1	1:U1:1:MET:N	2.21	0.72
3:A8:42:ILE:HD11	3:A8:96:LEU:HD11	1.72	0.72
3:J8:12:ASP:O	3:J8:82:GLN:NE2	2.23	0.72
3:J8:61:VAL:HG12	3:J8:62:GLN:H	1.55	0.72
2:K2:3:ASP:O	2:K2:47:ARG:NH1	2.21	0.72
1:T1:48:GLY:O	2:U2:25:LYS:NZ	2.18	0.72
2:T2:9:GLU:OE2	2:T4:13:PHE:N	2.23	0.72
2:V6:32:ILE:HG21	2:V6:90:GLY:HA3	1.72	0.72
3:W8:65:VAL:HG12	3:W8:76:GLU:HB3	1.70	0.72
2:X2:84:ASP:O	2:X2:92:THR:OG1	2.07	0.72
2:X5:2:ALA:O	2:X5:78:ARG:NH2	2.22	0.72
2:12:92:THR:O	2:12:94:GLY:N	2.22	0.72
2:L5:34:TYR:OH	2:L6:35:GLU:OE2	2.08	0.71
1:Q1:45:ASP:OD2	1:Q1:49:ALA:N	2.19	0.71
1:S1:53:GLU:OE2	2:S5:78:ARG:HB3	1.88	0.71
2:S7:8:ILE:HG12	2:S7:73:VAL:HG22	1.72	0.71
3:L8:8:TYR:HE2	3:L8:93:LEU:HD23	1.54	0.71
3:P8:18:LEU:O	3:P8:22:ILE:N	2.18	0.71
2:T2:84:ASP:O	2:T2:92:THR:OG1	2.08	0.71
2:U3:47:ARG:HH22	2:U3:79:PRO:HG2	1.55	0.71
3:A8:55:ALA:O	3:A8:59:THR:OG1	2.08	0.71
2:C2:8:ILE:HG12	2:C2:73:VAL:HG22	1.72	0.71
3:E8:121:GLN:NE2	3:Q8:49:ASN:OD1	2.23	0.71
3:I9:11:LEU:N	3:I9:37:SER:O	2.21	0.71
2:M2:3:ASP:O	2:M2:47:ARG:NH1	2.21	0.71
3:U8:109:MET:HB2	3:U8:144:GLU:HB3	1.71	0.71
3:V8:9:ILE:HB	3:V8:39:TRP:HB2	1.71	0.71
2:47:3:ASP:OD2	2:47:91:ARG:NH2	2.23	0.71
1:D1:1:MET:N	1:E1:75:ASP:OD1	2.22	0.71
2:E3:5:LEU:HD13	2:E3:47:ARG:HD3	1.71	0.71
3:E8:49:ASN:OD1	3:F8:121:GLN:NE2	2.24	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N7:8:ILE:HG12	2:N7:73:VAL:HG22	1.72	0.71
2:P2:8:ILE:HG12	2:P2:73:VAL:HG22	1.72	0.71
1:W1:53:GLU:OE2	2:W5:78:ARG:HB3	1.89	0.71
2:W2:47:ARG:NH2	2:W2:84:ASP:OD2	2.22	0.71
2:Y7:8:ILE:HG12	2:Y7:73:VAL:HG22	1.71	0.71
2:B3:47:ARG:HH12	2:B3:84:ASP:CG	1.99	0.71
2:D2:29:VAL:CG1	2:D2:46:VAL:HG22	2.21	0.71
3:H8:49:ASN:OD1	3:Y8:121:GLN:NE2	2.24	0.71
1:I1:54:VAL:HG21	1:I1:93:PHE:CE2	2.26	0.71
2:O2:47:ARG:NH2	2:O2:84:ASP:OD2	2.23	0.71
3:O8:109:MET:HB2	3:O8:144:GLU:HB3	1.73	0.71
2:V5:8:ILE:HG12	2:V5:73:VAL:HG22	1.70	0.71
2:X5:3:ASP:O	2:X5:47:ARG:NH2	2.24	0.71
2:37:87:LEU:HB3	2:37:89:LEU:HD13	1.72	0.71
3:A8:135:LEU:HD11	3:A8:138:GLU:OE2	1.90	0.71
2:C2:90:GLY:O	2:C2:92:THR:N	2.20	0.71
2:D3:48:ARG:HH12	2:D3:85:ASP:CG	1.98	0.71
2:E2:30:GLU:OE1	2:E2:91:ARG:NH1	2.22	0.71
3:P8:170:THR:HG1	3:P8:177:ARG:H	1.37	0.71
3:Y9:105:LYS:N	3:Y9:204:VAL:O	2.23	0.71
2:A5:10:VAL:HG11	2:A5:15:GLY:HA3	1.71	0.71
2:H7:17:VAL:HG11	2:I3:7:MET:HE1	1.73	0.71
2:J2:84:ASP:O	2:J2:92:THR:OG1	2.07	0.71
2:L2:47:ARG:HD3	2:L2:91:ARG:HG2	1.72	0.71
1:M1:75:ASP:OD2	1:N1:59:SER:N	2.18	0.71
2:N3:13:PHE:HB2	2:N4:37:THR:HG21	1.71	0.71
1:O1:18:ARG:NH1	1:P1:65:GLN:O	2.24	0.71
2:V2:17:VAL:HG21	2:W5:7:MET:HE1	1.73	0.71
1:31:22:LEU:HD12	1:31:44:ALA:HB1	1.73	0.71
2:E7:28:LYS:HA	2:Q3:78:ARG:NH1	2.06	0.71
3:R8:61:VAL:HG12	3:R8:62:GLN:H	1.56	0.71
3:T8:45:GLY:HA2	3:T8:48:ILE:HD13	1.71	0.71
2:W5:34:TYR:OH	2:W6:35:GLU:OE2	2.09	0.71
2:Y7:47:ARG:NH1	2:Y7:89:LEU:O	2.23	0.71
2:B3:47:ARG:HH22	2:B3:79:PRO:HG2	1.56	0.71
3:B8:55:ALA:O	3:B8:59:THR:OG1	2.07	0.71
3:D8:9:ILE:HG21	3:D8:153:LEU:HB2	1.72	0.71
2:L4:3:ASP:OD2	2:L4:91:ARG:NE	2.22	0.71
2:L6:32:ILE:HD13	2:L6:90:GLY:HA3	1.73	0.71
2:M3:17:VAL:HG21	2:M4:7:MET:HE1	1.71	0.71
1:V1:2:VAL:HG23	1:V1:57:TYR:CE1	2.25	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:V8:121:GLN:NE2	3:48:49:ASN:OD1	2.23	0.71
2:Z2:8:ILE:HG12	2:Z2:73:VAL:HG22	1.72	0.71
1:H1:59:SER:N	1:Z1:75:ASP:OD2	2.17	0.71
3:Q8:6:ARG:NH1	3:Q8:72:TYR:OH	2.23	0.71
1:R1:28:ARG:NH1	1:R1:36:PRO:HB2	2.05	0.71
2:T7:47:ARG:NH1	2:T7:89:LEU:O	2.23	0.71
3:T8:112:GLN:OE1	3:38:50:ARG:NE	2.24	0.71
2:V2:84:ASP:O	2:V2:92:THR:OG1	2.09	0.71
2:V2:92:THR:O	2:V2:94:GLY:N	2.24	0.71
2:24:10:VAL:HG11	2:24:15:GLY:HA3	1.73	0.71
2:46:36:LYS:NZ	2:47:35:GLU:OE1	2.24	0.71
2:D5:47:ARG:NH1	2:D5:84:ASP:OD1	2.24	0.70
2:36:13:PHE:HB2	2:37:37:THR:HG21	1.72	0.70
3:39:4:THR:N	3:39:43:ALA:O	2.22	0.70
2:C2:13:PHE:N	2:D5:9:GLU:OE2	2.22	0.70
1:F1:1:MET:N	1:R1:75:ASP:OD1	2.20	0.70
2:G3:21:ASP:OD2	2:G4:76:ILE:HD13	1.90	0.70
2:O3:8:ILE:HG12	2:O3:73:VAL:HG22	1.73	0.70
3:T8:16:PRO:HA	3:T8:33:PRO:HB3	1.72	0.70
2:23:32:ILE:HD13	2:23:90:GLY:HA3	1.72	0.70
2:35:10:VAL:HG11	2:35:15:GLY:HA3	1.73	0.70
2:D2:9:GLU:OE2	2:D4:13:PHE:N	2.23	0.70
3:F9:105:LYS:N	3:F9:204:VAL:O	2.21	0.70
2:R3:78:ARG:HH11	2:U7:28:LYS:HA	1.54	0.70
2:S3:17:VAL:HG21	2:S4:7:MET:HE1	1.74	0.70
3:U8:61:VAL:HG12	3:U8:62:GLN:H	1.56	0.70
2:25:3:ASP:O	2:25:47:ARG:NH2	2.23	0.70
3:A8:46:ILE:HD11	3:I8:177:ARG:HG2	1.74	0.70
2:D3:6:LEU:HD13	2:D3:48:ARG:HD3	1.74	0.70
1:K1:28:ARG:NH1	1:K1:36:PRO:HB2	2.06	0.70
2:L5:3:ASP:O	2:L5:47:ARG:NH2	2.24	0.70
2:N6:32:ILE:HD13	2:N6:90:GLY:HA3	1.73	0.70
3:G8:12:ASP:O	3:G8:82:GLN:NE2	2.23	0.70
3:O8:122:THR:HG21	3:O8:136:PRO:HA	1.73	0.70
2:W3:13:PHE:HB2	2:W4:37:THR:HG21	1.71	0.70
3:49:45:GLY:N	3:49:71:ALA:O	2.24	0.70
2:B2:90:GLY:O	2:B2:92:THR:N	2.25	0.70
3:B8:170:THR:HG1	3:B8:177:ARG:H	1.39	0.70
2:C2:13:PHE:HB2	2:D5:37:THR:HG21	1.74	0.70
3:C8:57:LYS:O	2:M7:78:ARG:NH2	2.25	0.70
2:G4:3:ASP:OD2	2:G4:91:ARG:NH2	2.18	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H7:52:ALA:O	2:H7:56:ALA:N	2.23	0.70
1:I1:22:LEU:HD12	1:I1:44:ALA:HB1	1.73	0.70
3:K8:61:VAL:HG12	3:K8:62:GLN:H	1.55	0.70
3:K8:167:VAL:HB	3:K8:179:TYR:HB2	1.73	0.70
3:L8:170:THR:HG1	3:L8:177:ARG:H	1.40	0.70
2:O7:54:LYS:NZ	2:O7:58:GLU:OE1	2.25	0.70
3:Q8:61:VAL:HG12	3:Q8:62:GLN:H	1.56	0.70
2:V5:13:PHE:N	2:V6:9:GLU:OE2	2.24	0.70
3:38:106:PRO:HG3	3:38:150:TYR:CE2	2.26	0.70
3:C8:49:ASN:OD1	3:M8:121:GLN:NE2	2.25	0.70
3:G8:9:ILE:HB	3:G8:39:TRP:HB2	1.74	0.70
1:K1:9:THR:OG1	1:L1:86:GLU:OE1	2.09	0.70
2:K3:13:PHE:HB2	2:K4:37:THR:HG21	1.74	0.70
3:N8:169:VAL:HG12	3:N8:171:PRO:HD3	1.73	0.70
2:O3:9:GLU:HB3	2:O3:43:THR:HG23	1.73	0.70
2:P6:32:ILE:HG21	2:P6:90:GLY:HA3	1.73	0.70
2:Y3:47:ARG:HH22	2:Y3:79:PRO:HG2	1.56	0.70
2:33:47:ARG:HH12	2:33:84:ASP:CG	2.00	0.70
2:A6:47:ARG:HH22	2:A6:79:PRO:HG3	1.57	0.70
2:E7:78:ARG:NE	3:Q8:59:THR:O	2.24	0.70
2:I3:47:ARG:HH22	2:I3:79:PRO:HG2	1.57	0.70
3:M8:61:VAL:HG12	3:M8:62:GLN:H	1.56	0.70
2:25:8:ILE:HG12	2:25:73:VAL:HG22	1.73	0.70
2:M5:35:GLU:HG2	2:N2:13:PHE:HE2	1.56	0.70
2:Z3:32:ILE:HD13	2:Z3:90:GLY:HA3	1.73	0.70
3:18:61:VAL:HG12	3:18:62:GLN:H	1.56	0.70
2:E5:16:MET:HG2	2:E5:44:ALA:HB2	1.74	0.70
2:L2:10:VAL:HG11	2:L2:15:GLY:HA3	1.74	0.70
2:Q2:45:VAL:HG11	2:Q2:89:LEU:HD12	1.74	0.70
2:Z5:3:ASP:O	2:Z5:47:ARG:NH2	2.24	0.70
3:A8:112:GLN:OE1	3:G8:50:ARG:NE	2.25	0.69
3:C8:12:ASP:O	3:C8:82:GLN:NE2	2.25	0.69
2:G3:17:VAL:HG21	2:G4:7:MET:HE1	1.73	0.69
2:Q6:45:VAL:HG11	2:Q6:89:LEU:HD22	1.74	0.69
3:X9:5:LEU:O	3:X9:103:ARG:HA	1.92	0.69
3:18:18:LEU:HD11	3:18:156:ASN:HA	1.74	0.69
2:47:8:ILE:HG12	2:47:73:VAL:HG22	1.73	0.69
1:I1:13:SER:OG	1:J1:83:ASP:OD2	2.06	0.69
2:J5:8:ILE:HG12	2:J5:73:VAL:HG22	1.72	0.69
3:L8:109:MET:HB2	3:L8:144:GLU:HB3	1.74	0.69
3:M8:122:THR:HG21	3:M8:136:PRO:HA	1.73	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T7:52:ALA:O	2:T7:56:ALA:N	2.25	0.69
2:V3:13:PHE:HB2	2:V4:37:THR:HG21	1.74	0.69
3:28:55:ALA:O	3:28:59:THR:OG1	2.09	0.69
2:I5:32:ILE:HD11	2:I5:47:ARG:HG3	1.74	0.69
3:M8:49:ASN:OD1	3:28:121:GLN:NE2	2.25	0.69
2:W7:24:VAL:O	2:Y3:78:ARG:NH2	2.24	0.69
2:A3:13:PHE:HB2	2:A4:37:THR:HG21	1.75	0.69
2:A3:17:VAL:HG21	2:A4:7:MET:HE1	1.74	0.69
2:A7:8:ILE:HD13	2:A7:19:ALA:HB1	1.74	0.69
3:E9:105:LYS:N	3:E9:204:VAL:O	2.25	0.69
3:F8:170:THR:HG1	3:F8:177:ARG:H	1.40	0.69
2:I3:3:ASP:OD1	2:I3:4:ALA:N	2.25	0.69
2:K2:47:ARG:NH2	2:K2:84:ASP:OD2	2.25	0.69
3:Q8:186:GLU:O	3:Q8:190:ALA:N	2.25	0.69
3:S8:177:ARG:HG2	3:U8:46:ILE:HD11	1.72	0.69
2:T7:78:ARG:HD3	3:38:60:LYS:HG2	1.74	0.69
3:V8:46:ILE:HD11	3:X8:177:ARG:HG2	1.73	0.69
2:E5:10:VAL:HG11	2:E5:15:GLY:HA3	1.74	0.69
3:H8:177:ARG:HG2	3:W8:46:ILE:HD11	1.74	0.69
2:L2:8:ILE:HG12	2:L2:73:VAL:HG22	1.72	0.69
2:S5:7:MET:HE1	2:32:17:VAL:HG21	1.74	0.69
2:V3:9:GLU:HB3	2:V3:43:THR:HG23	1.74	0.69
3:M8:186:GLU:O	3:M8:190:ALA:N	2.24	0.69
3:N8:8:TYR:CE2	3:N8:93:LEU:HD23	2.28	0.69
2:O7:8:ILE:HG12	2:O7:73:VAL:HG22	1.73	0.69
2:Q5:10:VAL:HG11	2:Q5:15:GLY:HA3	1.74	0.69
3:Q8:134:ILE:HG12	3:Q8:181:ALA:HB2	1.74	0.69
2:V3:47:ARG:HH12	2:V3:84:ASP:CG	2.00	0.69
2:X3:5:LEU:HD13	2:X3:47:ARG:HD3	1.74	0.69
3:A8:177:ARG:HG2	3:G8:46:ILE:HD11	1.73	0.69
2:I4:10:VAL:HG11	2:I4:15:GLY:HA3	1.74	0.69
2:L6:57:THR:HG21	2:L6:75:VAL:HG22	1.73	0.69
2:P2:84:ASP:O	2:P2:92:THR:OG1	2.08	0.69
3:Q9:105:LYS:N	3:Q9:204:VAL:O	2.23	0.69
1:T1:28:ARG:NH1	1:T1:36:PRO:HB2	2.08	0.69
3:28:12:ASP:O	3:28:82:GLN:NE2	2.25	0.69
2:A2:3:ASP:C	2:A2:47:ARG:HH12	1.99	0.69
2:E6:36:LYS:NZ	2:E7:35:GLU:OE1	2.21	0.69
2:F2:17:VAL:HG21	2:R5:7:MET:HE1	1.74	0.69
2:F2:69:GLU:O	2:F2:70:VAL:HG22	1.92	0.69
2:H3:19:ALA:HB2	2:H3:64:ALA:HB2	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H8:50:ARG:NE	3:Y8:112:GLN:OE1	2.26	0.69
3:I8:8:TYR:CE2	3:I8:93:LEU:HD23	2.27	0.69
2:J7:19:ALA:HB2	2:J7:64:ALA:HB2	1.74	0.69
2:M2:5:LEU:HD11	2:M2:7:MET:HE2	1.75	0.69
2:M7:17:VAL:HG11	2:N3:7:MET:HE1	1.74	0.69
1:O1:1:MET:N	1:31:75:ASP:OD1	2.23	0.69
2:P2:30:GLU:OE1	2:P2:91:ARG:NH2	2.25	0.69
1:Q1:28:ARG:HH11	1:Q1:36:PRO:HB2	1.58	0.69
2:R5:10:VAL:HG11	2:R5:15:GLY:HA3	1.73	0.69
2:T2:10:VAL:HG11	2:T2:15:GLY:HA3	1.74	0.69
2:V7:78:ARG:NH1	3:48:56:LEU:O	2.25	0.69
3:Y8:122:THR:HG21	3:Y8:136:PRO:HA	1.73	0.69
3:38:3:ILE:HD11	3:38:50:ARG:NH1	2.08	0.69
2:Q3:18:GLU:OE1	2:Q4:74:HIS:NE2	2.22	0.69
3:V8:12:ASP:O	3:V8:82:GLN:NE2	2.26	0.69
2:Z5:2:ALA:O	2:Z5:78:ARG:NH1	2.25	0.69
1:E1:53:GLU:OE2	2:E5:78:ARG:HB3	1.93	0.69
2:F5:9:GLU:OE2	2:G2:13:PHE:N	2.25	0.69
3:H8:112:GLN:OE1	3:W8:50:ARG:NE	2.24	0.69
3:I9:105:LYS:N	3:I9:204:VAL:O	2.21	0.69
3:28:122:THR:HG21	3:28:136:PRO:HA	1.72	0.69
2:B5:8:ILE:HG12	2:B5:73:VAL:HG22	1.75	0.68
2:H7:19:ALA:HB2	2:H7:64:ALA:HB2	1.74	0.68
2:L2:11:ARG:HB3	2:L2:69:GLU:HG2	1.74	0.68
2:T5:92:THR:O	2:T5:94:GLY:N	2.26	0.68
2:U4:16:MET:HG2	2:U4:44:ALA:HB2	1.75	0.68
3:Y8:8:TYR:CE2	3:Y8:93:LEU:HD23	2.29	0.68
1:B1:6:VAL:HG21	1:B1:50:GLY:O	1.92	0.68
3:K8:12:ASP:O	3:K8:82:GLN:NE2	2.26	0.68
2:O7:52:ALA:O	2:O7:56:ALA:N	2.26	0.68
3:X8:122:THR:HG21	3:X8:136:PRO:HA	1.74	0.68
2:E6:30:GLU:OE1	2:E6:91:ARG:NH2	2.23	0.68
3:J9:103:ARG:O	3:J9:204:VAL:N	2.26	0.68
3:K8:170:THR:HG1	3:K8:177:ARG:H	1.39	0.68
1:L1:75:ASP:OD1	1:21:1:MET:N	2.23	0.68
2:T7:19:ALA:HB2	2:T7:64:ALA:HB2	1.74	0.68
2:V7:78:ARG:NE	3:48:59:THR:O	2.25	0.68
3:W8:61:VAL:HG12	3:W8:62:GLN:H	1.58	0.68
2:13:9:GLU:HB3	2:13:43:THR:HG23	1.74	0.68
3:28:154:ALA:HB2	3:28:198:ILE:HD11	1.75	0.68
2:A5:34:TYR:OH	2:A6:35:GLU:OE2	2.07	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C4:10:VAL:HG11	2:C4:15:GLY:HA3	1.75	0.68
3:H8:55:ALA:O	3:H8:59:THR:OG1	2.11	0.68
3:M8:12:ASP:O	3:M8:82:GLN:NE2	2.26	0.68
2:P5:7:MET:HE1	2:Q2:17:VAL:HG21	1.75	0.68
2:R3:8:ILE:HD12	2:R3:19:ALA:HB1	1.75	0.68
3:R8:49:ASN:OD1	3:U8:121:GLN:NE2	2.27	0.68
3:S8:55:ALA:O	3:S8:59:THR:OG1	2.11	0.68
3:Y8:61:VAL:HG12	3:Y8:62:GLN:H	1.58	0.68
1:41:22:LEU:HD12	1:41:44:ALA:HB1	1.75	0.68
2:46:45:VAL:HG11	2:46:89:LEU:HD12	1.75	0.68
2:B6:7:MET:HG2	2:B6:45:VAL:HG12	1.75	0.68
1:K1:53:GLU:OE2	2:K5:78:ARG:HB3	1.93	0.68
2:Q5:7:MET:HE1	2:S2:17:VAL:HG21	1.75	0.68
2:R3:90:GLY:O	2:R3:92:THR:N	2.25	0.68
2:T2:5:LEU:HD23	2:T2:76:ILE:HD12	1.75	0.68
3:C8:55:ALA:O	3:C8:59:THR:OG1	2.10	0.68
3:E8:9:ILE:HB	3:E8:39:TRP:HB2	1.75	0.68
2:G4:10:VAL:HG11	2:G4:15:GLY:HA3	1.76	0.68
2:K7:78:ARG:NE	3:18:59:THR:O	2.26	0.68
3:V8:61:VAL:HG12	3:V8:62:GLN:H	1.59	0.68
2:Z2:10:VAL:HG11	2:Z2:15:GLY:HA3	1.75	0.68
3:B8:109:MET:HB2	3:B8:144:GLU:HB3	1.76	0.68
3:E8:55:ALA:O	3:E8:59:THR:OG1	2.11	0.68
3:X8:61:VAL:HG12	3:X8:62:GLN:H	1.59	0.68
2:Y2:10:VAL:HG11	2:Y2:15:GLY:HA3	1.76	0.68
2:46:32:ILE:HG21	2:46:90:GLY:HA3	1.74	0.68
3:A8:59:THR:O	2:I7:78:ARG:NE	2.27	0.68
2:D2:3:ASP:O	2:D2:47:ARG:NH1	2.23	0.68
2:K6:13:PHE:HB2	2:K7:37:THR:HG21	1.76	0.68
2:L3:90:GLY:O	2:L3:92:THR:N	2.27	0.68
2:M2:11:ARG:HB3	2:M2:69:GLU:HG2	1.75	0.68
2:M4:10:VAL:HG11	2:M4:15:GLY:HA3	1.75	0.68
3:P8:8:TYR:HE2	3:P8:93:LEU:HD23	1.57	0.68
3:V8:60:LYS:HG2	2:X7:78:ARG:HD3	1.75	0.68
2:X3:32:ILE:HD11	2:X3:47:ARG:HG3	1.76	0.68
2:Z3:90:GLY:O	2:Z3:92:THR:N	2.26	0.68
3:18:109:MET:HB2	3:18:144:GLU:HB3	1.75	0.68
2:26:55:ALA:HB1	3:28:115:ARG:HD2	1.76	0.68
3:B9:20:THR:O	3:B9:24:LYS:N	2.24	0.68
3:O8:45:GLY:HA3	3:O8:73:GLY:H	1.58	0.68
2:Y5:57:GLU:O	2:Y5:61:ARG:NH2	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:27:52:ALA:O	2:27:56:ALA:N	2.26	0.68
3:38:61:VAL:HG12	3:38:62:GLN:H	1.59	0.68
2:45:3:ASP:O	2:45:47:ARG:NH2	2.27	0.68
3:E8:177:ARG:HG2	3:Q8:46:ILE:HD11	1.76	0.68
1:H1:28:ARG:HH11	1:H1:36:PRO:HB2	1.58	0.68
2:H7:47:ARG:NH1	2:H7:89:LEU:O	2.26	0.68
2:Q5:18:GLU:OE1	2:Q6:74:HIS:NE2	2.27	0.68
3:28:9:ILE:HG21	3:28:153:LEU:HB2	1.76	0.68
1:H1:83:ASP:OD2	1:Z1:13:SER:OG	2.05	0.67
2:O3:3:ASP:OD2	2:O3:91:ARG:NE	2.24	0.67
3:O8:65:VAL:HG12	3:O8:76:GLU:HB3	1.75	0.67
3:W8:8:TYR:CE2	3:W8:93:LEU:HD23	2.29	0.67
3:W8:55:ALA:O	3:W8:59:THR:OG1	2.11	0.67
2:Y3:90:GLY:O	2:Y3:92:THR:N	2.26	0.67
2:42:32:ILE:HD11	2:42:90:GLY:HA3	1.76	0.67
2:A3:5:LEU:HD23	2:A3:47:ARG:HD3	1.76	0.67
3:I8:103:ARG:HH21	3:I8:201:VAL:HG13	1.59	0.67
3:I8:170:THR:HG1	3:I8:177:ARG:H	1.40	0.67
2:R6:13:PHE:HB2	2:R7:37:THR:HG21	1.74	0.67
3:Y8:8:TYR:HE2	3:Y8:93:LEU:HD23	1.57	0.67
3:B8:46:ILE:HD11	3:L8:177:ARG:HG2	1.77	0.67
2:D4:3:ASP:OD2	2:D4:91:ARG:NH2	2.22	0.67
3:D8:47:ALA:HB1	3:D8:50:ARG:HH12	1.59	0.67
2:G5:3:ASP:OD1	2:G5:78:ARG:NH1	2.27	0.67
2:V3:17:VAL:HG21	2:V4:7:MET:HE1	1.76	0.67
3:B8:169:VAL:HG22	3:B8:178:LEU:HD13	1.76	0.67
3:D8:61:VAL:HG12	3:D8:62:GLN:H	1.58	0.67
3:E8:183:SER:OG	3:E8:186:GLU:OE2	2.12	0.67
2:G7:78:ARG:HD3	3:I8:60:LYS:HG2	1.74	0.67
3:G8:154:ALA:HB2	3:G8:198:ILE:HD11	1.75	0.67
2:J3:9:GLU:HB3	2:J3:43:THR:HG23	1.75	0.67
2:T2:3:ASP:O	2:T2:47:ARG:NH1	2.22	0.67
3:V8:55:ALA:O	3:V8:59:THR:OG1	2.12	0.67
3:Z8:12:ASP:O	3:Z8:82:GLN:NE2	2.28	0.67
3:Z8:134:ILE:HD11	3:Z8:140:LEU:HD13	1.77	0.67
2:23:9:GLU:HB3	2:23:43:THR:HG23	1.75	0.67
2:D3:22:ASP:OD2	2:D4:76:ILE:HD13	1.95	0.67
3:T8:122:THR:HG21	3:T8:136:PRO:HA	1.76	0.67
2:Z3:13:PHE:HB2	2:Z4:37:THR:HG21	1.76	0.67
1:21:50:GLY:N	1:21:53:GLU:OE1	2.25	0.67
1:C1:28:ARG:NH1	1:C1:36:PRO:HB2	2.09	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C7:78:ARG:HD3	3:28:60:LYS:HG2	1.75	0.67
2:E7:8:ILE:HG12	2:E7:73:VAL:HG22	1.75	0.67
1:G1:18:ARG:O	1:G1:72:ARG:NH2	2.28	0.67
3:G8:109:MET:HB2	3:G8:144:GLU:HB3	1.74	0.67
3:H9:4:THR:N	3:H9:43:ALA:O	2.21	0.67
3:L8:61:VAL:HG12	3:L8:62:GLN:H	1.60	0.67
2:P7:50:ALA:O	2:P7:54:ALA:N	2.28	0.67
3:S8:170:THR:HG1	3:S8:177:ARG:H	1.38	0.67
1:V1:28:ARG:NH1	1:V1:36:PRO:HB2	2.10	0.67
2:V3:5:LEU:HD13	2:V3:47:ARG:HD3	1.77	0.67
2:35:3:ASP:OD2	2:35:91:ARG:NH2	2.25	0.67
3:B8:8:TYR:CE2	3:B8:93:LEU:HD23	2.30	0.67
2:H3:25:LYS:HB3	3:H8:160:LYS:HE3	1.77	0.67
2:J7:8:ILE:HG12	2:J7:73:VAL:HG22	1.77	0.67
2:S2:32:ILE:HD11	2:S2:90:GLY:HA3	1.77	0.67
2:S5:9:GLU:OE2	2:32:13:PHE:N	2.27	0.67
2:23:5:LEU:HD13	2:23:47:ARG:HD3	1.76	0.67
3:B9:47:ALA:O	3:B9:51:VAL:N	2.26	0.67
3:F8:61:VAL:HG12	3:F8:62:GLN:H	1.59	0.67
3:G9:67:VAL:N	3:G9:74:LEU:O	2.24	0.67
2:I4:3:ASP:OD2	2:I4:91:ARG:NH2	2.24	0.67
2:K5:9:GLU:OE2	2:L2:13:PHE:N	2.27	0.67
3:P8:61:VAL:HG12	3:P8:62:GLN:H	1.59	0.67
2:Q6:4:ALA:N	2:Q6:48:GLY:O	2.27	0.67
2:S3:9:GLU:HB3	2:S3:43:THR:HG23	1.76	0.67
2:U3:32:ILE:HD11	2:U3:47:ARG:HG3	1.77	0.67
2:X2:47:ARG:HD3	2:X2:91:ARG:HG2	1.77	0.67
2:X4:10:VAL:HG11	2:X4:15:GLY:HA3	1.76	0.67
3:48:45:GLY:HA2	3:48:48:ILE:HD13	1.77	0.67
2:B5:10:VAL:HG11	2:B5:15:GLY:HA3	1.75	0.67
2:D7:78:ARG:NE	3:N8:59:THR:O	2.27	0.67
3:F8:134:ILE:HG12	3:F8:181:ALA:HB2	1.76	0.67
2:O2:9:GLU:OE2	2:O4:13:PHE:N	2.26	0.67
2:S5:13:PHE:N	2:S6:9:GLU:OE1	2.28	0.67
3:U8:55:ALA:O	3:U8:59:THR:OG1	2.12	0.67
2:Z2:13:PHE:CE2	2:15:35:GLU:HG2	2.30	0.67
2:12:11:ARG:HB3	2:12:69:GLU:HG2	1.75	0.67
2:23:47:ARG:HH22	2:23:79:PRO:HG2	1.59	0.67
3:G8:61:VAL:HG12	3:G8:62:GLN:H	1.58	0.67
3:J8:121:GLN:NE2	3:L8:49:ASN:O	2.28	0.67
2:N2:3:ASP:OD2	2:N2:91:ARG:NE	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:W3:9:GLU:HB3	2:W3:43:THR:HG23	1.77	0.67
3:18:8:TYR:O	3:18:103:ARG:NH2	2.28	0.67
2:A2:17:VAL:HG21	2:B5:7:MET:HE1	1.76	0.66
2:C2:3:ASP:O	2:C2:47:ARG:NH2	2.27	0.66
3:C8:61:VAL:HG12	3:C8:62:GLN:H	1.60	0.66
2:F4:78:ARG:NH2	3:F8:159:GLU:OE2	2.28	0.66
3:H8:61:VAL:HG12	3:H8:62:GLN:H	1.58	0.66
2:I2:3:ASP:O	2:I2:47:ARG:NH2	2.27	0.66
3:L8:45:GLY:HA3	3:L8:73:GLY:H	1.59	0.66
3:O8:19:ALA:HB3	3:O8:33:PRO:HG3	1.77	0.66
3:P8:6:ARG:NH1	3:P8:72:TYR:OH	2.26	0.66
3:Q8:55:ALA:O	3:Q8:59:THR:OG1	2.12	0.66
2:T3:4:ALA:O	2:T3:47:ARG:HD2	1.94	0.66
2:W3:5:LEU:HD13	2:W3:47:ARG:HD3	1.77	0.66
2:B3:30:GLU:OE1	2:B3:91:ARG:NH1	2.26	0.66
2:B5:36:LYS:NZ	2:B6:35:GLU:OE2	2.27	0.66
3:E8:21:PHE:O	3:E8:25:THR:OG1	2.08	0.66
1:F1:50:GLY:N	1:F1:53:GLU:OE1	2.17	0.66
2:J7:28:LYS:HA	2:L3:78:ARG:NH1	2.10	0.66
1:M1:64:ARG:HD3	1:N1:62:SER:HB2	1.77	0.66
2:Q3:32:ILE:HD11	2:Q3:47:ARG:HG3	1.77	0.66
2:S6:19:ALA:HB2	2:S6:64:ALA:HB2	1.77	0.66
2:Y6:16:MET:HG2	2:Y6:44:ALA:HB2	1.77	0.66
2:C3:9:GLU:HB3	2:C3:43:THR:HG23	1.76	0.66
3:C8:65:VAL:HG12	3:C8:76:GLU:HB3	1.76	0.66
2:D2:45:VAL:HG11	2:D2:89:LEU:HD12	1.77	0.66
3:F8:46:ILE:HD11	3:Q8:177:ARG:HG2	1.76	0.66
3:L8:65:VAL:HG12	3:L8:76:GLU:HB3	1.76	0.66
3:Q8:103:ARG:HH21	3:Q8:201:VAL:HG13	1.59	0.66
2:R6:64:ALA:O	2:R6:66:ARG:N	2.28	0.66
2:W7:10:VAL:HG11	2:W7:15:GLY:HA3	1.77	0.66
3:W8:11:LEU:HB3	3:W8:14:LEU:HD21	1.76	0.66
1:Y1:53:GLU:OE2	2:Y5:77:ARG:HB3	1.94	0.66
2:Y6:32:ILE:HG21	2:Y6:90:GLY:HA3	1.77	0.66
3:38:109:MET:HB2	3:38:144:GLU:HB3	1.76	0.66
2:H5:3:ASP:C	2:H5:47:ARG:HH11	2.03	0.66
2:L2:54:LYS:HZ2	2:L5:55:ALA:HB2	1.59	0.66
2:L3:9:GLU:HB3	2:L3:43:THR:HG23	1.77	0.66
3:M9:20:THR:O	3:M9:24:LYS:N	2.27	0.66
1:X1:28:ARG:HH11	1:X1:36:PRO:HB2	1.61	0.66
2:34:10:VAL:HG11	2:34:15:GLY:HA3	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B5:47:ARG:NH1	2:B5:84:ASP:OD1	2.28	0.66
2:F2:32:ILE:HD13	2:F2:90:GLY:HA3	1.76	0.66
2:P7:6:ILE:HG12	2:P7:71:VAL:HG22	1.77	0.66
3:U8:186:GLU:O	3:U8:190:ALA:N	2.26	0.66
2:V7:78:ARG:HD3	3:48:60:LYS:HG2	1.78	0.66
2:Y5:12:PHE:HB2	2:Y6:37:THR:HG21	1.76	0.66
2:43:13:PHE:HB2	2:44:37:THR:HG21	1.77	0.66
2:A3:26:ALA:O	3:A8:12:ASP:HB3	1.96	0.66
3:A8:123:GLN:NE2	3:A9:31:PRO:O	2.29	0.66
3:G8:103:ARG:HH21	3:G8:201:VAL:HG13	1.61	0.66
2:H6:19:ALA:HB2	2:H6:64:ALA:HB2	1.75	0.66
2:O5:8:ILE:HG12	2:O5:73:VAL:HG22	1.78	0.66
2:O5:34:TYR:OH	2:O6:35:GLU:OE2	2.12	0.66
2:O6:32:ILE:HG21	2:O6:90:GLY:HA3	1.78	0.66
3:R9:7:THR:O	3:R9:41:GLU:N	2.28	0.66
2:S2:8:ILE:HG12	2:S2:73:VAL:HG22	1.77	0.66
2:V7:52:ALA:O	2:V7:56:ALA:N	2.27	0.66
2:A5:54:LYS:NZ	2:A5:58:GLU:OE1	2.29	0.66
3:D8:177:ARG:HG2	3:N8:46:ILE:HD11	1.78	0.66
2:H3:26:ALA:O	3:H8:12:ASP:HB3	1.95	0.66
3:M8:19:ALA:HB3	3:M8:33:PRO:HG3	1.77	0.66
1:N1:45:ASP:OD2	1:N1:49:ALA:N	2.27	0.66
2:N3:18:GLU:OE1	2:N4:74:HIS:NE2	2.27	0.66
3:N8:109:MET:HB2	3:N8:144:GLU:HB3	1.78	0.66
3:N9:20:THR:O	3:N9:24:LYS:N	2.28	0.66
2:S7:78:ARG:NE	3:U8:59:THR:O	2.28	0.66
3:T8:61:VAL:HG12	3:T8:62:GLN:H	1.61	0.66
3:U8:65:VAL:HG12	3:U8:76:GLU:HB3	1.76	0.66
2:Y7:52:ALA:O	2:Y7:56:ALA:N	2.28	0.66
3:B8:127:ARG:HH21	3:J8:67:VAL:HG12	1.61	0.66
1:J1:18:ARG:NH1	1:11:65:GLN:O	2.28	0.66
3:J8:9:ILE:HG21	3:J8:153:LEU:HB2	1.77	0.66
2:K4:3:ASP:OD2	2:K4:91:ARG:NH2	2.29	0.66
3:M8:69:GLU:CD	3:28:127:ARG:NH2	2.54	0.66
2:N5:34:TYR:OH	2:N6:35:GLU:OE2	2.13	0.66
2:Q5:37:THR:HG21	2:S2:13:PHE:HB2	1.77	0.66
1:T1:31:ASP:OD1	1:T1:35:THR:OG1	2.12	0.66
3:Y8:167:VAL:HB	3:Y8:179:TYR:HB2	1.78	0.66
1:A1:63:ALA:HB1	1:A1:77:THR:HG22	1.77	0.66
2:E5:21:ASP:OD2	2:E5:25:LYS:NZ	2.25	0.66
2:G2:8:ILE:HG12	2:G2:73:VAL:HG22	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I2:2:ALA:HB3	2:I2:78:ARG:NH1	2.11	0.66
3:J8:170:THR:HG1	3:J8:177:ARG:H	1.42	0.66
2:N2:8:ILE:HG12	2:N2:73:VAL:HG22	1.76	0.66
3:N8:154:ALA:HB2	3:N8:198:ILE:HD11	1.77	0.66
2:U2:3:ASP:HB2	2:U2:47:ARG:NH1	2.11	0.66
2:W7:52:ALA:O	2:W7:56:ALA:N	2.28	0.66
2:17:52:ALA:O	2:17:56:ALA:N	2.28	0.66
2:23:45:VAL:HG11	2:23:89:LEU:HD12	1.78	0.66
1:F1:83:ASP:OD2	1:R1:13:SER:OG	2.06	0.66
2:I3:90:GLY:O	2:I3:92:THR:N	2.29	0.66
2:K3:9:GLU:HB3	2:K3:43:THR:HG23	1.78	0.66
3:K8:42:ILE:HD11	3:K8:96:LEU:HD11	1.76	0.66
1:R1:31:ASP:OD1	1:R1:35:THR:OG1	2.14	0.66
2:U4:23:MET:HE3	2:U4:46:VAL:HG21	1.77	0.66
2:X5:10:VAL:HG11	2:X5:15:GLY:HA3	1.78	0.66
3:Z8:11:LEU:HD22	3:Z8:156:ASN:HD22	1.60	0.66
2:K3:47:ARG:NH1	2:K3:91:ARG:HB2	2.09	0.65
2:M2:10:VAL:HG11	2:M2:15:GLY:HA3	1.79	0.65
2:O3:13:PHE:HB2	2:O4:37:THR:HG21	1.77	0.65
2:W6:13:PHE:HB2	2:W7:37:THR:HG21	1.76	0.65
2:X3:78:ARG:NH1	2:47:28:LYS:HA	2.11	0.65
2:12:47:ARG:HD3	2:12:91:ARG:HG2	1.76	0.65
2:23:17:VAL:HG21	2:24:7:MET:HE1	1.78	0.65
2:43:8:ILE:HG23	2:43:73:VAL:HG22	1.78	0.65
2:A3:32:ILE:HD13	2:A3:90:GLY:HA3	1.78	0.65
2:D7:8:ILE:HG12	2:D7:73:VAL:HG22	1.77	0.65
2:K2:10:VAL:HG11	2:K2:15:GLY:HA3	1.78	0.65
2:K5:16:MET:HG2	2:K5:44:ALA:HB2	1.78	0.65
2:K6:32:ILE:HD13	2:K6:90:GLY:HA3	1.78	0.65
2:M2:78:ARG:HH12	2:M5:28:LYS:HD3	1.60	0.65
3:R8:55:ALA:O	3:R8:59:THR:OG1	2.13	0.65
2:Y3:19:ALA:HB2	2:Y3:64:ALA:HB2	1.76	0.65
2:B5:18:GLU:OE1	2:B6:74:HIS:NE2	2.30	0.65
2:D3:79:ARG:O	2:E7:25:LYS:NZ	2.25	0.65
1:I1:7:VAL:HG12	1:J1:87:MET:HG3	1.77	0.65
1:J1:28:ARG:NH2	1:J1:38:GLY:O	2.29	0.65
3:L8:122:THR:HG21	3:L8:136:PRO:HA	1.76	0.65
2:M5:16:MET:HG2	2:M5:44:ALA:HB2	1.78	0.65
2:P2:92:THR:O	2:P2:94:GLY:N	2.28	0.65
2:U3:25:LYS:HB3	3:U8:160:LYS:HE3	1.78	0.65
3:Y8:164:VAL:HG21	3:Y8:190:ALA:HB2	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:18:44:PRO:C	3:18:46:ILE:H	2.04	0.65
3:A8:16:PRO:HA	3:A8:33:PRO:HB2	1.79	0.65
3:C8:50:ARG:NE	3:M8:112:GLN:OE1	2.26	0.65
2:I3:18:GLU:OE1	2:I4:74:HIS:NE2	2.28	0.65
2:J7:78:ARG:NE	3:L8:59:THR:O	2.30	0.65
3:J8:4:THR:OG1	3:J8:43:ALA:O	2.12	0.65
1:U1:67:GLU:O	1:U1:69:THR:N	2.29	0.65
2:Y2:3:ASP:O	2:Y2:47:ARG:NH1	2.23	0.65
1:B1:66:THR:O	1:B1:68:VAL:N	2.29	0.65
1:H1:53:GLU:OE2	2:H5:78:ARG:HB3	1.96	0.65
2:M2:92:THR:O	2:M2:94:GLY:N	2.27	0.65
2:P7:15:VAL:HG11	2:Q3:7:MET:HE1	1.79	0.65
3:V8:112:GLN:OE1	3:48:50:ARG:NE	2.25	0.65
3:Y8:12:ASP:O	3:Y8:82:GLN:NE2	2.29	0.65
2:35:46:VAL:HG23	2:35:47:ARG:H	1.61	0.65
3:C8:45:GLY:HA2	3:C8:48:ILE:HD13	1.77	0.65
2:L2:90:GLY:O	2:L2:92:THR:N	2.28	0.65
2:O5:35:GLU:HG2	2:P2:13:PHE:HE2	1.61	0.65
2:P2:32:ILE:HD11	2:P2:90:GLY:HA3	1.77	0.65
2:Q2:3:ASP:O	2:Q2:47:ARG:NH1	2.25	0.65
3:R8:17:GLN:O	3:R8:20:THR:OG1	2.13	0.65
3:T8:139:SER:HB2	3:T8:187:ILE:HG13	1.79	0.65
2:X3:32:ILE:HD13	2:X3:90:GLY:HA3	1.77	0.65
3:19:105:LYS:N	3:19:204:VAL:O	2.26	0.65
3:B8:9:ILE:HD11	3:B8:150:TYR:HA	1.78	0.65
2:C3:47:ARG:HH22	2:C3:79:PRO:HG2	1.62	0.65
3:C8:46:ILE:HD11	3:M8:177:ARG:HG2	1.78	0.65
2:F3:10:VAL:HG11	2:F3:15:GLY:HA3	1.78	0.65
3:F8:109:MET:HB2	3:F8:144:GLU:HB3	1.78	0.65
2:J5:9:GLU:OE2	2:12:13:PHE:N	2.30	0.65
3:K8:103:ARG:HH21	3:K8:201:VAL:HG13	1.60	0.65
2:M2:32:ILE:HD11	2:M2:90:GLY:HA3	1.79	0.65
3:R8:7:THR:OG1	3:R8:41:GLU:N	2.25	0.65
3:U8:106:PRO:HG3	3:U8:150:TYR:CE2	2.31	0.65
3:X9:6:ARG:O	3:X9:104:LEU:N	2.28	0.65
2:Y2:47:ARG:HD3	2:Y2:91:ARG:HG2	1.79	0.65
3:A8:12:ASP:O	3:A8:82:GLN:NE2	2.28	0.65
3:C8:134:ILE:HG12	3:C8:181:ALA:HB2	1.77	0.65
3:R8:9:ILE:HD12	3:R8:150:TYR:HA	1.78	0.65
2:T3:5:LEU:HD22	2:T3:6:GLY:H	1.61	0.65
2:W6:32:ILE:HD13	2:W6:90:GLY:HA3	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:W7:78:ARG:NE	3:Y8:59:THR:O	2.29	0.65
2:B3:5:LEU:HD13	2:B3:47:ARG:HD3	1.77	0.65
3:C8:6:ARG:NH2	3:C8:72:TYR:OH	2.30	0.65
2:F3:30:GLU:OE1	2:F3:91:ARG:NH2	2.26	0.65
2:G6:5:LEU:HB3	2:G6:76:ILE:HB	1.79	0.65
2:K6:55:ALA:HB1	3:K8:115:ARG:HD2	1.77	0.65
1:L1:53:GLU:OE2	2:L5:78:ARG:HB3	1.97	0.65
1:N1:31:ASP:OD1	1:N1:35:THR:OG1	2.15	0.65
3:28:109:MET:HB2	3:28:144:GLU:HB3	1.78	0.65
1:41:31:ASP:OD1	1:41:35:THR:OG1	2.14	0.65
1:A1:61:SER:HB2	1:E1:61:SER:HB3	1.78	0.65
2:B6:13:PHE:HB2	2:B7:37:THR:HG21	1.77	0.65
2:H3:17:VAL:HG21	2:H4:7:MET:HE1	1.78	0.65
2:J2:16:MET:HG2	2:J2:44:ALA:HB2	1.78	0.65
2:N5:8:ILE:HG12	2:N5:73:VAL:HG22	1.79	0.65
3:N8:61:VAL:HG12	3:N8:62:GLN:H	1.60	0.65
2:Z3:47:ARG:HH22	2:Z3:79:PRO:HG2	1.62	0.65
3:18:7:THR:OG1	3:18:41:GLU:N	2.29	0.65
1:L1:28:ARG:NH1	1:L1:36:PRO:HB2	2.11	0.64
3:L8:55:ALA:O	3:L8:59:THR:OG1	2.15	0.64
3:P8:8:TYR:CE2	3:P8:93:LEU:HD23	2.32	0.64
2:Q7:52:ALA:O	2:Q7:56:ALA:N	2.29	0.64
2:S3:5:LEU:HD13	2:S3:47:ARG:HD3	1.80	0.64
2:Y3:47:ARG:HH12	2:Y3:84:ASP:CG	2.05	0.64
2:A2:13:PHE:HE2	2:B5:35:GLU:HG2	1.62	0.64
3:A8:9:ILE:HB	3:A8:39:TRP:HB2	1.79	0.64
3:B9:88:ALA:O	3:B9:92:ILE:N	2.30	0.64
1:C1:31:ASP:OD1	1:C1:35:THR:OG1	2.14	0.64
3:D9:103:ARG:O	3:D9:204:VAL:N	2.30	0.64
2:G5:16:MET:HG2	2:G5:44:ALA:HB2	1.78	0.64
1:I1:53:GLU:OE2	2:I5:78:ARG:HB3	1.97	0.64
3:Q8:170:THR:HG1	3:Q8:177:ARG:H	1.43	0.64
2:T6:13:PHE:HB2	2:T7:37:THR:HG21	1.78	0.64
2:U2:37:THR:HG21	2:U4:13:PHE:HB2	1.78	0.64
3:U8:20:THR:HG21	3:U9:135:LEU:HA	1.78	0.64
3:U8:50:ARG:HD2	3:U8:95:LYS:HD3	1.80	0.64
2:W7:8:ILE:HG12	2:W7:73:VAL:HG22	1.80	0.64
3:48:55:ALA:O	3:48:59:THR:OG1	2.14	0.64
2:A2:32:ILE:HD11	2:A2:90:GLY:HA3	1.79	0.64
2:A7:10:VAL:HG11	2:A7:15:GLY:HA3	1.80	0.64
2:C7:78:ARG:NH2	3:28:57:LYS:O	2.29	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G3:47:ARG:NH1	2:G3:84:ASP:OD1	2.29	0.64
2:G5:3:ASP:O	2:G5:47:ARG:NH2	2.30	0.64
3:G9:92:ILE:O	3:G9:96:LEU:N	2.21	0.64
3:N8:106:PRO:HG3	3:N8:150:TYR:CE2	2.32	0.64
2:O2:45:VAL:HG11	2:O2:89:LEU:HD12	1.78	0.64
2:O5:7:MET:HE1	2:P2:17:VAL:HG21	1.78	0.64
1:T1:64:ARG:HH11	1:U1:62:SER:HB3	1.63	0.64
2:W6:32:ILE:HG21	2:W6:90:GLY:HA3	1.79	0.64
2:X3:9:GLU:HB3	2:X3:43:THR:HG23	1.79	0.64
3:19:20:THR:O	3:19:24:LYS:N	2.30	0.64
3:C8:121:GLN:NE2	3:28:49:ASN:OD1	2.31	0.64
3:F9:139:SER:N	3:F9:182:GLY:O	2.27	0.64
2:M5:3:ASP:O	2:M5:47:ARG:NH2	2.26	0.64
3:O8:134:ILE:HG12	3:O8:181:ALA:HB2	1.78	0.64
2:P3:3:ASP:OD2	2:P3:91:ARG:NE	2.30	0.64
3:Q8:21:PHE:HE2	3:Q8:169:VAL:HB	1.62	0.64
1:S1:20:GLU:O	2:32:62:ARG:NH1	2.30	0.64
3:T8:109:MET:HB2	3:T8:144:GLU:HB3	1.80	0.64
3:T8:169:VAL:HG12	3:T8:171:PRO:HD3	1.80	0.64
2:U3:90:GLY:O	2:U3:92:THR:N	2.31	0.64
2:X3:26:ALA:O	3:X8:12:ASP:HB3	1.97	0.64
3:Y8:55:ALA:O	3:Y8:59:THR:OG1	2.13	0.64
2:Z2:47:ARG:HD3	2:Z2:91:ARG:HG2	1.80	0.64
2:A2:13:PHE:N	2:B5:9:GLU:OE2	2.31	0.64
3:D8:46:ILE:HD11	3:P8:177:ARG:HG2	1.79	0.64
2:G5:74:HIS:NE2	2:W2:18:GLU:OE1	2.30	0.64
3:J8:42:ILE:HD13	3:J8:96:LEU:HD21	1.79	0.64
3:N8:183:SER:OG	3:N8:186:GLU:OE2	2.14	0.64
2:R5:16:MET:HG2	2:R5:44:ALA:HB2	1.80	0.64
2:R6:55:ALA:HB1	3:R8:115:ARG:HD2	1.79	0.64
3:S9:20:THR:O	3:S9:24:LYS:N	2.31	0.64
1:T1:28:ARG:HH11	1:T1:36:PRO:HB2	1.62	0.64
3:V8:103:ARG:HH21	3:V8:201:VAL:HG13	1.62	0.64
2:23:32:ILE:HD11	2:23:47:ARG:HG3	1.78	0.64
2:25:30:GLU:OE1	2:25:91:ARG:NH2	2.30	0.64
2:33:47:ARG:HH11	2:33:91:ARG:HB2	1.63	0.64
3:J8:109:MET:HB2	3:J8:144:GLU:HB3	1.77	0.64
3:J9:20:THR:O	3:J9:24:LYS:N	2.30	0.64
2:M3:5:LEU:HD13	2:M3:47:ARG:HD3	1.79	0.64
3:R8:44:PRO:HG3	3:U8:110:THR:HG21	1.79	0.64
2:S4:10:VAL:HG11	2:S4:15:GLY:HA3	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S8:61:VAL:HG12	3:S8:62:GLN:H	1.61	0.64
2:X7:52:ALA:O	2:X7:56:ALA:N	2.29	0.64
1:21:22:LEU:HD12	1:21:44:ALA:HB1	1.79	0.64
3:G8:11:LEU:HB3	3:G8:14:LEU:HD21	1.80	0.64
2:H3:90:GLY:O	2:H3:92:THR:N	2.29	0.64
2:K2:7:MET:HE1	2:K4:17:VAL:HG11	1.80	0.64
3:O8:55:ALA:O	3:O8:59:THR:OG1	2.14	0.64
2:P2:47:ARG:HD3	2:P2:91:ARG:HG2	1.78	0.64
2:Q3:19:ALA:HB2	2:Q3:64:ALA:HB2	1.80	0.64
2:R7:52:ALA:O	2:R7:56:ALA:N	2.31	0.64
2:U7:8:ILE:HG12	2:U7:73:VAL:HG22	1.78	0.64
3:U8:9:ILE:CD1	3:U8:150:TYR:HA	2.28	0.64
1:V1:50:GLY:N	1:V1:53:GLU:OE1	2.24	0.64
3:48:61:VAL:HG12	3:48:62:GLN:H	1.61	0.64
2:A3:32:ILE:HD11	2:A3:47:ARG:HG3	1.78	0.64
2:L5:8:ILE:HG12	2:L5:73:VAL:HG22	1.79	0.64
2:S5:13:PHE:HD2	2:S6:43:THR:HG21	1.63	0.64
3:U8:9:ILE:HB	3:U8:39:TRP:HB2	1.79	0.64
3:W8:8:TYR:HE2	3:W8:93:LEU:HD23	1.63	0.64
3:Z8:104:LEU:HD12	3:Z8:147:PRO:HG3	1.78	0.64
3:K9:39:TRP:HA	3:K9:76:GLU:HA	1.79	0.64
2:L7:52:ALA:O	2:L7:56:ALA:N	2.31	0.64
3:U8:106:PRO:HG3	3:U8:150:TYR:HE2	1.63	0.64
3:V8:127:ARG:HD3	3:48:27:ARG:HD2	1.78	0.64
2:W5:47:ARG:NH1	2:W5:84:ASP:OD1	2.30	0.64
2:Y3:47:ARG:NH1	2:Y3:84:ASP:OD1	2.31	0.64
2:Z6:32:ILE:HD13	2:Z6:90:GLY:HA3	1.80	0.64
3:29:39:TRP:HA	3:29:76:GLU:HA	1.80	0.64
2:B3:7:MET:HE1	2:C7:17:VAL:HG21	1.80	0.64
2:D2:13:PHE:N	2:E5:9:GLU:OE2	2.30	0.64
3:I8:12:ASP:O	3:I8:82:GLN:NE2	2.30	0.64
2:L3:13:PHE:HB2	2:L4:37:THR:HG21	1.78	0.64
2:P3:90:GLY:O	2:P3:92:THR:N	2.31	0.64
2:T2:54:LYS:HZ1	2:T5:55:ALA:HB2	1.63	0.64
3:U8:17:GLN:NE2	3:U8:159:GLU:OE2	2.30	0.64
3:Y8:169:VAL:HG12	3:Y8:171:PRO:HD3	1.80	0.64
3:Z8:170:THR:OG1	3:Z8:177:ARG:N	2.19	0.64
3:18:6:ARG:NH1	3:18:72:TYR:OH	2.27	0.64
2:E2:32:ILE:CD1	2:E2:90:GLY:HA3	2.28	0.63
3:E8:61:VAL:HG12	3:E8:62:GLN:H	1.63	0.63
1:F1:95:LYS:HE3	2:F5:78:ARG:HH11	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K1:31:ASP:OD1	1:K1:35:THR:OG1	2.15	0.63
2:L3:47:ARG:HH22	2:L3:79:PRO:HG2	1.62	0.63
2:N6:25:LYS:NZ	3:P8:58:ALA:HA	2.13	0.63
3:O8:170:THR:HG1	3:O8:177:ARG:H	1.46	0.63
1:P1:7:VAL:HG12	1:Q1:87:MET:HG2	1.80	0.63
2:P4:23:MET:HE3	2:P4:46:VAL:HG21	1.78	0.63
2:Q3:90:GLY:O	2:Q3:92:THR:N	2.30	0.63
3:R8:18:LEU:O	3:R8:22:ILE:N	2.25	0.63
2:T2:32:ILE:HD11	2:T2:90:GLY:HA3	1.80	0.63
3:U8:134:ILE:HG12	3:U8:181:ALA:HB2	1.80	0.63
1:X1:28:ARG:NH1	1:X1:36:PRO:HB2	2.13	0.63
3:48:170:THR:HG1	3:48:177:ARG:H	1.46	0.63
2:D3:8:MET:HE1	2:E7:17:VAL:HG11	1.80	0.63
2:E5:47:ARG:NH1	2:E5:84:ASP:OD1	2.28	0.63
2:F2:37:THR:HG21	2:F4:13:PHE:HB2	1.80	0.63
2:G2:10:VAL:HG11	2:G2:15:GLY:HA3	1.79	0.63
3:H8:8:TYR:O	3:H8:103:ARG:NH2	2.31	0.63
3:I8:61:VAL:HG12	3:I8:62:GLN:H	1.62	0.63
3:L8:103:ARG:HH21	3:L8:201:VAL:HG13	1.63	0.63
3:M8:55:ALA:O	3:M8:59:THR:OG1	2.16	0.63
2:R3:17:VAL:HG21	2:R4:7:MET:HE1	1.79	0.63
2:V2:10:VAL:HG11	2:V2:15:GLY:HA3	1.80	0.63
3:V8:18:LEU:HD11	3:V8:156:ASN:HA	1.80	0.63
3:W9:4:THR:N	3:W9:43:ALA:O	2.22	0.63
3:X8:6:ARG:NH2	3:X8:72:TYR:OH	2.31	0.63
3:Z8:7:THR:OG1	3:Z8:41:GLU:N	2.31	0.63
3:A8:53:ASP:OD1	3:I8:121:GLN:NE2	2.32	0.63
3:B8:134:ILE:HG12	3:B8:181:ALA:HB2	1.81	0.63
2:C5:3:ASP:O	2:C5:47:ARG:NH2	2.29	0.63
3:C8:141:PHE:HB3	3:C8:180:LEU:HB2	1.81	0.63
2:D7:52:ALA:O	2:D7:56:ALA:N	2.31	0.63
3:D8:120:TYR:HD1	3:N8:29:PHE:CZ	2.17	0.63
2:F2:8:ILE:HG12	2:F2:73:VAL:HG22	1.80	0.63
2:H4:78:ARG:NH2	3:H8:159:GLU:OE1	2.31	0.63
3:J8:9:ILE:HD12	3:J8:150:TYR:HA	1.79	0.63
2:S3:4:ALA:HB2	2:S3:50:VAL:HG22	1.79	0.63
2:S4:53:VAL:O	2:S4:57:THR:OG1	2.16	0.63
2:U2:90:GLY:O	2:U2:92:THR:N	2.31	0.63
3:U8:11:LEU:HB3	3:U8:14:LEU:HD21	1.79	0.63
3:V8:186:GLU:O	3:V8:190:ALA:N	2.29	0.63
2:43:9:GLU:HB3	2:43:43:THR:HG23	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E7:52:ALA:O	2:E7:56:ALA:N	2.31	0.63
2:F5:7:MET:HE1	2:G2:17:VAL:HG21	1.80	0.63
3:G8:50:ARG:HD2	3:G8:95:LYS:HD3	1.79	0.63
3:K8:50:ARG:HD2	3:K8:95:LYS:HD3	1.80	0.63
3:N8:9:ILE:HD12	3:N8:150:TYR:HA	1.81	0.63
2:P4:16:MET:HG2	2:P4:44:ALA:HB2	1.80	0.63
2:Q7:50:VAL:HG21	2:Q7:77:PRO:HB3	1.80	0.63
3:S8:134:ILE:HG12	3:S8:181:ALA:HB2	1.79	0.63
2:12:47:ARG:NH1	2:12:84:ASP:OD2	2.31	0.63
3:18:134:ILE:HG12	3:18:181:ALA:HB2	1.80	0.63
3:B8:61:VAL:HG12	3:B8:62:GLN:H	1.63	0.63
2:C7:52:ALA:O	2:C7:56:ALA:N	2.30	0.63
2:D3:10:GLU:HB3	2:D3:44:THR:HG23	1.80	0.63
3:E8:56:LEU:O	2:F7:78:ARG:NH2	2.32	0.63
2:U6:13:PHE:N	2:U7:9:GLU:OE2	2.29	0.63
2:Y3:5:LEU:HB3	2:Y3:47:ARG:HH21	1.64	0.63
2:Z3:7:MET:HE1	2:17:17:VAL:HG11	1.81	0.63
3:Z8:61:VAL:HG12	3:Z8:62:GLN:H	1.63	0.63
2:D2:29:VAL:HG11	2:D2:46:VAL:HG22	1.81	0.63
3:D8:105:LYS:N	3:D8:204:VAL:O	2.25	0.63
2:F7:10:VAL:HG11	2:F7:15:GLY:HA3	1.79	0.63
2:G2:3:ASP:O	2:G2:47:ARG:NH1	2.31	0.63
1:J1:64:ARG:HD3	1:11:62:SER:HB2	1.81	0.63
2:O2:4:ALA:O	2:O2:47:ARG:NH1	2.31	0.63
2:P4:31:LEU:HA	2:P4:46:VAL:HG12	1.81	0.63
3:T8:17:GLN:O	3:T8:20:THR:OG1	2.14	0.63
2:W5:16:MET:HG2	2:W5:44:ALA:HB2	1.81	0.63
3:X8:6:ARG:HA	3:X8:104:LEU:HG	1.80	0.63
2:Y3:18:GLU:OE1	2:Y4:74:HIS:NE2	2.21	0.63
3:A8:27:ARG:HD2	3:I8:127:ARG:HH21	1.63	0.63
3:B8:7:THR:HG23	3:B8:41:GLU:HB3	1.80	0.63
2:C7:8:ILE:HG13	2:C7:73:VAL:HG22	1.80	0.63
3:C8:9:ILE:HD12	3:C8:150:TYR:HA	1.81	0.63
2:H3:7:MET:HE1	2:Z7:17:VAL:HG21	1.80	0.63
2:I7:52:ALA:O	2:I7:56:ALA:N	2.30	0.63
2:K5:10:VAL:HG11	2:K5:15:GLY:HA3	1.79	0.63
3:L8:9:ILE:HB	3:L8:39:TRP:HB2	1.81	0.63
2:N2:3:ASP:O	2:N2:47:ARG:NH1	2.30	0.63
2:V2:19:ALA:HB2	2:V2:64:ALA:HB2	1.79	0.63
3:28:9:ILE:HD12	3:28:150:TYR:HA	1.81	0.63
3:28:103:ARG:HH21	3:28:201:VAL:HG13	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A1:1:MET:N	1:B1:75:ASP:OD1	2.25	0.63
2:A3:7:MET:HE1	2:B7:17:VAL:HG21	1.79	0.63
3:G8:19:ALA:HB3	3:G8:33:PRO:HG3	1.81	0.63
3:H8:111:HIS:ND1	3:H8:195:GLU:OE2	2.31	0.63
2:N6:32:ILE:HD11	2:N6:47:ARG:HD2	1.80	0.63
1:O1:63:ALA:HB1	1:O1:77:THR:HG22	1.81	0.63
3:P8:55:ALA:O	3:P8:59:THR:OG1	2.16	0.63
2:T5:32:ILE:HD13	2:T5:90:GLY:HA3	1.81	0.63
2:X2:19:ALA:HB2	2:X2:64:ALA:HB2	1.78	0.63
3:X8:104:LEU:HD12	3:X8:147:PRO:HG3	1.80	0.63
2:Z2:92:THR:O	2:Z2:94:GLY:N	2.31	0.63
3:18:111:HIS:HA	3:18:142:ILE:O	1.99	0.63
2:32:10:VAL:HG11	2:32:15:GLY:HA3	1.81	0.63
2:42:45:VAL:HG11	2:42:89:LEU:HD12	1.80	0.63
3:A8:21:PHE:HE2	3:A8:169:VAL:HB	1.64	0.63
3:B8:8:TYR:HE2	3:B8:93:LEU:HD23	1.64	0.63
3:G8:170:THR:HG1	3:G8:177:ARG:H	1.45	0.63
3:I8:47:ALA:HB1	3:I8:50:ARG:HH12	1.63	0.63
3:M8:60:LYS:HG2	2:27:78:ARG:HD3	1.80	0.63
3:C8:183:SER:OG	3:C8:186:GLU:OE2	2.14	0.62
3:D8:42:ILE:HD11	3:D8:96:LEU:HD11	1.81	0.62
3:G8:55:ALA:O	3:G8:59:THR:OG1	2.17	0.62
2:L5:16:MET:HG2	2:L5:44:ALA:HB2	1.80	0.62
3:M8:59:THR:O	2:27:78:ARG:NE	2.32	0.62
3:O8:42:ILE:HD11	3:O8:96:LEU:HD11	1.81	0.62
3:P8:145:THR:HG21	3:P8:198:ILE:HG21	1.81	0.62
3:Q8:110:THR:O	3:Q8:143:LEU:HA	1.99	0.62
3:S8:50:ARG:HD2	3:S8:95:LYS:HD3	1.81	0.62
3:39:20:THR:O	3:39:24:LYS:N	2.32	0.62
2:E2:37:THR:HG21	2:E4:13:PHE:HB2	1.81	0.62
2:G5:37:THR:HG21	2:W2:13:PHE:HB2	1.81	0.62
2:G6:8:ILE:HG12	2:G6:73:VAL:HG12	1.79	0.62
3:I9:20:THR:O	3:I9:24:LYS:N	2.28	0.62
1:J1:64:ARG:HH11	1:11:62:SER:CB	2.12	0.62
2:J3:90:GLY:O	2:J3:92:THR:N	2.32	0.62
3:J8:106:PRO:HG3	3:J8:150:TYR:CE2	2.34	0.62
2:K2:32:ILE:HD11	2:K2:90:GLY:HA3	1.81	0.62
3:L8:134:ILE:HG12	3:L8:181:ALA:HB2	1.82	0.62
2:O7:19:ALA:HB2	2:O7:64:ALA:HB2	1.81	0.62
2:R3:4:ALA:O	2:R3:47:ARG:HD2	2.00	0.62
2:T2:54:LYS:NZ	2:T5:55:ALA:HB2	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:W8:5:LEU:HD12	3:W8:42:ILE:HD11	1.80	0.62
2:X3:90:GLY:O	2:X3:92:THR:N	2.32	0.62
3:X8:109:MET:HB2	3:X8:144:GLU:HB3	1.81	0.62
2:Y3:30:GLU:OE1	2:Y3:91:ARG:NH2	2.27	0.62
1:21:68:VAL:C	1:21:72:ARG:HH12	2.07	0.62
2:23:26:ALA:O	3:28:12:ASP:HB3	1.99	0.62
2:33:10:VAL:HG11	2:33:15:GLY:HA3	1.79	0.62
1:A1:62:SER:HB2	1:B1:64:ARG:HD3	1.81	0.62
2:A2:29:VAL:HG11	2:A2:46:VAL:HG22	1.80	0.62
2:A2:47:ARG:NH2	2:A2:84:ASP:OD2	2.32	0.62
2:B4:78:ARG:NH2	3:B8:159:GLU:OE1	2.33	0.62
2:B7:10:VAL:HG11	2:B7:15:GLY:HA3	1.80	0.62
3:E8:42:ILE:HD11	3:E8:96:LEU:HD11	1.80	0.62
1:K1:86:GLU:HG2	1:K1:87:MET:N	2.13	0.62
1:L1:64:ARG:HD3	1:21:62:SER:HB2	1.80	0.62
1:O1:21:GLY:HA2	2:P2:58:GLU:HB3	1.80	0.62
2:P5:8:ILE:HG12	2:P5:73:VAL:HG22	1.79	0.62
2:P5:10:VAL:HG11	2:P5:15:GLY:HA3	1.81	0.62
2:T5:34:TYR:OH	2:T6:35:GLU:OE2	2.12	0.62
2:T7:17:VAL:HG11	2:U3:7:MET:HE1	1.81	0.62
3:V8:134:ILE:HG12	3:V8:181:ALA:HB2	1.81	0.62
2:X3:47:ARG:HH12	2:X3:84:ASP:CG	2.06	0.62
3:X8:12:ASP:O	3:X8:82:GLN:NE2	2.27	0.62
3:29:20:THR:O	3:29:24:LYS:N	2.31	0.62
2:34:78:ARG:NH2	3:38:159:GLU:O	2.33	0.62
3:48:24:LYS:HE2	3:49:122:THR:O	1.99	0.62
1:B1:54:VAL:HG21	1:B1:93:PHE:CE2	2.34	0.62
3:C8:24:LYS:HG2	3:C9:127:ARG:HA	1.80	0.62
3:F8:8:TYR:HA	3:F8:40:VAL:HG22	1.80	0.62
2:J3:18:GLU:OE1	2:J4:74:HIS:NE2	2.30	0.62
2:J5:18:GLU:OE1	2:J6:74:HIS:NE2	2.31	0.62
2:N4:10:VAL:HG11	2:N4:15:GLY:HA3	1.80	0.62
3:P8:134:ILE:HG12	3:P8:181:ALA:HB2	1.80	0.62
2:R2:43:THR:HG21	2:R4:13:PHE:HD2	1.62	0.62
2:T3:32:ILE:HD11	2:T3:47:ARG:HG3	1.81	0.62
3:V8:123:GLN:HG3	3:V9:23:GLY:HA3	1.81	0.62
3:18:106:PRO:HG3	3:18:150:TYR:CE2	2.34	0.62
2:32:45:VAL:HG11	2:32:89:LEU:HD12	1.80	0.62
1:L1:68:VAL:HA	1:L1:72:ARG:HH12	1.63	0.62
2:M7:52:ALA:O	2:M7:56:ALA:N	2.32	0.62
2:Q3:61:GLN:HB2	2:Q3:73:VAL:HG21	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R8:141:PHE:HB3	3:R8:180:LEU:HB2	1.81	0.62
3:R8:144:GLU:HB2	3:S8:46:ILE:HD11	1.79	0.62
1:T1:64:ARG:HD3	1:U1:62:SER:HB2	1.79	0.62
2:V6:13:PHE:N	2:V7:9:GLU:OE2	2.29	0.62
2:12:32:ILE:CD1	2:12:90:GLY:HA3	2.29	0.62
2:43:47:ARG:NH1	2:43:84:ASP:OD1	2.31	0.62
2:D7:78:ARG:NH2	3:N8:56:LEU:O	2.32	0.62
2:F2:3:ASP:O	2:F2:47:ARG:NH1	2.31	0.62
2:G6:32:ILE:HD13	2:G6:90:GLY:HA3	1.80	0.62
2:G7:10:VAL:HG11	2:G7:15:GLY:HA3	1.81	0.62
2:H3:47:ARG:HH11	2:H3:91:ARG:HB2	1.64	0.62
2:I5:34:TYR:OH	2:I6:35:GLU:OE2	2.13	0.62
2:K2:47:ARG:HD3	2:K2:91:ARG:HG2	1.81	0.62
2:L6:19:ALA:HB2	2:L6:64:ALA:HB2	1.80	0.62
2:T4:57:THR:HG22	2:T4:73:VAL:HG13	1.81	0.62
2:V3:90:GLY:O	2:V3:92:THR:N	2.32	0.62
3:V8:45:GLY:HA2	3:V8:48:ILE:HD13	1.79	0.62
1:C1:66:THR:O	1:C1:69:THR:OG1	2.15	0.62
2:E7:10:VAL:HG11	2:E7:15:GLY:HA3	1.81	0.62
3:K8:123:GLN:NE2	3:K9:31:PRO:O	2.32	0.62
2:Q2:8:ILE:HG12	2:Q2:73:VAL:HG22	1.82	0.62
2:T2:3:ASP:OD2	2:T2:91:ARG:NE	2.31	0.62
2:14:3:ASP:OD2	2:14:91:ARG:NH2	2.32	0.62
2:15:47:ARG:NH1	2:15:91:ARG:HB2	2.15	0.62
3:F8:18:LEU:HD11	3:F8:156:ASN:HA	1.81	0.62
2:Q3:26:ALA:O	3:Q8:12:ASP:HB3	1.98	0.62
2:12:19:ALA:HB2	2:12:64:ALA:HB2	1.82	0.62
2:22:32:ILE:CD1	2:22:90:GLY:HA3	2.29	0.62
3:D8:8:TYR:CE2	3:D8:93:LEU:HD23	2.34	0.62
2:P6:13:PHE:HB2	2:P7:35:THR:HG21	1.81	0.62
2:R2:32:ILE:CD1	2:R2:90:GLY:HA3	2.30	0.62
2:R5:47:ARG:NH1	2:R5:84:ASP:OD1	2.30	0.62
3:R8:8:TYR:CE2	3:R8:93:LEU:HD23	2.34	0.62
2:V7:8:ILE:HG12	2:V7:73:VAL:HG22	1.82	0.62
3:W9:121:GLN:O	3:W9:125:ILE:N	2.31	0.62
3:49:88:ALA:O	3:49:92:ILE:N	2.30	0.62
1:G1:64:ARG:HD3	1:W1:62:SER:HB2	1.81	0.62
2:H2:19:ALA:HB2	2:H2:64:ALA:HB2	1.82	0.62
3:M8:154:ALA:HB2	3:M8:198:ILE:HD11	1.82	0.62
3:N8:45:GLY:HA3	3:N8:73:GLY:H	1.64	0.62
2:O3:7:MET:HE1	2:37:17:VAL:HG11	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O9:154:ALA:HB1	3:O9:194:ALA:HB1	1.81	0.62
2:T5:7:MET:HE1	2:U2:17:VAL:HG21	1.81	0.62
3:Y8:134:ILE:HG12	3:Y8:181:ALA:HB2	1.82	0.62
3:19:45:GLY:N	3:19:71:ALA:O	2.33	0.62
1:41:53:GLU:OE2	2:45:78:ARG:HB3	2.00	0.62
2:D2:13:PHE:HB2	2:E5:37:THR:HG21	1.81	0.61
3:D8:123:GLN:NE2	3:D9:31:PRO:O	2.33	0.61
2:I6:45:VAL:HG11	2:I6:89:LEU:HD22	1.82	0.61
2:J5:7:MET:HE1	2:12:17:VAL:HG21	1.81	0.61
3:J8:112:GLN:OE1	3:L8:50:ARG:NE	2.30	0.61
3:T9:103:ARG:O	3:T9:204:VAL:N	2.18	0.61
2:W2:78:ARG:HG3	2:W5:28:LYS:N	2.14	0.61
1:X1:16:GLU:CD	1:X1:17:PRO:HD2	2.24	0.61
3:X8:42:ILE:HD11	3:X8:96:LEU:HD11	1.80	0.61
2:Y5:33:TYR:OH	2:Y6:35:GLU:OE2	2.10	0.61
2:14:54:LYS:HD2	2:14:75:VAL:HG11	1.81	0.61
3:18:61:VAL:HG21	3:18:88:ALA:HB2	1.81	0.61
3:38:42:ILE:HD13	3:38:96:LEU:HD21	1.82	0.61
2:45:16:MET:HG2	2:45:44:ALA:HB2	1.82	0.61
3:B8:29:PHE:CZ	3:L8:120:TYR:HD1	2.17	0.61
2:C2:32:ILE:HD11	2:C2:90:GLY:HA3	1.81	0.61
3:N8:50:ARG:HD2	3:N8:95:LYS:HD3	1.83	0.61
3:N9:88:ALA:O	3:N9:92:ILE:N	2.32	0.61
2:O5:16:MET:HG2	2:O5:44:ALA:HB2	1.81	0.61
2:O6:57:THR:HG21	2:O6:75:VAL:HG22	1.82	0.61
3:S8:93:LEU:HB2	3:S8:98:VAL:O	1.99	0.61
3:U8:24:LYS:NZ	3:U9:134:ILE:O	2.30	0.61
2:X3:13:PHE:HB2	2:X4:37:THR:HG21	1.81	0.61
2:Y5:7:ILE:HG12	2:Y5:72:VAL:HG22	1.81	0.61
2:32:32:ILE:HD11	2:32:90:GLY:HA3	1.82	0.61
2:43:19:ALA:HB2	2:43:64:ALA:HB2	1.82	0.61
3:A8:8:TYR:HE2	3:A8:93:LEU:HD23	1.64	0.61
2:F2:19:ALA:HB2	2:F2:64:ALA:HB2	1.83	0.61
2:G3:90:GLY:O	2:G3:92:THR:N	2.31	0.61
2:H3:13:PHE:HD2	2:H4:43:THR:HG21	1.65	0.61
2:J7:52:ALA:O	2:J7:56:ALA:N	2.33	0.61
2:P3:26:ALA:O	3:P8:12:ASP:HB3	2.01	0.61
1:Q1:28:ARG:NH1	1:Q1:36:PRO:HB2	2.16	0.61
3:X8:67:VAL:HG12	3:48:127:ARG:HH21	1.65	0.61
2:42:9:GLU:OE2	2:44:13:PHE:N	2.30	0.61
2:A2:4:ALA:O	2:A2:47:ARG:NH1	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C8:17:GLN:O	3:C8:20:THR:OG1	2.19	0.61
2:E3:47:ARG:NH1	2:E3:91:ARG:HB2	2.09	0.61
1:H1:1:MET:N	1:Z1:75:ASP:OD1	2.23	0.61
3:L8:16:PRO:HA	3:L8:33:PRO:HB3	1.81	0.61
1:V1:61:SER:HB3	1:W1:61:SER:HB2	1.82	0.61
3:V8:59:THR:O	2:X7:78:ARG:NE	2.33	0.61
2:15:34:TYR:OH	2:16:35:GLU:OE2	2.09	0.61
3:A8:169:VAL:HG12	3:A8:171:PRO:HD3	1.81	0.61
3:H8:122:THR:HG21	3:H8:136:PRO:HA	1.81	0.61
2:I2:3:ASP:OD2	2:I2:91:ARG:NH2	2.31	0.61
1:O1:70:ASN:C	1:O1:72:ARG:H	2.09	0.61
3:O8:50:ARG:HD2	3:O8:95:LYS:HD3	1.83	0.61
2:P3:47:ARG:HH22	2:P3:79:PRO:HG2	1.66	0.61
2:Q4:53:VAL:O	2:Q4:57:THR:OG1	2.14	0.61
2:R3:7:MET:HE1	2:V7:17:VAL:HG11	1.81	0.61
2:S2:16:MET:HG2	2:S2:44:ALA:HB2	1.82	0.61
3:T8:55:ALA:O	3:T8:59:THR:OG1	2.18	0.61
2:U2:32:ILE:HD11	2:U2:90:GLY:HA3	1.82	0.61
2:V5:13:PHE:HB2	2:V6:37:THR:HG21	1.81	0.61
2:V7:60:GLY:O	2:V7:64:ALA:N	2.32	0.61
1:W1:28:ARG:HH12	1:W1:36:PRO:C	2.08	0.61
2:17:8:ILE:HG12	2:17:73:VAL:HG22	1.82	0.61
3:18:21:PHE:HE2	3:18:169:VAL:HB	1.66	0.61
2:46:55:ALA:HB1	3:48:115:ARG:HD2	1.82	0.61
3:C8:60:LYS:HG2	2:M7:78:ARG:HD3	1.82	0.61
2:E2:3:ASP:C	2:E2:47:ARG:HH12	2.09	0.61
3:G9:20:THR:O	3:G9:24:LYS:N	2.33	0.61
1:R1:87:MET:HG2	1:V1:7:VAL:HG12	1.83	0.61
3:R8:48:ILE:HG23	3:R8:75:LEU:HB2	1.81	0.61
3:W8:111:HIS:HA	3:W8:142:ILE:O	2.00	0.61
3:28:127:ARG:O	3:28:127:ARG:HD3	2.00	0.61
1:D1:68:VAL:C	1:D1:72:ARG:HH12	2.09	0.61
3:G8:42:ILE:HD11	3:G8:96:LEU:HD11	1.82	0.61
2:J7:5:LEU:HD23	2:J7:76:ILE:HD12	1.83	0.61
3:L9:170:THR:N	3:L9:177:ARG:O	2.21	0.61
2:N2:19:ALA:HB2	2:N2:64:ALA:HB2	1.82	0.61
2:N3:19:ALA:HB2	2:N3:64:ALA:HB2	1.83	0.61
2:P6:45:VAL:HG11	2:P6:89:LEU:HD22	1.83	0.61
2:R2:8:ILE:HG12	2:R2:73:VAL:HG22	1.82	0.61
3:S8:154:ALA:HB2	3:S8:198:ILE:HD11	1.82	0.61
3:U8:47:ALA:HB1	3:U8:50:ARG:HH12	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:W6:47:ARG:NH2	2:W6:84:ASP:OD1	2.34	0.61
3:A8:134:ILE:HD13	3:A8:181:ALA:HB2	1.82	0.61
2:E6:47:ARG:NH2	2:E6:84:ASP:OD1	2.34	0.61
2:F2:13:PHE:HB2	2:R5:37:THR:HG21	1.82	0.61
3:F8:106:PRO:HG3	3:F8:150:TYR:CE2	2.35	0.61
3:I8:65:VAL:HG12	3:I8:76:GLU:HB3	1.81	0.61
1:L1:70:ASN:C	1:L1:72:ARG:H	2.09	0.61
3:O8:123:GLN:NE2	3:O9:31:PRO:O	2.34	0.61
2:P4:10:VAL:HG11	2:P4:15:GLY:HA3	1.81	0.61
2:T3:17:VAL:HG21	2:T4:7:MET:HE1	1.82	0.61
2:T3:47:ARG:HH11	2:T3:91:ARG:HB2	1.65	0.61
2:W3:47:ARG:HH22	2:W3:79:PRO:HG2	1.65	0.61
1:Z1:63:ALA:HB1	1:Z1:77:THR:HG22	1.82	0.61
2:42:54:LYS:HZ2	2:45:55:ALA:HB2	1.66	0.61
2:C2:19:ALA:HB2	2:C2:64:ALA:HB2	1.82	0.61
2:D6:30:GLU:OE1	2:D6:91:ARG:NH2	2.32	0.61
3:E9:20:THR:O	3:E9:24:LYS:N	2.30	0.61
3:F8:186:GLU:O	3:F8:190:ALA:N	2.33	0.61
3:G8:111:HIS:HA	3:G8:142:ILE:O	2.01	0.61
2:M7:47:ARG:NH1	2:M7:89:LEU:O	2.34	0.61
2:Q3:17:VAL:HG21	2:Q4:7:MET:HE1	1.81	0.61
2:Q3:47:ARG:HH22	2:Q3:79:PRO:HG2	1.66	0.61
3:R8:59:THR:O	2:U7:78:ARG:NE	2.33	0.61
1:U1:53:GLU:OE2	2:U5:78:ARG:HB3	2.00	0.61
3:18:169:VAL:HG12	3:18:171:PRO:HD3	1.82	0.61
2:23:12:GLY:HA2	2:24:9:GLU:OE2	2.01	0.61
2:46:4:ALA:N	2:46:48:GLY:O	2.27	0.61
2:A2:29:VAL:HG12	2:A2:46:VAL:HG22	1.83	0.61
2:B3:9:GLU:HB3	2:B3:43:THR:HG23	1.83	0.61
2:B7:78:ARG:NE	3:J8:59:THR:O	2.33	0.61
2:D2:54:LYS:NZ	2:D5:55:ALA:HB2	2.15	0.61
3:F8:8:TYR:CE2	3:F8:93:LEU:HD23	2.36	0.61
3:G8:112:GLN:OE1	3:I8:50:ARG:NE	2.26	0.61
1:M1:32:PRO:HG3	1:M1:87:MET:CE	2.31	0.61
3:N8:42:ILE:HD11	3:N8:96:LEU:HD11	1.82	0.61
3:O8:9:ILE:HD12	3:O8:150:TYR:HA	1.81	0.61
3:P8:12:ASP:O	3:P8:82:GLN:NE2	2.31	0.61
3:S8:122:THR:HG21	3:S8:136:PRO:HA	1.82	0.61
2:U3:9:GLU:HB3	2:U3:43:THR:HG23	1.82	0.61
2:U5:10:VAL:HG11	2:U5:15:GLY:HA3	1.82	0.61
3:28:11:LEU:HD22	3:28:156:ASN:HD22	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:48:111:HIS:ND1	3:48:195:GLU:OE2	2.34	0.61
2:A2:3:ASP:OD2	2:A2:91:ARG:NE	2.30	0.60
2:A3:5:LEU:HB3	2:A3:76:ILE:HB	1.81	0.60
3:A8:8:TYR:CE2	3:A8:93:LEU:HD23	2.36	0.60
3:F8:170:THR:OG1	3:F8:177:ARG:N	2.23	0.60
2:H7:8:ILE:HG12	2:H7:73:VAL:HG22	1.81	0.60
2:M5:35:GLU:HG2	2:N2:13:PHE:CE2	2.36	0.60
2:M7:10:VAL:HG11	2:M7:15:GLY:HA3	1.82	0.60
3:M8:8:TYR:CE2	3:M8:93:LEU:HD23	2.36	0.60
1:N1:22:LEU:HD22	1:N1:44:ALA:HB1	1.82	0.60
2:T6:18:GLU:OE1	2:T7:74:HIS:NE2	2.32	0.60
3:V8:3:ILE:HD13	3:V8:47:ALA:HB1	1.83	0.60
2:W2:19:ALA:HB2	2:W2:64:ALA:HB2	1.83	0.60
2:Z3:8:ILE:HD12	2:Z3:19:ALA:HB1	1.83	0.60
3:Z8:55:ALA:O	3:Z8:59:THR:OG1	2.17	0.60
3:Z9:93:LEU:O	3:Z9:97:GLU:N	2.34	0.60
2:13:10:VAL:HG11	2:13:15:GLY:HA3	1.82	0.60
3:L8:21:PHE:CE2	3:L8:169:VAL:HB	2.36	0.60
3:P9:37:SER:HA	3:P9:78:HIS:HA	1.83	0.60
2:U7:52:ALA:O	2:U7:56:ALA:N	2.34	0.60
3:Y8:134:ILE:HD11	3:Y8:140:LEU:HD13	1.82	0.60
3:A9:105:LYS:N	3:A9:204:VAL:O	2.32	0.60
2:C7:50:VAL:HG21	2:C7:77:PRO:HB3	1.83	0.60
3:H8:142:ILE:HD12	3:W8:46:ILE:HG22	1.84	0.60
3:O8:145:THR:HG21	3:O8:198:ILE:HG21	1.82	0.60
2:P7:8:VAL:HG11	2:P7:13:GLY:HA3	1.83	0.60
3:X9:66:GLN:HA	3:X9:75:LEU:HA	1.82	0.60
2:16:13:PHE:HB2	2:17:37:THR:HG21	1.83	0.60
3:28:170:THR:HG1	3:28:177:ARG:H	1.49	0.60
2:A5:35:GLU:HG2	2:E2:13:PHE:CE2	2.37	0.60
2:B2:17:VAL:HG21	2:C5:7:MET:HE1	1.84	0.60
2:C3:47:ARG:HH12	2:C3:84:ASP:CG	2.08	0.60
2:F5:16:MET:HG2	2:F5:44:ALA:HB2	1.83	0.60
2:G3:32:ILE:HD12	2:G3:90:GLY:HA3	1.83	0.60
2:J7:10:VAL:HG22	2:J7:70:VAL:HA	1.83	0.60
3:J8:41:GLU:HB2	3:J8:74:LEU:HD13	1.83	0.60
3:J8:177:ARG:HG2	3:L8:46:ILE:HD11	1.83	0.60
2:N3:3:ASP:OD1	2:N3:4:ALA:N	2.34	0.60
2:P3:4:ALA:O	2:P3:47:ARG:HD2	2.01	0.60
3:P8:170:THR:OG1	3:P8:177:ARG:N	2.21	0.60
2:Q3:47:ARG:NH1	2:Q3:91:ARG:HB2	2.07	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R2:45:VAL:HG11	2:R2:89:LEU:HD12	1.83	0.60
3:V8:122:THR:HG21	3:V8:136:PRO:HA	1.82	0.60
2:46:13:PHE:HB2	2:47:37:THR:HG21	1.83	0.60
2:B7:52:ALA:O	2:B7:56:ALA:N	2.31	0.60
2:C6:11:ARG:NH1	2:C7:41:TYR:OH	2.34	0.60
3:C8:123:GLN:CG	3:C9:23:GLY:HA3	2.32	0.60
2:H2:3:ASP:O	2:H2:47:ARG:NH2	2.33	0.60
2:H4:54:LYS:HD2	2:H4:75:VAL:HG11	1.81	0.60
3:M8:183:SER:OG	3:M8:186:GLU:OE2	2.18	0.60
2:R2:3:ASP:O	2:R2:47:ARG:NH1	2.27	0.60
3:V8:65:VAL:HG12	3:V8:76:GLU:HB3	1.83	0.60
3:V8:177:ARG:HB3	3:48:46:ILE:HD11	1.83	0.60
3:Z9:144:GLU:HA	3:Z9:176:GLY:O	2.01	0.60
3:38:3:ILE:HD11	3:38:50:ARG:HH12	1.64	0.60
2:E3:90:GLY:O	2:E3:92:THR:N	2.35	0.60
3:E8:59:THR:O	2:F7:78:ARG:NE	2.34	0.60
2:F6:32:ILE:HG21	2:F6:90:GLY:HA3	1.84	0.60
3:M9:88:ALA:O	3:M9:92:ILE:N	2.34	0.60
2:O3:90:GLY:O	2:O3:92:THR:N	2.35	0.60
2:T3:13:PHE:HB2	2:T4:37:THR:HG21	1.82	0.60
3:18:44:PRO:HG2	3:18:47:ALA:H	1.65	0.60
2:23:90:GLY:O	2:23:92:THR:N	2.34	0.60
3:39:93:LEU:O	3:39:97:GLU:HA	2.01	0.60
2:43:90:GLY:O	2:43:92:THR:N	2.34	0.60
2:A5:32:ILE:HD12	2:A5:47:ARG:HG3	1.82	0.60
2:A7:78:ARG:NH2	3:G8:57:LYS:O	2.34	0.60
1:D1:50:GLY:N	1:D1:53:GLU:OE1	2.18	0.60
2:D5:36:LYS:NZ	2:D6:35:GLU:OE2	2.32	0.60
3:E9:101:GLU:HA	3:E9:203:GLY:HA2	1.82	0.60
2:F3:18:GLU:OE1	2:F4:74:HIS:NE2	2.29	0.60
3:F8:27:ARG:HB2	3:Q8:127:ARG:HH11	1.67	0.60
3:G8:21:PHE:HE2	3:G8:169:VAL:HB	1.65	0.60
1:H1:62:SER:HB2	1:Z1:64:ARG:HD3	1.82	0.60
2:L7:16:MET:HG3	2:L7:42:VAL:HG12	1.84	0.60
2:N2:54:LYS:NZ	2:N5:55:ALA:HB2	2.17	0.60
2:T3:9:GLU:HB3	2:T3:43:THR:HG23	1.83	0.60
2:X2:32:ILE:CD1	2:X2:90:GLY:HA3	2.32	0.60
2:Z2:18:GLU:OE1	2:15:74:HIS:NE2	2.34	0.60
2:33:90:GLY:O	2:33:92:THR:N	2.34	0.60
3:C8:27:ARG:HD2	3:M8:127:ARG:NE	2.17	0.60
1:F1:32:PRO:HG2	1:F1:87:MET:HE1	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H8:65:VAL:HG12	3:H8:76:GLU:HB3	1.84	0.60
2:I7:47:ARG:NH1	2:I7:89:LEU:O	2.35	0.60
3:I8:42:ILE:HD11	3:I8:96:LEU:HD11	1.84	0.60
3:K8:65:VAL:HG12	3:K8:76:GLU:HB3	1.84	0.60
2:L3:26:ALA:O	3:L8:12:ASP:HB3	2.02	0.60
2:L5:35:GLU:HG2	2:22:13:PHE:CE2	2.37	0.60
2:L6:55:ALA:HB1	3:L8:115:ARG:HD2	1.82	0.60
2:O6:19:ALA:HB2	2:O6:64:ALA:HB2	1.83	0.60
2:O7:17:VAL:HG11	2:P3:7:MET:HE1	1.84	0.60
2:P3:47:ARG:NH1	2:P3:91:ARG:HB2	2.15	0.60
3:38:42:ILE:HD11	3:38:96:LEU:HD11	1.84	0.60
3:D8:169:VAL:HG22	3:D8:178:LEU:HD13	1.84	0.60
2:F2:47:ARG:HD3	2:F2:91:ARG:HG2	1.83	0.60
3:J9:42:ILE:O	3:J9:73:GLY:N	2.30	0.60
1:K1:50:GLY:N	1:K1:53:GLU:OE1	2.25	0.60
3:L8:106:PRO:HG3	3:L8:150:TYR:CE2	2.35	0.60
2:P2:19:ALA:HB2	2:P2:64:ALA:HB2	1.83	0.60
2:V3:26:ALA:O	3:V8:12:ASP:HB3	2.01	0.60
2:W2:10:VAL:HG11	2:W2:15:GLY:HA3	1.83	0.60
2:X6:32:ILE:HG21	2:X6:90:GLY:HA3	1.84	0.60
1:Y1:45:ASP:OD1	1:Y1:47:VAL:N	2.27	0.60
1:31:17:PRO:HA	1:31:20:GLU:HG3	1.84	0.60
2:36:47:ARG:HH22	2:36:79:PRO:HG3	1.67	0.60
3:B8:106:PRO:HG3	3:B8:150:TYR:HE2	1.67	0.60
2:C2:37:THR:HG21	2:C4:13:PHE:HB2	1.84	0.60
2:I5:16:MET:HG2	2:I5:44:ALA:HB2	1.84	0.60
3:K8:150:TYR:HE2	3:K8:201:VAL:HG11	1.66	0.60
2:N3:17:VAL:HG21	2:N4:7:MET:HE1	1.83	0.60
3:R8:122:THR:HG22	3:R8:134:ILE:HG22	1.83	0.60
2:U2:47:ARG:NH2	2:U2:79:PRO:HG2	2.16	0.60
2:Z7:60:GLY:O	2:Z7:64:ALA:N	2.29	0.60
2:13:26:ALA:O	3:18:12:ASP:HB3	2.01	0.60
2:15:13:PHE:HD2	2:16:43:THR:HG21	1.66	0.60
3:38:7:THR:OG1	3:38:41:GLU:N	2.35	0.60
2:B3:8:ILE:HG22	2:B3:73:VAL:HG22	1.83	0.59
3:B8:15:GLN:HG2	3:B8:156:ASN:OD1	2.02	0.59
2:J4:20:ALA:HB1	2:J4:31:LEU:HD22	1.84	0.59
3:J8:127:ARG:HD3	3:L8:27:ARG:HH11	1.67	0.59
3:L8:17:GLN:O	3:L8:20:THR:OG1	2.19	0.59
2:O2:32:ILE:HD11	2:O2:90:GLY:HA3	1.83	0.59
2:Q4:16:MET:HG3	2:Q4:42:VAL:HG12	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R2:19:ALA:HB2	2:R2:64:ALA:HB2	1.83	0.59
2:S5:16:MET:HG2	2:S5:44:ALA:HB2	1.83	0.59
2:T5:3:ASP:O	2:T5:47:ARG:NH2	2.34	0.59
2:T6:19:ALA:HB2	2:T6:64:ALA:HB2	1.82	0.59
2:U3:47:ARG:HH12	2:U3:84:ASP:CG	2.10	0.59
2:V3:18:GLU:OE1	2:V4:74:HIS:NE2	2.32	0.59
3:G8:150:TYR:HE2	3:G8:201:VAL:HG11	1.67	0.59
2:I3:9:GLU:HB3	2:I3:43:THR:HG23	1.82	0.59
1:N1:70:ASN:C	1:N1:72:ARG:H	2.10	0.59
2:O5:3:ASP:O	2:O5:47:ARG:NH2	2.34	0.59
2:R3:51:ALA:HB2	2:U7:51:ALA:HB2	1.83	0.59
2:X2:32:ILE:HD11	2:X2:90:GLY:HA3	1.84	0.59
3:Z8:21:PHE:CE2	3:Z8:169:VAL:HB	2.38	0.59
2:27:10:VAL:HG11	2:27:15:GLY:HA3	1.83	0.59
3:38:9:ILE:HD12	3:38:150:TYR:HA	1.84	0.59
3:39:87:ALA:O	3:39:91:THR:N	2.32	0.59
2:46:19:ALA:HB2	2:46:64:ALA:HB2	1.83	0.59
3:A8:120:TYR:HD1	3:G8:29:PHE:CZ	2.19	0.59
2:B7:78:ARG:NH2	3:J8:57:LYS:O	2.35	0.59
2:D3:48:ARG:NH1	2:D3:85:ASP:OD1	2.36	0.59
2:O2:13:PHE:CE2	2:35:35:GLU:HG2	2.37	0.59
2:P3:17:VAL:HG21	2:P4:7:MET:HE1	1.85	0.59
2:R3:9:GLU:HB3	2:R3:43:THR:HG23	1.85	0.59
2:S3:32:ILE:HD13	2:S3:90:GLY:HA3	1.83	0.59
3:48:18:LEU:HD11	3:48:156:ASN:HA	1.83	0.59
3:A8:58:ALA:HA	2:I6:25:LYS:HZ1	1.68	0.59
2:E2:84:ASP:O	2:E2:92:THR:OG1	2.17	0.59
2:F5:74:HIS:NE2	2:G2:18:GLU:OE1	2.34	0.59
2:G2:16:MET:O	2:G2:20:ALA:N	2.29	0.59
2:G3:26:ALA:O	3:G8:12:ASP:HB3	2.02	0.59
2:G7:78:ARG:NE	3:I8:59:THR:O	2.35	0.59
2:I3:32:ILE:HD12	2:I3:90:GLY:HA3	1.85	0.59
2:I5:13:PHE:HD2	2:I6:43:THR:HG21	1.68	0.59
2:L2:32:ILE:CD1	2:L2:90:GLY:HA3	2.33	0.59
2:M3:51:ALA:HB2	2:27:51:ALA:HB2	1.84	0.59
3:T8:145:THR:HG21	3:T8:198:ILE:HG21	1.83	0.59
2:U7:19:ALA:HB2	2:U7:64:ALA:HB2	1.84	0.59
1:X1:16:GLU:OE1	1:X1:16:GLU:C	2.45	0.59
2:Y3:9:GLU:HB3	2:Y3:43:THR:HG23	1.84	0.59
2:Y4:10:VAL:HG11	2:Y4:15:GLY:HA3	1.84	0.59
2:17:50:VAL:HG21	2:17:77:PRO:HB3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B2:32:ILE:HD11	2:B2:90:GLY:HA3	1.85	0.59
2:D6:55:ALA:HB1	3:D8:115:ARG:HD2	1.84	0.59
3:D8:121:GLN:NE2	3:N8:49:ASN:OD1	2.35	0.59
2:F7:60:GLY:O	2:F7:64:ALA:N	2.29	0.59
2:H2:36:LYS:NZ	2:Z5:35:GLU:OE2	2.22	0.59
2:K7:17:VAL:CG1	2:L3:7:MET:HE1	2.29	0.59
3:K8:142:ILE:HB	3:18:46:ILE:HG21	1.84	0.59
2:L3:17:VAL:HG21	2:L4:7:MET:HE1	1.84	0.59
3:M8:56:LEU:O	2:27:78:ARG:NH2	2.35	0.59
2:Q3:9:GLU:HB3	2:Q3:43:THR:HG23	1.84	0.59
3:R8:6:ARG:NH1	3:R8:72:TYR:OH	2.35	0.59
1:S1:68:VAL:CA	1:S1:72:ARG:HH12	2.13	0.59
3:S8:65:VAL:HG12	3:S8:76:GLU:HB3	1.84	0.59
3:X8:9:ILE:HG21	3:X8:153:LEU:HB2	1.85	0.59
3:Z8:111:HIS:ND1	3:Z8:195:GLU:OE2	2.35	0.59
3:48:9:ILE:CD1	3:48:150:TYR:HA	2.32	0.59
2:A4:62:ARG:NE	2:A5:66:ARG:NH1	2.49	0.59
3:A8:170:THR:OG1	3:A8:177:ARG:N	2.23	0.59
3:F8:6:ARG:NH1	3:F8:72:TYR:OH	2.36	0.59
2:H4:78:ARG:NH2	3:H8:159:GLU:O	2.35	0.59
3:H8:15:GLN:HG3	3:H8:160:LYS:HB2	1.85	0.59
2:K2:19:ALA:HB2	2:K2:64:ALA:HB2	1.84	0.59
3:Q8:50:ARG:HD2	3:Q8:95:LYS:HD3	1.84	0.59
3:Q8:111:HIS:HB3	3:Q8:143:LEU:HD13	1.85	0.59
2:W3:90:GLY:O	2:W3:92:THR:N	2.33	0.59
1:Z1:50:GLY:N	1:Z1:53:GLU:OE1	2.24	0.59
1:31:18:ARG:NH2	1:31:71:ASN:O	2.35	0.59
3:38:11:LEU:HD21	3:38:153:LEU:HA	1.83	0.59
2:C3:7:MET:HE1	2:D7:17:VAL:HG21	1.85	0.59
2:E4:50:VAL:HG11	3:E8:186:GLU:HG3	1.84	0.59
3:H8:20:THR:HG21	3:H9:135:LEU:HA	1.85	0.59
3:K8:134:ILE:HG12	3:K8:181:ALA:HB2	1.83	0.59
3:R8:5:LEU:HD12	3:R8:42:ILE:HD11	1.85	0.59
3:S8:134:ILE:HD11	3:S8:140:LEU:HD13	1.85	0.59
2:V3:47:ARG:HH22	2:V3:79:PRO:HG2	1.68	0.59
3:Z8:17:GLN:NE2	3:Z8:159:GLU:HG3	2.18	0.59
2:13:47:ARG:HH12	2:13:79:PRO:HG2	1.66	0.59
2:33:17:VAL:HG21	2:34:7:MET:HE1	1.85	0.59
3:A8:60:LYS:HD2	2:I7:2:ALA:HB3	1.84	0.59
3:B8:17:GLN:O	3:B8:20:THR:OG1	2.20	0.59
3:B8:115:ARG:NH1	3:B8:188:ASP:OD2	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F3:21:ASP:OD2	2:F4:76:ILE:HD13	2.03	0.59
3:F8:51:VAL:HG13	3:F8:92:ILE:HG12	1.83	0.59
3:F8:183:SER:OG	3:F8:186:GLU:OE2	2.21	0.59
2:G2:45:VAL:HG11	2:G2:89:LEU:HD12	1.84	0.59
2:O7:10:VAL:HG11	2:O7:15:GLY:HA3	1.83	0.59
1:P1:64:ARG:HD3	1:Q1:62:SER:HB2	1.84	0.59
1:Q1:28:ARG:HH12	1:Q1:36:PRO:C	2.10	0.59
3:R8:106:PRO:HG3	3:R8:150:TYR:CE2	2.38	0.59
2:S3:90:GLY:O	2:S3:92:THR:N	2.35	0.59
2:V2:9:GLU:OE2	2:V4:13:PHE:N	2.35	0.59
3:V8:170:THR:HG1	3:V8:177:ARG:H	1.50	0.59
2:33:18:GLU:OE1	2:34:74:HIS:NE2	2.35	0.59
2:44:47:ARG:NH1	2:44:89:LEU:O	2.36	0.59
3:A8:183:SER:OG	3:A8:186:GLU:OE2	2.21	0.59
3:A9:4:THR:O	3:A9:43:ALA:N	2.26	0.59
1:C1:47:VAL:HG13	1:D1:14:ARG:NH1	2.18	0.59
2:C7:28:LYS:HA	2:23:78:ARG:NH1	2.18	0.59
3:C8:169:VAL:HG12	3:C8:171:PRO:HD3	1.84	0.59
3:C8:186:GLU:O	3:C8:190:ALA:N	2.33	0.59
1:E1:33:ASP:HB3	1:E1:35:THR:HG23	1.85	0.59
3:H8:59:THR:O	2:Y7:78:ARG:NE	2.36	0.59
3:L8:143:LEU:O	3:L8:177:ARG:HA	2.03	0.59
2:N3:47:ARG:HH11	2:N3:91:ARG:HB2	1.67	0.59
2:O2:32:ILE:CD1	2:O2:90:GLY:HA3	2.33	0.59
2:P3:9:GLU:HB3	2:P3:43:THR:HG23	1.84	0.59
2:P3:13:PHE:HB2	2:P4:37:THR:HG21	1.83	0.59
3:P8:110:THR:O	3:P8:143:LEU:HA	2.03	0.59
2:U5:37:THR:HG21	2:42:13:PHE:HB2	1.84	0.59
3:W8:154:ALA:HB2	3:W8:198:ILE:HD11	1.85	0.59
3:X8:46:ILE:HD11	3:48:177:ARG:HG2	1.85	0.59
3:Y8:52:THR:OG1	3:Y8:66:GLN:NE2	2.32	0.59
2:17:10:VAL:HG11	2:17:15:GLY:HA3	1.85	0.59
3:38:169:VAL:HG12	3:38:171:PRO:HD3	1.84	0.59
2:A3:9:GLU:HB3	2:A3:43:THR:HG23	1.83	0.59
2:A5:16:MET:HG2	2:A5:44:ALA:HB2	1.84	0.59
2:B5:16:MET:HG2	2:B5:44:ALA:HB2	1.84	0.59
3:B8:127:ARG:HD3	3:J8:27:ARG:HH11	1.68	0.59
3:G8:21:PHE:CE2	3:G8:169:VAL:HB	2.38	0.59
3:H8:21:PHE:CE2	3:H8:169:VAL:HB	2.38	0.59
3:J8:8:TYR:CE2	3:J8:93:LEU:HD23	2.38	0.59
2:O2:13:PHE:HE2	2:35:35:GLU:HG2	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O7:17:VAL:HG21	2:P3:7:MET:HE1	1.85	0.59
3:P8:21:PHE:CE2	3:P8:169:VAL:HB	2.38	0.59
2:T4:78:ARG:NH2	3:T8:159:GLU:OE1	2.35	0.59
2:13:16:MET:HG2	2:13:44:ALA:HB2	1.85	0.59
2:34:16:MET:HG3	2:34:42:VAL:HG12	1.85	0.59
2:37:47:ARG:NH1	2:37:89:LEU:O	2.35	0.59
3:A8:45:GLY:HA3	3:A8:73:GLY:H	1.68	0.58
3:G9:66:GLN:HA	3:G9:75:LEU:HA	1.84	0.58
2:S2:32:ILE:CD1	2:S2:90:GLY:HA3	2.33	0.58
2:S3:10:VAL:HG11	2:S3:15:GLY:HA3	1.85	0.58
2:S7:52:ALA:O	2:S7:56:ALA:N	2.33	0.58
3:S8:169:VAL:HG12	3:S8:171:PRO:HD3	1.84	0.58
2:T5:16:MET:HG2	2:T5:44:ALA:HB2	1.84	0.58
3:V8:47:ALA:HB1	3:V8:50:ARG:HH12	1.68	0.58
3:W8:120:TYR:HD1	3:Y8:29:PHE:CZ	2.20	0.58
2:C2:45:VAL:HG11	2:C2:89:LEU:HD12	1.84	0.58
1:F1:2:VAL:HG23	1:F1:57:TYR:CE1	2.38	0.58
2:G7:8:ILE:HG12	2:G7:73:VAL:HG22	1.84	0.58
2:I2:47:ARG:HH12	2:I2:79:PRO:HG2	1.69	0.58
2:I4:16:MET:HG2	2:I4:44:ALA:HB2	1.85	0.58
2:K3:47:ARG:HH11	2:K3:91:ARG:CB	2.12	0.58
2:L2:37:THR:HG21	2:L4:13:PHE:HB2	1.85	0.58
2:N2:45:VAL:HG11	2:N2:89:LEU:HD12	1.85	0.58
2:N5:2:ALA:O	2:N5:78:ARG:NH1	2.36	0.58
2:Q7:17:VAL:HG11	2:S3:7:MET:HE1	1.84	0.58
2:S6:57:THR:HG21	2:S6:75:VAL:HG22	1.85	0.58
2:T3:26:ALA:O	3:T8:12:ASP:HB3	2.03	0.58
2:U3:8:ILE:HG12	2:U3:73:VAL:HG22	1.84	0.58
2:U7:25:LYS:O	2:V7:25:LYS:NZ	2.24	0.58
2:Z7:47:ARG:NH1	2:Z7:89:LEU:O	2.35	0.58
2:26:19:ALA:HB2	2:26:64:ALA:HB2	1.85	0.58
2:47:52:ALA:O	2:47:56:ALA:N	2.36	0.58
3:48:186:GLU:O	3:48:190:ALA:N	2.32	0.58
2:B3:36:LYS:NZ	2:B4:35:GLU:OE2	2.26	0.58
3:B8:48:ILE:HG22	3:B8:66:GLN:HE22	1.68	0.58
3:E8:21:PHE:CE2	3:E8:169:VAL:HB	2.38	0.58
2:G6:47:ARG:HH22	2:G6:79:PRO:HG3	1.67	0.58
3:G8:8:TYR:HE2	3:G8:93:LEU:HD23	1.67	0.58
2:J7:27:ALA:O	2:L3:78:ARG:NH1	2.36	0.58
2:L7:17:VAL:HG11	2:23:7:MET:HE1	1.84	0.58
2:M3:13:PHE:HB2	2:M4:37:THR:HG21	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N9:39:TRP:HA	3:N9:76:GLU:HA	1.86	0.58
2:25:13:PHE:HB2	2:26:37:THR:HG21	1.85	0.58
1:A1:64:ARG:HD3	1:E1:62:SER:HB2	1.85	0.58
3:B8:53:ASP:O	3:B8:57:LYS:N	2.25	0.58
3:G8:122:THR:HG21	3:G8:136:PRO:HA	1.85	0.58
3:K8:126:ASN:O	3:K8:129:SER:HB3	2.02	0.58
2:S3:47:ARG:HH21	2:S3:91:ARG:HB2	1.68	0.58
3:T8:103:ARG:HH21	3:T8:201:VAL:HG13	1.67	0.58
2:U2:16:MET:HE2	2:U2:42:VAL:HG11	1.85	0.58
2:V3:3:ASP:OD2	2:V3:91:ARG:NE	2.34	0.58
3:V8:50:ARG:NE	3:X8:112:GLN:OE1	2.36	0.58
2:W6:57:THR:HG21	2:W6:75:VAL:HG22	1.85	0.58
1:B1:33:ASP:HB3	1:B1:35:THR:HG23	1.85	0.58
3:D8:12:ASP:O	3:D8:82:GLN:NE2	2.36	0.58
1:F1:21:GLY:HA2	2:G2:58:GLU:HB3	1.86	0.58
2:F5:3:ASP:O	2:F5:47:ARG:NH2	2.36	0.58
2:I5:9:GLU:OE2	2:J2:13:PHE:N	2.37	0.58
2:K3:26:ALA:O	3:K8:12:ASP:HB3	2.03	0.58
2:L6:32:ILE:HG21	2:L6:90:GLY:HA3	1.86	0.58
1:R1:1:MET:N	1:V1:75:ASP:OD1	2.30	0.58
2:T4:16:MET:HG2	2:T4:44:ALA:HB2	1.84	0.58
2:U5:92:THR:O	2:U5:94:GLY:N	2.36	0.58
3:V9:20:THR:O	3:V9:24:LYS:N	2.35	0.58
2:13:32:ILE:HD12	2:13:47:ARG:HG3	1.85	0.58
1:C1:1:MET:N	1:D1:75:ASP:OD1	2.31	0.58
3:E8:128:ASN:O	3:E8:130:GLN:N	2.36	0.58
2:G7:78:ARG:NH2	3:I8:57:LYS:O	2.36	0.58
3:I8:186:GLU:O	3:I8:190:ALA:N	2.33	0.58
2:L3:47:ARG:NH1	2:L3:91:ARG:HB2	2.11	0.58
1:M1:32:PRO:HG3	1:M1:87:MET:HE3	1.84	0.58
2:O2:3:ASP:OD2	2:O2:91:ARG:NH2	2.37	0.58
3:U8:24:LYS:HE2	3:U9:122:THR:O	2.04	0.58
1:11:53:GLU:OE2	2:15:78:ARG:HB3	2.03	0.58
2:D2:29:VAL:HG12	2:D2:46:VAL:HG22	1.84	0.58
2:D7:28:LYS:HA	2:N3:78:ARG:NH2	2.17	0.58
2:F2:47:ARG:NH2	2:F2:84:ASP:OD1	2.37	0.58
2:I5:32:ILE:CD1	2:I5:47:ARG:HG3	2.33	0.58
2:L5:10:VAL:HG11	2:L5:15:GLY:HA3	1.86	0.58
2:M5:61:GLN:HB2	2:M5:73:VAL:HG21	1.84	0.58
2:N5:16:MET:HG2	2:N5:44:ALA:HB2	1.86	0.58
1:T1:64:ARG:HH11	1:U1:62:SER:CB	2.15	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X1:32:PRO:HG3	1:X1:87:MET:HE1	1.84	0.58
1:Y1:32:PRO:HG3	1:Y1:87:MET:HE1	1.86	0.58
3:38:45:GLY:HA3	3:38:72:TYR:HB2	1.84	0.58
3:38:126:ASN:O	3:38:129:SER:HB3	2.03	0.58
1:B1:1:MET:SD	1:C1:74:VAL:HG23	2.44	0.58
1:B1:69:THR:H	1:B1:72:ARG:NH2	2.01	0.58
3:C8:109:MET:HB2	3:C8:144:GLU:HB3	1.84	0.58
2:I5:5:LEU:HB3	2:I5:76:ILE:HB	1.85	0.58
2:N3:8:ILE:HG23	2:N3:73:VAL:HG22	1.86	0.58
1:O1:68:VAL:O	1:O1:72:ARG:NH1	2.37	0.58
3:T8:123:GLN:HA	3:T8:126:ASN:HD22	1.69	0.58
2:W2:32:ILE:CD1	2:W2:90:GLY:HA3	2.33	0.58
2:W6:32:ILE:HD11	2:W6:47:ARG:HD2	1.84	0.58
2:Y2:45:VAL:HG11	2:Y2:89:LEU:HD12	1.84	0.58
2:Z3:47:ARG:HH11	2:Z3:91:ARG:HB2	1.69	0.58
2:35:47:ARG:HH12	2:35:84:ASP:CG	2.12	0.58
1:C1:28:ARG:HH11	1:C1:36:PRO:HB2	1.68	0.58
3:C8:170:THR:HG1	3:C8:177:ARG:H	1.48	0.58
2:F4:31:LEU:HA	2:F4:46:VAL:HG12	1.85	0.58
3:F8:55:ALA:O	3:F8:59:THR:OG1	2.21	0.58
3:F8:59:THR:O	2:Q7:78:ARG:NE	2.36	0.58
2:K7:78:ARG:NH2	3:18:57:LYS:O	2.37	0.58
3:P8:119:ALA:O	3:P8:122:THR:OG1	2.22	0.58
3:P8:139:SER:HB2	3:P8:187:ILE:HG13	1.84	0.58
2:V5:16:MET:HG2	2:V5:44:ALA:HB2	1.85	0.58
3:X8:8:TYR:CE2	3:X8:93:LEU:HD23	2.38	0.58
3:Z8:169:VAL:HG12	3:Z8:171:PRO:HD3	1.84	0.58
3:28:8:TYR:CE2	3:28:93:LEU:HD23	2.38	0.58
2:34:50:VAL:HG11	3:38:186:GLU:HG3	1.85	0.58
3:48:128:ASN:O	3:48:130:GLN:N	2.32	0.58
2:B3:90:GLY:O	2:B3:92:THR:N	2.37	0.58
3:B8:13:ALA:HA	3:B8:35:GLN:O	2.04	0.58
3:C8:8:TYR:CE2	3:C8:93:LEU:HD23	2.39	0.58
3:J8:65:VAL:HG12	3:J8:76:GLU:HB3	1.85	0.58
2:L7:50:VAL:HG21	2:L7:77:PRO:HB3	1.86	0.58
3:M8:20:THR:HG21	3:M9:135:LEU:HA	1.85	0.58
3:P8:18:LEU:HD11	3:P8:156:ASN:HA	1.86	0.58
3:P8:45:GLY:HA2	3:P8:48:ILE:HD13	1.86	0.58
2:Q6:14:VAL:HG23	2:Q7:9:GLU:HB2	1.85	0.58
2:T3:47:ARG:NH1	2:T3:84:ASP:OD1	2.37	0.58
2:U3:47:ARG:NH1	2:U3:91:ARG:HB2	2.17	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:21:70:ASN:C	1:21:72:ARG:H	2.12	0.58
2:37:52:ALA:O	2:37:56:ALA:N	2.37	0.58
3:D8:21:PHE:CE2	3:D8:169:VAL:HB	2.39	0.57
2:F5:10:VAL:HG11	2:F5:15:GLY:HA3	1.85	0.57
3:O8:170:THR:OG1	3:O8:177:ARG:N	2.23	0.57
2:S6:83:VAL:HG13	2:S6:87:LEU:HD12	1.86	0.57
3:S8:167:VAL:HB	3:S8:179:TYR:HB2	1.85	0.57
3:S9:121:GLN:O	3:S9:125:ILE:N	2.37	0.57
3:T8:21:PHE:CE2	3:T8:169:VAL:HB	2.38	0.57
2:W2:78:ARG:HG3	2:W5:28:LYS:H	1.68	0.57
3:48:21:PHE:HE2	3:48:169:VAL:HB	1.69	0.57
2:C3:25:LYS:HB3	3:C8:160:LYS:HE3	1.86	0.57
1:F1:73:PRO:O	1:G1:79:MET:HE1	2.04	0.57
1:H1:7:VAL:HG11	1:I1:87:MET:HE2	1.85	0.57
1:H1:31:ASP:C	1:H1:33:ASP:H	2.11	0.57
2:M4:31:LEU:HA	2:M4:46:VAL:HG12	1.86	0.57
3:N8:13:ALA:HA	3:N8:35:GLN:O	2.04	0.57
2:P2:32:ILE:CD1	2:P2:90:GLY:HA3	2.35	0.57
3:P8:9:ILE:CD1	3:P8:150:TYR:HA	2.30	0.57
1:R1:28:ARG:HH12	1:R1:36:PRO:C	2.11	0.57
3:S8:7:THR:OG1	3:S8:41:GLU:N	2.38	0.57
2:X6:10:VAL:HG11	2:X6:15:GLY:HA3	1.85	0.57
1:Z1:5:LYS:HD3	1:Z1:36:PRO:HD3	1.86	0.57
3:38:134:ILE:HG12	3:38:181:ALA:HB2	1.85	0.57
2:46:16:MET:HG3	2:46:42:VAL:HG12	1.86	0.57
3:48:119:ALA:O	3:48:122:THR:OG1	2.22	0.57
2:C3:26:ALA:O	3:C8:12:ASP:HB3	2.04	0.57
1:D1:68:VAL:HA	1:D1:72:ARG:HH12	1.69	0.57
2:D3:79:ARG:NH1	2:P7:26:LYS:HA	2.19	0.57
2:D5:13:PHE:HD2	2:D6:43:THR:HG21	1.69	0.57
3:G8:17:GLN:O	3:G8:20:THR:OG1	2.20	0.57
2:H7:28:LYS:HA	2:W3:78:ARG:NH1	2.18	0.57
3:K8:18:LEU:HD11	3:K8:156:ASN:HA	1.86	0.57
2:O5:10:VAL:HG11	2:O5:15:GLY:HA3	1.86	0.57
2:U3:4:ALA:O	2:U3:47:ARG:HD2	2.04	0.57
2:W7:26:ALA:O	2:Y3:77:PRO:HB2	2.03	0.57
3:Z8:142:ILE:HA	3:Z8:178:LEU:O	2.05	0.57
3:48:9:ILE:HD11	3:48:150:TYR:CD1	2.38	0.57
2:A2:32:ILE:CD1	2:A2:90:GLY:HA3	2.33	0.57
1:B1:45:ASP:OD2	1:B1:49:ALA:N	2.32	0.57
2:D2:54:LYS:HZ2	2:D5:55:ALA:HB2	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D5:3:ASP:O	2:D5:47:ARG:NH2	2.28	0.57
3:D8:141:PHE:HB3	3:D8:180:LEU:HB2	1.86	0.57
3:E8:121:GLN:O	3:E8:125:ILE:HG13	2.04	0.57
2:G6:3:ASP:O	2:G6:47:ARG:NH1	2.35	0.57
2:H6:18:GLU:CD	2:H7:74:HIS:HE2	2.11	0.57
2:O2:8:ILE:HG12	2:O2:73:VAL:HG22	1.87	0.57
3:O9:105:LYS:N	3:O9:204:VAL:O	2.21	0.57
1:S1:10:VAL:HG13	1:31:82:VAL:HG13	1.86	0.57
2:T2:3:ASP:C	2:T2:47:ARG:HH12	2.09	0.57
3:T8:128:ASN:O	3:T8:130:GLN:N	2.33	0.57
3:38:17:GLN:CD	3:38:159:GLU:HG3	2.28	0.57
3:A8:29:PHE:CZ	3:I8:120:TYR:HD1	2.23	0.57
1:B1:62:SER:HB2	1:C1:64:ARG:HD3	1.86	0.57
3:B8:9:ILE:HD13	3:B8:153:LEU:HB2	1.87	0.57
3:B8:49:ASN:O	3:L8:121:GLN:NE2	2.34	0.57
3:B8:130:GLN:NE2	3:B8:172:TYR:OH	2.24	0.57
3:C8:103:ARG:HH21	3:C8:201:VAL:HG13	1.67	0.57
2:D2:37:THR:HG21	2:D4:13:PHE:HB2	1.85	0.57
3:D8:154:ALA:HB2	3:D8:198:ILE:HD11	1.85	0.57
2:L2:54:LYS:NZ	2:L5:55:ALA:HB2	2.19	0.57
2:L7:10:VAL:HG11	2:L7:15:GLY:HA3	1.86	0.57
2:M6:13:PHE:HB2	2:M7:37:THR:HG21	1.86	0.57
2:P3:47:ARG:NH1	2:P3:84:ASP:OD1	2.37	0.57
2:S4:8:ILE:HD12	2:S4:73:VAL:HG22	1.85	0.57
3:S8:24:LYS:HD3	3:S9:126:ASN:O	2.04	0.57
2:T4:30:GLU:OE1	2:T4:91:ARG:NH2	2.34	0.57
3:T8:116:ALA:HA	3:T8:137:GLY:HA2	1.85	0.57
3:Y8:63:PRO:HA	3:Y8:77:VAL:HA	1.86	0.57
3:18:60:LYS:HB2	3:18:84:GLU:HG2	1.85	0.57
3:28:111:HIS:HA	3:28:142:ILE:O	2.04	0.57
2:32:32:ILE:CD1	2:32:90:GLY:HA3	2.35	0.57
2:32:92:THR:O	2:32:94:GLY:N	2.37	0.57
1:A1:68:VAL:C	1:A1:72:ARG:NH1	2.62	0.57
3:B8:21:PHE:O	3:B8:25:THR:OG1	2.14	0.57
2:C3:13:PHE:HB2	2:C4:37:THR:HG21	1.86	0.57
3:F8:125:ILE:HD12	3:F8:134:ILE:HD12	1.86	0.57
2:G6:32:ILE:HG21	2:G6:90:GLY:HA3	1.86	0.57
2:G7:17:VAL:HG11	2:W3:7:MET:HE1	1.87	0.57
3:J8:127:ARG:HH22	3:L8:67:VAL:HG12	1.70	0.57
3:L9:45:GLY:N	3:L9:71:ALA:O	2.38	0.57
1:O1:83:ASP:OD2	1:31:13:SER:N	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Q9:65:VAL:O	3:Q9:76:GLU:N	2.36	0.57
1:Y1:32:PRO:HG3	1:Y1:87:MET:CE	2.34	0.57
3:28:128:ASN:O	3:28:130:GLN:N	2.37	0.57
3:48:9:ILE:HD11	3:48:150:TYR:HA	1.87	0.57
1:A1:45:ASP:OD1	1:A1:47:VAL:N	2.32	0.57
2:B2:13:PHE:HE2	2:C5:35:GLU:HG2	1.70	0.57
3:B9:39:TRP:HA	3:B9:76:GLU:HA	1.85	0.57
2:C7:78:ARG:NE	3:28:59:THR:O	2.38	0.57
3:D8:29:PHE:CZ	3:P8:120:TYR:HD1	2.23	0.57
2:G6:5:LEU:HD23	2:G6:76:ILE:HD12	1.86	0.57
3:H8:21:PHE:HE2	3:H8:169:VAL:HB	1.69	0.57
3:H8:109:MET:HB2	3:H8:144:GLU:HB3	1.86	0.57
2:J4:54:LYS:HD2	2:J4:75:VAL:HG11	1.86	0.57
2:N6:56:ALA:O	2:N6:60:GLY:N	2.38	0.57
1:P1:28:ARG:NH1	1:P1:36:PRO:HB2	2.19	0.57
2:R6:32:ILE:HG21	2:R6:90:GLY:HA3	1.87	0.57
3:T9:50:ARG:O	3:T9:54:ALA:N	2.34	0.57
2:Y3:8:ILE:HG23	2:Y3:73:VAL:HG22	1.86	0.57
3:18:143:LEU:O	3:18:177:ARG:HA	2.05	0.57
2:46:83:VAL:HG23	2:46:87:LEU:HD13	1.87	0.57
2:A2:13:PHE:CE2	2:B5:35:GLU:HG2	2.40	0.57
2:C3:9:GLU:HG3	2:C3:71:VAL:HB	1.87	0.57
2:E7:16:MET:HG3	2:E7:42:VAL:HG12	1.87	0.57
2:F4:10:VAL:HG11	2:F4:15:GLY:HA3	1.86	0.57
2:I2:47:ARG:NH1	2:I2:79:PRO:HG2	2.20	0.57
2:M3:9:GLU:HB3	2:M3:43:THR:HG23	1.87	0.57
2:O3:47:ARG:NH2	2:O3:84:ASP:OD1	2.37	0.57
2:T5:18:GLU:OE1	2:T6:74:HIS:NE2	2.37	0.57
2:U7:17:VAL:HG21	2:43:7:MET:HE1	1.87	0.57
3:W8:123:GLN:HG3	3:W9:23:GLY:HA3	1.87	0.57
2:15:16:MET:HG2	2:15:44:ALA:HB2	1.85	0.57
2:25:13:PHE:HD2	2:26:43:THR:HG21	1.69	0.57
2:32:30:GLU:OE1	2:32:91:ARG:NH2	2.34	0.57
3:38:17:GLN:O	3:38:20:THR:OG1	2.20	0.57
2:B7:50:VAL:HG21	2:B7:77:PRO:HB3	1.86	0.57
2:F7:13:PHE:HB3	2:G3:43:THR:HG21	1.86	0.57
1:H1:68:VAL:C	1:H1:72:ARG:HH12	2.13	0.57
2:I3:8:ILE:HG12	2:I3:73:VAL:HG22	1.86	0.57
3:K8:164:VAL:HG21	3:K8:190:ALA:HB2	1.85	0.57
3:L8:61:VAL:HG11	3:L8:77:VAL:HB	1.87	0.57
1:O1:64:ARG:HD3	1:P1:62:SER:HB2	1.84	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P6:32:ILE:HD11	2:P6:47:ARG:HD2	1.86	0.57
2:Q6:3:ASP:O	2:Q6:47:ARG:NH1	2.36	0.57
1:T1:18:ARG:NH1	1:U1:65:GLN:O	2.38	0.57
3:T8:18:LEU:HD22	3:T8:22:ILE:HG13	1.87	0.57
3:W8:128:ASN:O	3:W8:130:GLN:N	2.36	0.57
1:Z1:70:ASN:C	1:Z1:72:ARG:H	2.13	0.57
1:41:32:PRO:HG3	1:41:87:MET:HE1	1.87	0.57
2:43:9:GLU:HG3	2:43:71:VAL:HB	1.87	0.57
2:B6:32:ILE:HD13	2:B6:90:GLY:HA3	1.87	0.57
2:F3:34:TYR:OH	2:F4:35:GLU:OE2	2.22	0.57
1:H1:61:SER:HB2	1:I1:61:SER:HB3	1.86	0.57
2:H2:13:PHE:HB2	2:Z5:37:THR:HG21	1.86	0.57
3:H8:9:ILE:CD1	3:H8:150:TYR:HA	2.32	0.57
3:H8:64:ALA:HB3	3:H8:76:GLU:OE1	2.05	0.57
2:I4:60:GLY:O	2:I4:64:ALA:N	2.36	0.57
1:J1:70:ASN:C	1:J1:72:ARG:H	2.13	0.57
3:J9:105:LYS:N	3:J9:204:VAL:O	2.21	0.57
3:K8:17:GLN:O	3:K8:20:THR:OG1	2.19	0.57
1:L1:68:VAL:C	1:L1:72:ARG:HH12	2.11	0.57
2:L5:9:GLU:OE2	2:22:13:PHE:N	2.38	0.57
2:M3:18:GLU:OE1	2:M4:74:HIS:NE2	2.35	0.57
3:P8:19:ALA:HB3	3:P8:33:PRO:HG3	1.86	0.57
2:S2:9:GLU:HB2	2:S4:14:VAL:HG23	1.87	0.57
3:U8:123:GLN:HG3	3:U9:23:GLY:HA3	1.87	0.57
1:W1:63:ALA:HB1	1:W1:77:THR:HG22	1.87	0.57
2:W3:34:TYR:OH	2:W4:35:GLU:OE2	2.21	0.57
3:W8:143:LEU:HB3	3:W8:178:LEU:HB3	1.86	0.57
1:X1:31:ASP:OD1	1:X1:35:THR:OG1	2.20	0.57
3:39:65:VAL:O	3:39:75:LEU:HA	2.04	0.57
3:B8:63:PRO:HA	3:B8:77:VAL:HA	1.86	0.56
2:E5:18:GLU:CD	2:E6:74:HIS:HE2	2.12	0.56
2:F6:27:ALA:HA	3:F8:116:ALA:HB2	1.87	0.56
3:F8:8:TYR:HE2	3:F8:93:LEU:HB3	1.70	0.56
1:G1:75:ASP:OD2	1:W1:59:SER:N	2.36	0.56
2:G2:47:ARG:NH2	2:G2:84:ASP:OD1	2.37	0.56
2:I3:10:VAL:O	2:I3:12:GLY:N	2.38	0.56
1:K1:18:ARG:NH1	1:L1:65:GLN:O	2.37	0.56
1:L1:68:VAL:CA	1:L1:72:ARG:HH12	2.17	0.56
1:N1:41:VAL:HG11	1:N1:57:TYR:CZ	2.39	0.56
2:O3:5:LEU:HD12	2:O3:6:GLY:H	1.70	0.56
2:P2:90:GLY:C	2:P2:92:THR:H	2.11	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R2:32:ILE:HD11	2:R2:90:GLY:HA3	1.86	0.56
2:R3:47:ARG:HH22	2:R3:79:PRO:HG2	1.70	0.56
3:R8:130:GLN:NE2	3:R8:172:TYR:OH	2.38	0.56
3:R8:186:GLU:O	3:R8:190:ALA:N	2.33	0.56
1:T1:7:VAL:HG12	1:U1:87:MET:HG2	1.87	0.56
1:U1:45:ASP:OD1	1:U1:47:VAL:N	2.29	0.56
2:X2:10:VAL:HG11	2:X2:15:GLY:HA3	1.86	0.56
3:Y8:103:ARG:HH21	3:Y8:201:VAL:HG13	1.69	0.56
3:Z8:17:GLN:HE21	3:Z8:159:GLU:HG3	1.69	0.56
2:47:10:VAL:HG11	2:47:15:GLY:HA3	1.87	0.56
3:A8:7:THR:OG1	3:A8:41:GLU:N	2.38	0.56
3:C8:9:ILE:HG21	3:C8:153:LEU:HB2	1.87	0.56
3:O8:21:PHE:HE2	3:O8:169:VAL:HB	1.70	0.56
2:Q5:2:ALA:HB1	2:Q5:78:ARG:NH1	2.21	0.56
3:R8:167:VAL:HB	3:R8:179:TYR:HB2	1.87	0.56
2:S6:45:VAL:HG11	2:S6:89:LEU:HD22	1.86	0.56
3:X8:57:LYS:O	2:47:78:ARG:NH2	2.38	0.56
1:Y1:70:ASN:C	1:Y1:72:ARG:H	2.13	0.56
2:13:8:ILE:O	2:13:44:ALA:N	2.30	0.56
3:18:8:TYR:CE2	3:18:93:LEU:HD23	2.40	0.56
3:18:17:GLN:CD	3:18:159:GLU:HG3	2.31	0.56
3:38:64:ALA:HB3	3:38:76:GLU:OE1	2.05	0.56
3:49:38:LEU:N	3:49:77:VAL:O	2.35	0.56
2:A6:10:VAL:HG11	2:A6:15:GLY:HA3	1.86	0.56
2:B2:47:ARG:NH2	2:B2:84:ASP:OD1	2.38	0.56
3:B8:7:THR:OG1	3:B8:41:GLU:N	2.38	0.56
2:C3:7:MET:HE1	2:D7:17:VAL:HG11	1.87	0.56
1:D1:66:THR:HG22	1:D1:67:GLU:O	2.05	0.56
2:D5:16:MET:HG2	2:D5:44:ALA:HB2	1.85	0.56
2:E3:47:ARG:HH12	2:E3:84:ASP:CG	2.10	0.56
3:H8:121:GLN:O	3:H8:125:ILE:HG13	2.05	0.56
2:I2:37:THR:HG21	2:I4:13:PHE:HB2	1.86	0.56
2:J3:21:ASP:OD2	2:J4:76:ILE:HD13	2.05	0.56
3:K8:29:PHE:HB2	3:K8:63:PRO:O	2.05	0.56
3:K8:177:ARG:HG2	3:18:46:ILE:HD11	1.86	0.56
1:L1:74:VAL:HG11	1:L1:77:THR:HG23	1.87	0.56
2:L4:16:MET:HG2	2:L4:44:ALA:HB2	1.87	0.56
3:L8:7:THR:OG1	3:L8:41:GLU:N	2.37	0.56
2:N6:47:ARG:NH2	2:N6:84:ASP:OD1	2.38	0.56
3:N8:105:LYS:N	3:N8:204:VAL:O	2.30	0.56
2:Q2:82:ASN:OD1	2:Q4:31:LEU:N	2.34	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Q8:47:ALA:HB1	3:Q8:50:ARG:HH12	1.69	0.56
2:R5:57:THR:O	2:R5:60:GLY:N	2.35	0.56
2:R6:32:ILE:HD13	2:R6:90:GLY:HA3	1.86	0.56
3:R8:18:LEU:HD11	3:R8:156:ASN:HA	1.86	0.56
1:S1:22:LEU:HG	1:S1:44:ALA:HB1	1.86	0.56
2:U5:3:ASP:O	2:U5:47:ARG:NH2	2.38	0.56
3:W8:134:ILE:HG12	3:W8:181:ALA:HB2	1.86	0.56
3:X8:29:PHE:CZ	3:48:120:TYR:HD1	2.23	0.56
3:X9:88:ALA:O	3:X9:92:ILE:N	2.33	0.56
2:Y4:16:MET:HG2	2:Y4:44:ALA:HB2	1.87	0.56
3:Y8:42:ILE:HD11	3:Y8:96:LEU:HD11	1.86	0.56
3:Y9:47:ALA:O	3:Y9:51:VAL:N	2.38	0.56
3:Z8:9:ILE:HB	3:Z8:39:TRP:HB2	1.86	0.56
2:16:30:GLU:OE1	2:16:91:ARG:NH2	2.29	0.56
2:25:47:ARG:NH1	2:25:84:ASP:OD1	2.37	0.56
3:28:106:PRO:HG3	3:28:150:TYR:CE2	2.40	0.56
2:34:16:MET:HG2	2:34:44:ALA:HB2	1.86	0.56
3:38:35:GLN:HG2	3:38:80:PHE:CG	2.40	0.56
2:A6:34:TYR:OH	2:A6:36:LYS:NZ	2.38	0.56
3:A8:65:VAL:HG12	3:A8:76:GLU:HB3	1.87	0.56
2:F3:5:LEU:HD13	2:F3:47:ARG:HD3	1.88	0.56
1:I1:61:SER:HB2	1:J1:61:SER:HB3	1.87	0.56
2:J7:29:VAL:H	2:L3:78:ARG:HH12	1.54	0.56
1:P1:28:ARG:HH11	1:P1:36:PRO:HB2	1.70	0.56
1:Q1:55:VAL:HG21	1:Q1:78:ILE:HD13	1.86	0.56
2:Q3:10:VAL:O	2:Q3:12:GLY:N	2.39	0.56
2:R2:13:PHE:N	2:V5:9:GLU:OE2	2.39	0.56
3:R8:41:GLU:HB2	3:R8:74:LEU:HD13	1.87	0.56
3:R8:103:ARG:HH21	3:R8:201:VAL:HG13	1.70	0.56
2:V3:13:PHE:HD2	2:V4:43:THR:HG21	1.69	0.56
2:Y6:19:ALA:HB2	2:Y6:64:ALA:HB2	1.87	0.56
2:42:3:ASP:OD2	2:42:91:ARG:NH2	2.34	0.56
3:A8:58:ALA:HA	2:I6:25:LYS:HZ3	1.68	0.56
3:A8:116:ALA:N	3:A8:138:GLU:O	2.28	0.56
3:C8:27:ARG:HD2	3:M8:127:ARG:HE	1.70	0.56
1:F1:87:MET:HG2	1:R1:7:VAL:HG12	1.88	0.56
3:F8:16:PRO:HA	3:F8:33:PRO:CB	2.34	0.56
3:M8:29:PHE:HB2	3:M8:63:PRO:O	2.06	0.56
3:O8:15:GLN:HG2	3:O8:156:ASN:OD1	2.06	0.56
3:Y8:13:ALA:HA	3:Y8:35:GLN:O	2.05	0.56
1:Z1:31:ASP:O	1:Z1:33:ASP:N	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:42:10:VAL:HG11	2:42:15:GLY:HA3	1.86	0.56
3:A8:29:PHE:HB2	3:A8:63:PRO:O	2.06	0.56
3:C8:9:ILE:HD11	3:C8:150:TYR:CD2	2.40	0.56
3:F8:167:VAL:HB	3:F8:179:TYR:HB2	1.87	0.56
3:I8:111:HIS:ND1	3:I8:195:GLU:OE2	2.39	0.56
2:J3:13:PHE:HB2	2:J4:37:THR:HG21	1.87	0.56
2:M4:16:MET:HG2	2:M4:44:ALA:HB2	1.87	0.56
2:N4:62:ARG:NE	2:N5:66:ARG:NH1	2.53	0.56
2:Q5:47:ARG:NH1	2:Q5:84:ASP:OD1	2.39	0.56
2:R6:16:MET:HG2	2:R6:44:ALA:HB2	1.87	0.56
3:V8:120:TYR:HD1	3:48:29:PHE:CZ	2.24	0.56
2:Z4:47:ARG:NH1	2:Z4:89:LEU:HB3	2.20	0.56
2:13:90:GLY:O	2:13:92:THR:N	2.37	0.56
1:31:60:GLY:N	1:31:75:ASP:O	2.26	0.56
2:F4:66:ARG:NH1	2:F5:62:ARG:CZ	2.69	0.56
1:G1:2:VAL:HG23	1:G1:57:TYR:CE1	2.40	0.56
1:I1:18:ARG:NH1	1:J1:65:GLN:O	2.38	0.56
2:I2:47:ARG:NH1	2:I2:84:ASP:OD1	2.39	0.56
3:K8:21:PHE:CE2	3:K8:169:VAL:HB	2.41	0.56
3:L8:79:HIS:CE1	3:L8:81:ASP:H	2.23	0.56
3:N8:7:THR:OG1	3:N8:41:GLU:N	2.39	0.56
3:P8:143:LEU:O	3:P8:177:ARG:HA	2.06	0.56
1:Q1:28:ARG:NH2	1:Q1:38:GLY:H	2.03	0.56
2:T3:90:GLY:O	2:T3:92:THR:N	2.38	0.56
3:T8:20:THR:OG1	3:T8:21:PHE:N	2.39	0.56
3:48:38:LEU:O	3:48:76:GLU:HA	2.06	0.56
3:B8:186:GLU:OE1	3:B8:186:GLU:N	2.29	0.56
2:F6:3:ASP:O	2:F6:47:ARG:NH2	2.39	0.56
2:G4:4:ALA:O	2:G4:47:ARG:NE	2.36	0.56
2:G6:30:GLU:OE1	2:G6:91:ARG:NH2	2.31	0.56
3:G8:64:ALA:HB3	3:G8:76:GLU:OE1	2.05	0.56
2:H2:47:ARG:NH1	2:H2:84:ASP:OD1	2.38	0.56
3:L8:24:LYS:HG2	3:L9:127:ARG:HA	1.86	0.56
3:M8:9:ILE:HD11	3:M8:150:TYR:CD2	2.41	0.56
3:N9:139:SER:N	3:N9:182:GLY:O	2.32	0.56
1:P1:13:SER:OG	1:Q1:83:ASP:OD2	2.17	0.56
2:Q3:47:ARG:NH1	2:Q3:84:ASP:OD1	2.38	0.56
3:Q9:20:THR:O	3:Q9:24:LYS:N	2.31	0.56
2:T5:36:LYS:NZ	2:T6:35:GLU:OE2	2.34	0.56
3:U8:124:ILE:O	3:U8:127:ARG:HB2	2.06	0.56
2:W6:18:GLU:OE1	2:W7:74:HIS:NE2	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X5:45:VAL:HG11	2:X5:89:LEU:HD22	1.88	0.56
3:Y8:11:LEU:HB3	3:Y8:14:LEU:HD21	1.87	0.56
3:Y8:29:PHE:HB2	3:Y8:63:PRO:O	2.05	0.56
3:Y8:186:GLU:OE1	3:Y8:186:GLU:N	2.29	0.56
2:Z3:17:VAL:HG21	2:Z4:7:MET:HE1	1.88	0.56
2:23:47:ARG:NH2	2:23:79:PRO:HG2	2.21	0.56
2:46:57:THR:HG21	2:46:75:VAL:HG22	1.86	0.56
2:D3:19:GLU:OE1	2:D4:74:HIS:NE2	2.38	0.56
2:H3:8:ILE:HG22	2:H3:73:VAL:HG22	1.87	0.56
2:I7:19:ALA:HB2	2:I7:64:ALA:HB2	1.87	0.56
1:J1:31:ASP:O	1:J1:33:ASP:N	2.39	0.56
2:K2:32:ILE:CD1	2:K2:90:GLY:HA3	2.36	0.56
1:Q1:64:ARG:HD3	1:S1:62:SER:HB2	1.88	0.56
3:T8:12:ASP:O	3:T8:82:GLN:NE2	2.39	0.56
1:X1:75:ASP:OD1	1:Y1:1:MET:N	2.25	0.56
2:X2:92:THR:O	2:X2:94:GLY:N	2.35	0.56
2:Y5:12:PHE:HD2	2:Y6:43:THR:HG21	1.71	0.56
3:Z8:45:GLY:HA2	3:Z8:48:ILE:HD13	1.88	0.56
2:B5:58:GLU:O	2:B5:62:ARG:NH2	2.39	0.56
1:D1:68:VAL:CA	1:D1:72:ARG:HH12	2.18	0.56
3:E8:18:LEU:HD11	3:E8:156:ASN:HA	1.86	0.56
3:E8:126:ASN:O	3:E8:129:SER:HB3	2.06	0.56
2:F2:3:ASP:OD2	2:F2:91:ARG:NH2	2.38	0.56
3:F8:47:ALA:HB1	3:F8:50:ARG:HH12	1.70	0.56
1:H1:14:ARG:HG3	1:I1:47:VAL:HG12	1.88	0.56
3:H8:111:HIS:HA	3:H8:142:ILE:O	2.05	0.56
3:H8:128:ASN:O	3:H8:130:GLN:N	2.39	0.56
1:I1:70:ASN:C	1:I1:72:ARG:H	2.14	0.56
1:L1:61:SER:HB2	1:21:61:SER:HB3	1.88	0.56
1:Q1:32:PRO:HG3	1:Q1:87:MET:CE	2.36	0.56
3:R8:65:VAL:HG12	3:R8:76:GLU:HB3	1.87	0.56
2:T6:3:ASP:O	2:T6:47:ARG:NH1	2.36	0.56
2:U3:17:VAL:HG21	2:U4:7:MET:HE1	1.88	0.56
2:W6:13:PHE:N	2:W7:9:GLU:OE2	2.31	0.56
3:W8:35:GLN:HG2	3:W8:80:PHE:CG	2.40	0.56
3:X9:105:LYS:N	3:X9:204:VAL:O	2.34	0.56
2:Y2:19:ALA:HB2	2:Y2:64:ALA:HB2	1.88	0.56
3:18:12:ASP:O	3:18:82:GLN:NE2	2.38	0.56
2:A6:30:GLU:OE1	2:A6:91:ARG:NH2	2.37	0.55
2:A7:51:ALA:HB2	2:G3:51:ALA:HB2	1.88	0.55
1:B1:87:MET:HG2	1:C1:7:VAL:HG12	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D3:26:LYS:HB3	3:D8:160:LYS:HE3	1.88	0.55
2:F3:90:GLY:O	2:F3:92:THR:N	2.38	0.55
2:F6:47:ARG:NH1	2:F6:84:ASP:OD1	2.38	0.55
3:H8:29:PHE:HB2	3:H8:63:PRO:O	2.04	0.55
3:O8:35:GLN:HG2	3:O8:80:PHE:CG	2.40	0.55
2:T3:47:ARG:HH12	2:T3:84:ASP:CG	2.14	0.55
3:U8:21:PHE:O	3:U8:25:THR:OG1	2.11	0.55
2:W2:3:ASP:HB2	2:W2:47:ARG:NH1	2.20	0.55
2:W7:60:GLY:O	2:W7:64:ALA:N	2.36	0.55
2:X6:13:PHE:N	2:X7:9:GLU:OE2	2.39	0.55
3:Y8:128:ASN:O	3:Y8:130:GLN:N	2.38	0.55
3:Z8:6:ARG:HG2	3:Z8:104:LEU:HD11	1.87	0.55
3:18:110:THR:O	3:18:143:LEU:HA	2.06	0.55
2:25:34:TYR:OH	2:26:35:GLU:OE2	2.18	0.55
2:A7:78:ARG:NE	3:G8:59:THR:O	2.39	0.55
2:B3:10:VAL:HG11	2:B3:15:GLY:HA3	1.87	0.55
1:D1:62:SER:HB2	1:E1:64:ARG:HD3	1.88	0.55
1:F1:31:ASP:O	1:F1:33:ASP:N	2.39	0.55
2:F4:52:ALA:O	2:F4:56:ALA:N	2.28	0.55
2:F4:57:THR:HG22	2:F4:73:VAL:HG13	1.86	0.55
2:F5:45:VAL:HG11	2:F5:89:LEU:HD22	1.88	0.55
2:G5:32:ILE:HD12	2:G5:47:ARG:HG3	1.87	0.55
2:J2:32:ILE:CD1	2:J2:90:GLY:HA3	2.36	0.55
2:L4:78:ARG:NH2	3:L8:159:GLU:OE1	2.40	0.55
2:M7:17:VAL:CG1	2:N3:7:MET:HE1	2.36	0.55
3:M8:45:GLY:HA3	3:M8:73:GLY:H	1.71	0.55
3:N8:134:ILE:HG12	3:N8:181:ALA:HB2	1.87	0.55
3:P8:65:VAL:HG12	3:P8:76:GLU:HB3	1.88	0.55
2:R6:3:ASP:O	2:R6:47:ARG:NH1	2.38	0.55
2:V4:3:ASP:OD2	2:V4:91:ARG:NH2	2.35	0.55
3:28:35:GLN:HG2	3:28:80:PHE:CG	2.41	0.55
3:38:18:LEU:HD11	3:38:156:ASN:HA	1.87	0.55
3:38:111:HIS:HA	3:38:142:ILE:O	2.05	0.55
2:47:50:VAL:HG21	2:47:77:PRO:HB3	1.88	0.55
1:A1:68:VAL:O	1:A1:72:ARG:NH1	2.39	0.55
2:A3:19:ALA:HB2	2:A3:64:ALA:HB2	1.88	0.55
2:A4:30:GLU:OE1	2:A4:91:ARG:NH2	2.37	0.55
1:C1:62:SER:HA	1:D1:64:ARG:HH11	1.71	0.55
2:D2:8:ILE:HG12	2:D2:73:VAL:HG22	1.86	0.55
2:D3:48:ARG:HH22	2:D3:80:PRO:HG2	1.70	0.55
3:G8:142:ILE:HA	3:G8:178:LEU:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H4:66:ARG:NH1	2:H5:62:ARG:NE	2.54	0.55
2:H5:37:THR:HG21	2:I2:13:PHE:HB2	1.87	0.55
2:J3:57:THR:HG22	2:J3:73:VAL:HG13	1.87	0.55
3:J8:20:THR:HB	3:J8:24:LYS:NZ	2.21	0.55
2:L2:5:LEU:HD23	2:L2:76:ILE:HD12	1.88	0.55
2:L7:53:VAL:HA	2:L7:56:ALA:HB3	1.88	0.55
2:O7:47:ARG:NH1	2:O7:89:LEU:O	2.40	0.55
2:P2:10:VAL:HG11	2:P2:15:GLY:HA3	1.89	0.55
3:R8:126:ASN:O	3:R8:129:SER:HB3	2.07	0.55
3:T9:20:THR:O	3:T9:24:LYS:N	2.36	0.55
2:U2:32:ILE:CD1	2:U2:90:GLY:HA3	2.37	0.55
3:U8:128:ASN:O	3:U8:130:GLN:N	2.39	0.55
1:V1:31:ASP:OD1	1:V1:35:THR:OG1	2.23	0.55
3:49:4:THR:N	3:49:43:ALA:O	2.40	0.55
2:B6:10:VAL:HG11	2:B6:15:GLY:HA3	1.88	0.55
3:B8:45:GLY:HA2	3:B8:48:ILE:HD13	1.89	0.55
2:G5:9:GLU:HG3	2:G5:43:THR:OG1	2.06	0.55
2:K5:47:ARG:NH1	2:K5:84:ASP:OD1	2.39	0.55
1:L1:31:ASP:OD1	1:L1:35:THR:OG1	2.25	0.55
1:L1:32:PRO:HG3	1:L1:87:MET:CE	2.36	0.55
1:L1:32:PRO:HG3	1:L1:87:MET:HE3	1.87	0.55
3:M8:61:VAL:HG11	3:M8:77:VAL:HB	1.88	0.55
2:N6:47:ARG:HH22	2:N6:79:PRO:HG3	1.70	0.55
3:N8:170:THR:HG1	3:N8:177:ARG:H	1.52	0.55
2:P3:18:GLU:OE1	2:P4:74:HIS:NE2	2.34	0.55
3:P8:103:ARG:HH21	3:P8:201:VAL:HG13	1.70	0.55
3:R8:11:LEU:HB3	3:R8:14:LEU:HD21	1.89	0.55
2:S6:16:MET:HG3	2:S6:42:VAL:HG12	1.89	0.55
3:S8:106:PRO:HG3	3:S8:150:TYR:CD2	2.41	0.55
2:U2:3:ASP:O	2:U2:47:ARG:NH1	2.37	0.55
1:X1:45:ASP:OD1	1:X1:47:VAL:N	2.31	0.55
2:Y5:15:MET:HG2	2:Y5:43:ALA:HB2	1.87	0.55
3:Z8:35:GLN:HG2	3:Z8:80:PHE:CG	2.41	0.55
2:14:20:ALA:HB1	2:14:31:LEU:HD22	1.89	0.55
2:26:10:VAL:HG11	2:26:15:GLY:HA3	1.89	0.55
2:33:5:LEU:HD13	2:33:47:ARG:HD3	1.88	0.55
1:I1:16:GLU:OE2	1:I1:66:THR:HG23	2.07	0.55
3:J8:17:GLN:CD	3:J8:159:GLU:HG3	2.32	0.55
3:J8:120:TYR:HD1	3:L8:29:PHE:CZ	2.25	0.55
3:O8:7:THR:HG22	3:O8:150:TYR:CE1	2.41	0.55
2:Q5:5:LEU:HB3	2:Q5:76:ILE:HB	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R3:10:VAL:O	2:R3:12:GLY:N	2.40	0.55
2:R7:51:ALA:HB2	2:S3:51:ALA:HB2	1.87	0.55
1:U1:31:ASP:OD1	1:U1:35:THR:OG1	2.22	0.55
1:U1:32:PRO:HG3	1:U1:87:MET:CE	2.36	0.55
2:V2:32:ILE:CD1	2:V2:90:GLY:HA3	2.35	0.55
2:Y2:16:MET:O	2:Y2:20:ALA:N	2.28	0.55
3:Z8:141:PHE:HB3	3:Z8:180:LEU:HB2	1.88	0.55
3:18:16:PRO:HA	3:18:33:PRO:CB	2.31	0.55
3:38:21:PHE:HE2	3:38:169:VAL:HB	1.71	0.55
2:43:13:PHE:N	2:44:9:GLU:OE2	2.39	0.55
2:A3:34:TYR:OH	2:A4:35:GLU:OE2	2.25	0.55
3:A9:37:SER:HA	3:A9:78:HIS:HA	1.89	0.55
3:B8:169:VAL:HG12	3:B8:171:PRO:HD3	1.87	0.55
3:I8:62:GLN:O	3:I8:78:HIS:N	2.29	0.55
3:L8:128:ASN:O	3:L8:130:GLN:N	2.39	0.55
2:M3:47:ARG:HH12	2:M3:84:ASP:CG	2.14	0.55
3:M8:167:VAL:HB	3:M8:179:TYR:HB2	1.88	0.55
2:N5:18:GLU:OE1	2:N6:74:HIS:NE2	2.37	0.55
2:R5:9:GLU:HG3	2:R5:43:THR:OG1	2.07	0.55
2:U3:32:ILE:CD1	2:U3:47:ARG:HG3	2.37	0.55
3:U8:7:THR:OG1	3:U8:41:GLU:N	2.40	0.55
2:X4:31:LEU:HA	2:X4:46:VAL:HG12	1.89	0.55
2:33:10:VAL:O	2:33:12:GLY:N	2.40	0.55
3:48:154:ALA:HB2	3:48:198:ILE:HD11	1.89	0.55
3:A8:63:PRO:HA	3:A8:77:VAL:HA	1.89	0.55
3:E8:17:GLN:CD	3:E8:159:GLU:HG3	2.32	0.55
2:F7:52:ALA:O	2:F7:56:ALA:N	2.38	0.55
1:J1:66:THR:O	1:J1:69:THR:OG1	2.17	0.55
2:J3:26:ALA:O	3:J8:12:ASP:HB3	2.05	0.55
2:J7:60:GLY:O	2:J7:64:ALA:N	2.33	0.55
3:J8:15:GLN:HG3	3:J8:160:LYS:HB2	1.89	0.55
2:L4:66:ARG:NH1	2:L5:62:ARG:CZ	2.69	0.55
3:O8:93:LEU:O	3:O8:97:GLU:N	2.40	0.55
3:O8:134:ILE:HD11	3:O8:140:LEU:HD13	1.89	0.55
3:Q8:109:MET:HB2	3:Q8:144:GLU:HB3	1.89	0.55
3:T8:177:ARG:HG2	3:38:46:ILE:HD11	1.88	0.55
2:W5:13:PHE:HD2	2:W6:43:THR:HG21	1.71	0.55
2:A3:47:ARG:HH12	2:A3:84:ASP:CG	2.13	0.55
2:C3:90:GLY:O	2:C3:92:THR:N	2.40	0.55
2:C5:13:PHE:HD2	2:C6:43:THR:HG21	1.72	0.55
2:D5:8:ILE:HG12	2:D5:73:VAL:HG22	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D8:59:THR:O	2:P7:76:ARG:NE	2.38	0.55
1:G1:28:ARG:HH12	1:G1:36:PRO:C	2.15	0.55
2:G4:53:VAL:O	2:G4:57:THR:OG1	2.17	0.55
2:H2:54:LYS:NZ	2:H5:58:GLU:OE2	2.36	0.55
2:K3:24:VAL:HG11	2:K4:82:ASN:HB3	1.88	0.55
2:N3:4:ALA:HB3	2:N3:48:GLY:O	2.07	0.55
2:Q3:84:ASP:O	2:Q3:92:THR:OG1	2.21	0.55
2:X3:4:ALA:O	2:X3:47:ARG:HD2	2.07	0.55
3:48:62:GLN:O	3:48:78:HIS:N	2.35	0.55
3:48:143:LEU:O	3:48:177:ARG:HA	2.07	0.55
2:A4:78:ARG:HD3	3:A8:163:ASN:CG	2.32	0.55
2:A7:29:VAL:H	2:G3:78:ARG:HH21	1.55	0.55
2:B3:4:ALA:O	2:B3:47:ARG:HD2	2.07	0.55
2:B7:28:LYS:HA	2:J3:78:ARG:HH12	1.71	0.55
2:E2:19:ALA:HB2	2:E2:64:ALA:HB2	1.89	0.55
2:E6:47:ARG:HH22	2:E6:79:PRO:HG3	1.71	0.55
2:F3:78:ARG:HH21	2:Q7:29:VAL:H	1.54	0.55
2:G5:3:ASP:OD1	2:G5:3:ASP:N	2.38	0.55
3:G8:29:PHE:HB2	3:G8:63:PRO:O	2.07	0.55
3:G9:10:PHE:HA	3:G9:38:LEU:HA	1.87	0.55
2:H3:47:ARG:NH1	2:H3:84:ASP:OD1	2.40	0.55
2:M6:32:ILE:HG21	2:M6:90:GLY:HA3	1.87	0.55
3:O8:143:LEU:O	3:O8:177:ARG:HA	2.07	0.55
2:R5:13:PHE:HD2	2:R6:43:THR:HG21	1.72	0.55
3:R8:57:LYS:O	2:U7:78:ARG:NH2	2.40	0.55
3:S8:35:GLN:HG2	3:S8:80:PHE:CG	2.42	0.55
3:S8:106:PRO:HG3	3:S8:150:TYR:CE2	2.41	0.55
2:T3:13:PHE:N	2:T4:9:GLU:OE2	2.39	0.55
3:T8:110:THR:O	3:T8:143:LEU:HA	2.07	0.55
2:Y7:10:VAL:HG11	2:Y7:15:GLY:HA3	1.87	0.55
1:Z1:45:ASP:OD1	1:Z1:47:VAL:N	2.28	0.55
2:Z7:58:GLU:O	2:Z7:62:ARG:NE	2.40	0.55
2:C3:5:LEU:HD12	2:C3:6:GLY:H	1.72	0.55
2:F2:32:ILE:CD1	2:F2:90:GLY:HA3	2.37	0.55
3:F8:3:ILE:HD13	3:F8:47:ALA:HB1	1.88	0.55
2:G3:8:ILE:HD13	2:G3:19:ALA:HB1	1.88	0.55
1:M1:63:ALA:HB1	1:M1:77:THR:HG22	1.88	0.55
3:S8:63:PRO:HA	3:S8:77:VAL:HA	1.89	0.55
1:V1:68:VAL:HA	1:V1:72:ARG:HH12	1.72	0.55
2:16:32:ILE:HG21	2:16:90:GLY:HA3	1.88	0.55
2:33:9:GLU:HB3	2:33:43:THR:HG23	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:38:8:TYR:CE2	3:38:93:LEU:HD23	2.42	0.55
3:38:53:ASP:O	3:38:57:LYS:N	2.26	0.55
3:48:29:PHE:CD2	3:48:63:PRO:HD2	2.42	0.55
3:48:147:PRO:HD2	3:48:150:TYR:CE2	2.42	0.55
3:B8:62:GLN:O	3:B8:78:HIS:N	2.30	0.54
3:E8:46:ILE:HD11	3:F8:177:ARG:HG2	1.89	0.54
3:F8:21:PHE:CE2	3:F8:169:VAL:HB	2.42	0.54
2:I3:21:ASP:OD1	2:I4:83:VAL:HG21	2.07	0.54
2:J7:23:MET:HG2	2:J7:56:ALA:O	2.07	0.54
2:K3:90:GLY:O	2:K3:92:THR:N	2.40	0.54
2:P3:5:LEU:HD13	2:P3:47:ARG:HD3	1.88	0.54
3:P8:119:ALA:HA	3:P8:136:PRO:HB3	1.89	0.54
1:S1:70:ASN:C	1:S1:72:ARG:H	2.16	0.54
2:S3:34:TYR:OH	2:S4:35:GLU:OE2	2.20	0.54
3:S8:120:TYR:HD1	3:U8:29:PHE:CZ	2.25	0.54
2:W3:47:ARG:HH11	2:W3:91:ARG:HB2	1.71	0.54
3:X8:11:LEU:HB3	3:X8:14:LEU:HD21	1.89	0.54
2:Y2:32:ILE:CD1	2:Y2:90:GLY:HA3	2.37	0.54
1:31:15:LYS:NZ	1:31:19:ILE:HG13	2.21	0.54
2:33:47:ARG:HH11	2:33:91:ARG:CG	2.19	0.54
3:38:167:VAL:HB	3:38:179:TYR:HB2	1.88	0.54
3:48:111:HIS:HA	3:48:142:ILE:O	2.06	0.54
3:C8:123:GLN:HG3	3:C9:23:GLY:HA3	1.88	0.54
1:D1:68:VAL:C	1:D1:72:ARG:NH1	2.65	0.54
2:D6:32:ILE:HG21	2:D6:90:GLY:HA3	1.88	0.54
2:G5:10:VAL:HG13	2:G5:69:GLU:O	2.06	0.54
2:I3:5:LEU:HD13	2:I3:47:ARG:HD3	1.88	0.54
2:M3:19:ALA:HB2	2:M3:64:ALA:HB2	1.89	0.54
2:M3:26:ALA:O	3:M8:12:ASP:HB3	2.07	0.54
2:O2:3:ASP:O	2:O2:47:ARG:NH1	2.21	0.54
1:Q1:10:VAL:HG13	1:S1:82:VAL:HG13	1.87	0.54
3:T8:7:THR:OG1	3:T8:41:GLU:N	2.39	0.54
1:V1:63:ALA:HB1	1:V1:77:THR:HG22	1.89	0.54
2:V4:31:LEU:HA	2:V4:46:VAL:HG12	1.87	0.54
2:V6:32:ILE:HG21	2:V6:90:GLY:CA	2.37	0.54
3:W9:20:THR:O	3:W9:24:LYS:N	2.36	0.54
1:X1:7:VAL:HG12	1:Y1:87:MET:HG2	1.88	0.54
2:X5:35:GLU:HG2	2:Y2:13:PHE:HE2	1.72	0.54
2:Y6:60:GLY:O	2:Y6:64:ALA:N	2.37	0.54
2:Z6:19:ALA:HB2	2:Z6:64:ALA:HB2	1.87	0.54
2:42:47:ARG:HH22	2:42:79:PRO:HG2	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B3:47:ARG:NH1	2:B3:84:ASP:OD1	2.39	0.54
2:C5:16:MET:O	2:C5:20:ALA:N	2.32	0.54
2:E6:10:VAL:HG11	2:E6:15:GLY:HA3	1.89	0.54
3:G8:122:THR:HG22	3:G8:134:ILE:HG22	1.88	0.54
2:J3:30:GLU:OE1	2:J3:91:ARG:NH2	2.40	0.54
2:J5:10:VAL:HG11	2:J5:15:GLY:HA3	1.88	0.54
3:K8:11:LEU:HB3	3:K8:14:LEU:HD21	1.89	0.54
2:N2:78:ARG:HD3	2:N5:28:LYS:HB2	1.88	0.54
2:Q6:36:LYS:NZ	2:Q7:35:GLU:OE1	2.38	0.54
3:S8:144:GLU:HA	3:S8:176:GLY:O	2.06	0.54
2:W3:61:GLN:O	2:W3:65:GLU:HG3	2.06	0.54
3:W8:18:LEU:HD11	3:W8:156:ASN:HA	1.90	0.54
2:X5:35:GLU:HG2	2:Y2:13:PHE:CE2	2.42	0.54
2:X6:16:MET:HG2	2:X6:44:ALA:HB2	1.90	0.54
2:Y5:8:GLU:HG3	2:Y5:42:THR:OG1	2.06	0.54
1:Z1:31:ASP:C	1:Z1:33:ASP:H	2.15	0.54
2:23:19:ALA:HB2	2:23:64:ALA:HB2	1.88	0.54
3:38:7:THR:HG23	3:38:41:GLU:HB3	1.89	0.54
2:A5:37:THR:HG21	2:E2:13:PHE:HB2	1.89	0.54
3:B8:7:THR:HG22	3:B8:150:TYR:CE1	2.42	0.54
2:D7:50:VAL:HG21	2:D7:77:PRO:HB3	1.89	0.54
3:D8:128:ASN:O	3:D8:130:GLN:N	2.38	0.54
1:H1:61:SER:HB3	1:Z1:61:SER:HB2	1.88	0.54
1:J1:68:VAL:C	1:J1:72:ARG:HH12	2.16	0.54
2:K6:47:ARG:NH2	2:K6:84:ASP:OD1	2.41	0.54
3:L8:167:VAL:HB	3:L8:179:TYR:HB2	1.88	0.54
2:O5:9:GLU:OE2	2:P2:13:PHE:N	2.40	0.54
2:O5:35:GLU:HG2	2:P2:13:PHE:CE2	2.41	0.54
3:O8:128:ASN:O	3:O8:130:GLN:N	2.39	0.54
3:P8:42:ILE:HD11	3:P8:96:LEU:HD11	1.90	0.54
2:T5:31:LEU:HB3	2:T6:82:ASN:OD1	2.08	0.54
2:Z6:16:MET:HG2	2:Z6:44:ALA:HB2	1.88	0.54
3:28:143:LEU:O	3:28:177:ARG:HA	2.07	0.54
2:34:47:ARG:HH22	2:34:84:ASP:CG	2.16	0.54
2:45:10:VAL:HG11	2:45:15:GLY:HA3	1.89	0.54
3:C8:19:ALA:HB3	3:C8:33:PRO:HG3	1.89	0.54
3:C8:126:ASN:O	3:C8:129:SER:HB3	2.08	0.54
2:E6:5:LEU:HB3	2:E6:76:ILE:HB	1.90	0.54
1:F1:70:ASN:C	1:F1:72:ARG:H	2.15	0.54
2:F7:12:GLY:HA2	2:G3:9:GLU:OE2	2.07	0.54
2:G3:21:ASP:OD1	2:G4:83:VAL:HG21	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G8:127:ARG:NH1	3:I8:67:VAL:HG12	2.20	0.54
3:J8:21:PHE:HE2	3:J8:169:VAL:HB	1.73	0.54
2:N3:9:GLU:HB3	2:N3:43:THR:HG23	1.89	0.54
2:X4:20:ALA:HB1	2:X4:31:LEU:HD22	1.90	0.54
3:Z8:21:PHE:HE2	3:Z8:169:VAL:HB	1.73	0.54
2:37:19:ALA:HB2	2:37:64:ALA:HB2	1.88	0.54
2:43:47:ARG:NH1	2:43:91:ARG:HB2	2.09	0.54
3:B8:60:LYS:HD2	2:L7:78:ARG:HE	1.72	0.54
2:D2:30:GLU:OE1	2:D2:91:ARG:NH1	2.30	0.54
3:D8:56:LEU:O	2:P7:76:ARG:NH2	2.41	0.54
3:D8:70:ARG:HG2	3:D8:172:TYR:HB2	1.89	0.54
2:E2:16:MET:HG2	2:E2:44:ALA:HB2	1.89	0.54
2:E3:18:GLU:OE1	2:E4:74:HIS:NE2	2.38	0.54
3:H8:42:ILE:HD11	3:H8:96:LEU:HD11	1.90	0.54
2:J2:8:ILE:HG12	2:J2:73:VAL:HG22	1.90	0.54
3:J8:183:SER:OG	3:J8:186:GLU:OE2	2.26	0.54
3:K8:6:ARG:HA	3:K8:104:LEU:HG	1.90	0.54
2:M2:32:ILE:CD1	2:M2:90:GLY:HA3	2.37	0.54
1:O1:28:ARG:NH1	1:O1:36:PRO:HB2	2.23	0.54
2:P5:9:GLU:OE2	2:Q2:13:PHE:N	2.41	0.54
1:S1:63:ALA:HB1	1:S1:77:THR:HG22	1.90	0.54
2:V4:10:VAL:HG11	2:V4:15:GLY:HA3	1.88	0.54
2:Y3:10:VAL:O	2:Y3:12:GLY:N	2.41	0.54
3:38:36:ALA:N	3:38:79:HIS:O	2.41	0.54
3:A8:45:GLY:HA2	3:A8:48:ILE:HD13	1.88	0.54
2:D6:16:MET:HG3	2:D6:42:VAL:HG12	1.90	0.54
2:E3:9:GLU:HB3	2:E3:43:THR:HG23	1.90	0.54
2:H2:13:PHE:N	2:Z5:9:GLU:OE2	2.41	0.54
2:L6:10:VAL:HG21	2:L6:16:MET:N	2.22	0.54
3:L9:20:THR:O	3:L9:24:LYS:N	2.38	0.54
3:L9:103:ARG:O	3:L9:204:VAL:N	2.41	0.54
3:N8:21:PHE:HE2	3:N8:169:VAL:HB	1.71	0.54
1:O1:26:LEU:HD23	1:P1:87:MET:CE	2.38	0.54
2:P6:16:MET:HG3	2:P6:42:VAL:HG12	1.88	0.54
2:Q2:10:VAL:HG11	2:Q2:15:GLY:HA3	1.90	0.54
1:R1:32:PRO:HG3	1:R1:87:MET:HE1	1.89	0.54
2:U2:3:ASP:HB2	2:U2:47:ARG:HH11	1.73	0.54
2:Y6:10:VAL:HG11	2:Y6:15:GLY:HA3	1.88	0.54
3:18:44:PRO:HB2	3:18:46:ILE:HG13	1.90	0.54
2:26:13:PHE:HB2	2:27:37:THR:HG21	1.90	0.54
3:28:13:ALA:HA	3:28:35:GLN:O	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A6:32:ILE:HD13	2:A6:90:GLY:HA3	1.90	0.54
1:B1:31:ASP:O	1:B1:33:ASP:N	2.41	0.54
2:B3:53:VAL:O	2:B3:57:THR:OG1	2.21	0.54
2:D3:27:ALA:O	3:D8:12:ASP:HB3	2.07	0.54
3:D8:183:SER:OG	3:D8:186:GLU:OE2	2.23	0.54
3:K8:150:TYR:CE2	3:K8:201:VAL:HG11	2.42	0.54
1:N1:32:PRO:HG3	1:N1:87:MET:CE	2.38	0.54
3:N8:143:LEU:O	3:N8:177:ARG:HA	2.07	0.54
1:O1:16:GLU:OE1	1:O1:17:PRO:HD2	2.06	0.54
2:P5:57:THR:O	2:P5:60:GLY:N	2.41	0.54
2:R2:13:PHE:HB2	2:V5:37:THR:HG21	1.90	0.54
2:S5:10:VAL:HG11	2:S5:15:GLY:HA3	1.88	0.54
2:V3:7:MET:HE1	2:W7:17:VAL:CG1	2.34	0.54
3:Y8:65:VAL:HG12	3:Y8:76:GLU:HB3	1.90	0.54
2:Z6:32:ILE:HD11	2:Z6:47:ARG:HD2	1.89	0.54
3:29:6:ARG:N	3:29:41:GLU:O	2.41	0.54
2:42:54:LYS:NZ	2:45:55:ALA:HB2	2.22	0.54
2:F2:18:GLU:OE1	2:R5:74:HIS:NE2	2.40	0.54
2:G7:47:ARG:HH22	2:G7:84:ASP:CG	2.16	0.54
3:H8:41:GLU:HA	3:H8:74:LEU:CD1	2.38	0.54
2:L3:30:GLU:OE1	2:L3:91:ARG:NH2	2.34	0.54
3:L8:111:HIS:HA	3:L8:142:ILE:O	2.08	0.54
3:L8:142:ILE:HA	3:L8:178:LEU:O	2.07	0.54
3:N8:21:PHE:HE1	3:N8:130:GLN:HB3	1.73	0.54
2:Q5:52:ALA:O	2:Q5:56:ALA:N	2.39	0.54
3:R9:6:ARG:H	3:R9:42:ILE:HA	1.73	0.54
3:T8:122:THR:HG22	3:T8:134:ILE:HG22	1.89	0.54
2:U5:35:GLU:HG2	2:42:13:PHE:CE2	2.42	0.54
3:U8:36:ALA:N	3:U8:79:HIS:O	2.41	0.54
1:V1:59:SER:HA	1:V1:76:ALA:HA	1.90	0.54
3:W8:61:VAL:HG11	3:W8:77:VAL:HB	1.90	0.54
3:X8:19:ALA:HB3	3:X8:33:PRO:HG3	1.90	0.54
3:X8:55:ALA:O	3:X8:59:THR:OG1	2.25	0.54
3:X8:186:GLU:O	3:X8:190:ALA:N	2.40	0.54
2:Y6:47:ARG:HH22	2:Y6:79:PRO:CG	2.21	0.54
3:Z9:105:LYS:N	3:Z9:204:VAL:O	2.33	0.54
3:A8:38:LEU:O	3:A8:76:GLU:HA	2.07	0.54
2:D6:13:PHE:HB2	2:D7:37:THR:HG21	1.90	0.54
3:E8:142:ILE:HA	3:E8:178:LEU:O	2.08	0.54
1:F1:28:ARG:NH1	1:F1:36:PRO:HB2	2.22	0.54
3:G8:143:LEU:O	3:G8:177:ARG:HA	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H5:10:VAL:HG11	2:H5:15:GLY:HA3	1.90	0.54
2:O6:47:ARG:NH2	2:O6:84:ASP:OD2	2.41	0.54
3:O9:41:GLU:HA	3:O9:73:GLY:O	2.08	0.54
2:P6:19:ALA:HB2	2:P6:64:ALA:HB2	1.89	0.54
1:Q1:31:ASP:O	1:Q1:33:ASP:N	2.39	0.54
2:Q3:5:LEU:HD13	2:Q3:47:ARG:HD3	1.89	0.54
3:Q8:126:ASN:O	3:Q8:129:SER:HB3	2.08	0.54
3:Q8:167:VAL:HB	3:Q8:179:TYR:HB2	1.89	0.54
3:S8:47:ALA:HB1	3:S8:50:ARG:HH12	1.73	0.54
2:T3:4:ALA:HB3	2:T3:48:GLY:O	2.07	0.54
1:W1:70:ASN:C	1:W1:72:ARG:H	2.16	0.54
3:W9:139:SER:N	3:W9:182:GLY:O	2.31	0.54
1:Y1:68:VAL:C	1:Y1:72:ARG:HH12	2.16	0.54
3:Y8:183:SER:OG	3:Y8:186:GLU:OE2	2.25	0.54
2:25:90:GLY:O	2:25:91:ARG:HG2	2.08	0.54
2:33:47:ARG:HH11	2:33:91:ARG:CB	2.20	0.54
2:45:32:ILE:HD12	2:45:47:ARG:HG3	1.90	0.54
2:A3:10:VAL:O	2:A3:12:GLY:N	2.41	0.53
3:C8:144:GLU:HB2	3:28:46:ILE:HD11	1.89	0.53
2:F3:47:ARG:HH11	2:F3:91:ARG:HB2	1.73	0.53
2:H2:16:MET:HG2	2:H2:44:ALA:HB2	1.89	0.53
3:I8:142:ILE:HA	3:I8:178:LEU:O	2.07	0.53
2:N7:10:VAL:HG11	2:N7:15:GLY:HA3	1.89	0.53
1:O1:86:GLU:HG2	1:O1:87:MET:N	2.22	0.53
2:Q5:2:ALA:HB1	2:Q5:78:ARG:HH12	1.72	0.53
2:R6:27:ALA:HA	3:R8:116:ALA:HB2	1.90	0.53
3:R8:51:VAL:HG13	3:R8:92:ILE:HG12	1.90	0.53
3:R8:170:THR:HG1	3:R8:177:ARG:H	1.52	0.53
3:R9:41:GLU:HA	3:R9:74:LEU:HA	1.90	0.53
1:S1:7:VAL:HG12	1:31:87:MET:HG2	1.90	0.53
3:S8:183:SER:OG	3:S8:186:GLU:OE2	2.25	0.53
2:U3:12:GLY:HA2	2:U4:9:GLU:OE2	2.07	0.53
2:X5:13:PHE:HD2	2:X6:43:THR:HG21	1.71	0.53
2:Y3:34:TYR:OH	2:Y4:35:GLU:OE2	2.22	0.53
3:Z8:111:HIS:HA	3:Z8:142:ILE:O	2.08	0.53
2:14:16:MET:HG3	2:14:42:VAL:HG12	1.90	0.53
3:18:29:PHE:CD2	3:18:63:PRO:HD2	2.43	0.53
2:32:30:GLU:CD	2:32:91:ARG:HH22	2.15	0.53
3:38:16:PRO:HA	3:38:33:PRO:CB	2.30	0.53
2:D4:16:MET:HG3	2:D4:42:VAL:HG12	1.90	0.53
2:D7:23:MET:HG2	2:D7:56:ALA:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F7:87:LEU:HB3	2:F7:89:LEU:HD13	1.89	0.53
1:G1:31:ASP:OD1	1:G1:35:THR:OG1	2.22	0.53
1:H1:63:ALA:HB1	1:H1:77:THR:HG22	1.90	0.53
2:H3:4:ALA:O	2:H3:47:ARG:HD2	2.08	0.53
2:H5:13:PHE:HD2	2:H6:43:THR:HG21	1.73	0.53
3:Q9:88:ALA:O	3:Q9:92:ILE:N	2.37	0.53
2:S5:74:HIS:NE2	2:32:18:GLU:OE1	2.39	0.53
2:T2:5:LEU:HB3	2:T2:76:ILE:HB	1.89	0.53
2:T2:16:MET:O	2:T2:20:ALA:N	2.31	0.53
2:T5:4:ALA:HB2	2:T5:50:VAL:HA	1.88	0.53
3:T8:63:PRO:HB3	3:T8:77:VAL:HG12	1.90	0.53
2:V2:32:ILE:HD11	2:V2:90:GLY:HA3	1.89	0.53
1:Z1:31:ASP:OD1	1:Z1:35:THR:OG1	2.23	0.53
1:B1:32:PRO:HG3	1:B1:87:MET:CE	2.38	0.53
2:B2:3:ASP:O	2:B2:47:ARG:NH1	2.39	0.53
3:D8:9:ILE:CD1	3:D8:150:TYR:HA	2.38	0.53
3:D8:123:GLN:HA	3:D8:126:ASN:HD22	1.72	0.53
3:D8:128:ASN:O	3:D8:168:ASN:ND2	2.41	0.53
3:D8:186:GLU:OE1	3:D8:186:GLU:N	2.30	0.53
2:E6:57:THR:HG21	2:E6:75:VAL:HG22	1.90	0.53
1:H1:33:ASP:HB3	1:H1:35:THR:HG23	1.89	0.53
1:H1:68:VAL:C	1:H1:72:ARG:NH1	2.67	0.53
2:I3:9:GLU:HG3	2:I3:71:VAL:HB	1.90	0.53
2:J2:90:GLY:C	2:J2:92:THR:H	2.12	0.53
1:P1:86:GLU:C	1:P1:87:MET:SD	2.92	0.53
2:P5:5:LEU:HB3	2:P5:76:ILE:HB	1.89	0.53
3:P8:126:ASN:O	3:P8:129:SER:HB3	2.08	0.53
1:Q1:19:ILE:O	1:Q1:22:LEU:HB2	2.08	0.53
3:V8:21:PHE:O	3:V8:25:THR:OG1	2.16	0.53
1:X1:22:LEU:HG	1:X1:44:ALA:HB1	1.89	0.53
3:Y8:121:GLN:O	3:Y8:125:ILE:HG13	2.08	0.53
1:Z1:28:ARG:NH1	1:Z1:36:PRO:HB2	2.22	0.53
2:Z5:10:VAL:HG11	2:Z5:15:GLY:HA3	1.90	0.53
3:18:123:GLN:HG3	3:19:23:GLY:HA3	1.91	0.53
2:23:18:GLU:OE1	2:24:74:HIS:NE2	2.32	0.53
3:28:47:ALA:HB1	3:28:50:ARG:HH12	1.73	0.53
3:A8:141:PHE:HB3	3:A8:180:LEU:HB2	1.91	0.53
3:B8:16:PRO:CA	3:B8:33:PRO:HB3	2.35	0.53
2:D2:85:ALA:HA	2:D2:92:THR:HG23	1.90	0.53
2:D6:10:VAL:HG11	2:D6:15:GLY:HA3	1.90	0.53
3:D8:11:LEU:HD12	3:D8:39:TRP:HE1	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E8:142:ILE:HB	3:Q8:46:ILE:HG21	1.91	0.53
3:E9:66:GLN:HA	3:E9:75:LEU:HA	1.90	0.53
2:F3:84:ASP:O	2:F3:92:THR:OG1	2.22	0.53
3:G9:87:ALA:O	3:G9:91:THR:N	2.34	0.53
2:I2:32:ILE:HD11	2:I2:90:GLY:HA3	1.89	0.53
2:J3:34:TYR:OH	2:J4:35:GLU:OE2	2.24	0.53
3:K8:16:PRO:HA	3:K8:33:PRO:CB	2.35	0.53
2:M2:47:ARG:HH22	2:M2:79:PRO:HG2	1.74	0.53
2:M6:14:VAL:HG23	2:M7:9:GLU:HB2	1.91	0.53
3:P8:167:VAL:HB	3:P8:179:TYR:HB2	1.91	0.53
2:S6:32:ILE:HG21	2:S6:90:GLY:HA3	1.91	0.53
1:U1:63:ALA:HB1	1:U1:77:THR:HG22	1.90	0.53
2:V6:32:ILE:HD13	2:V6:90:GLY:HA3	1.89	0.53
3:V8:88:ALA:O	3:V8:91:THR:OG1	2.26	0.53
2:W3:4:ALA:O	2:W3:47:ARG:HD2	2.08	0.53
3:Z8:17:GLN:O	3:Z8:20:THR:OG1	2.20	0.53
2:A3:5:LEU:HD11	2:A3:7:MET:HE3	1.91	0.53
2:A3:5:LEU:HD22	2:A3:6:GLY:H	1.73	0.53
2:A6:32:ILE:HG21	2:A6:90:GLY:CA	2.37	0.53
3:A8:128:ASN:O	3:A8:130:GLN:N	2.39	0.53
2:B7:49:ASP:OD1	2:B7:50:VAL:N	2.41	0.53
2:I2:32:ILE:CD1	2:I2:90:GLY:HA3	2.38	0.53
3:I8:134:ILE:HG12	3:I8:181:ALA:HB2	1.90	0.53
3:I9:44:PRO:HA	3:I9:71:ALA:O	2.09	0.53
2:J7:78:ARG:HD3	3:L8:60:LYS:HG2	1.90	0.53
3:J8:127:ARG:NH2	3:L8:67:VAL:HG12	2.24	0.53
3:N8:38:LEU:O	3:N8:76:GLU:HA	2.09	0.53
3:S8:38:LEU:O	3:S8:76:GLU:HA	2.09	0.53
2:T3:47:ARG:HH22	2:T3:79:PRO:HG2	1.73	0.53
3:T8:65:VAL:HG12	3:T8:76:GLU:HB3	1.89	0.53
2:V3:5:LEU:HD12	2:V3:6:GLY:H	1.73	0.53
3:V8:142:ILE:HA	3:V8:178:LEU:O	2.09	0.53
2:W4:20:ALA:HB1	2:W4:31:LEU:HD22	1.90	0.53
2:W5:13:PHE:HB2	2:W6:37:THR:HG21	1.91	0.53
2:W7:78:ARG:NH2	3:Y8:56:LEU:O	2.42	0.53
2:Y2:32:ILE:HD11	2:Y2:90:GLY:HA3	1.90	0.53
2:13:9:GLU:HG3	2:13:71:VAL:HB	1.90	0.53
3:28:42:ILE:HD13	3:28:96:LEU:HD11	1.90	0.53
3:D8:162:ALA:HB3	3:D8:190:ALA:HB2	1.90	0.53
3:E8:13:ALA:HA	3:E8:35:GLN:O	2.09	0.53
3:E8:63:PRO:HB3	3:E8:77:VAL:HG12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K8:59:THR:HB	3:K8:61:VAL:HG23	1.90	0.53
2:L4:62:ARG:NE	2:L5:66:ARG:NH1	2.57	0.53
2:O3:12:GLY:HA2	2:O4:9:GLU:OE2	2.08	0.53
3:O8:141:PHE:CZ	3:O8:143:LEU:HB2	2.44	0.53
2:Q3:8:ILE:HG23	2:Q3:73:VAL:HG22	1.91	0.53
1:S1:68:VAL:HA	1:S1:72:ARG:NH1	2.19	0.53
3:S8:18:LEU:HD11	3:S8:156:ASN:HA	1.90	0.53
2:T2:32:ILE:CD1	2:T2:90:GLY:HA3	2.38	0.53
2:U5:18:GLU:CD	2:U6:74:HIS:HE2	2.17	0.53
2:V6:5:LEU:HD23	2:V6:76:ILE:HD12	1.89	0.53
3:V9:144:GLU:HA	3:V9:176:GLY:O	2.08	0.53
3:W8:41:GLU:HB2	3:W8:74:LEU:HD13	1.90	0.53
2:X5:16:MET:HG2	2:X5:44:ALA:HB2	1.90	0.53
3:18:126:ASN:O	3:18:129:SER:HB3	2.08	0.53
3:28:7:THR:OG1	3:28:41:GLU:N	2.41	0.53
1:F1:31:ASP:C	1:F1:33:ASP:H	2.17	0.53
2:F5:60:GLY:O	2:F5:64:ALA:N	2.42	0.53
2:H6:30:GLU:OE1	2:H6:91:ARG:NH2	2.39	0.53
2:H7:47:ARG:HH22	2:H7:84:ASP:CG	2.17	0.53
2:J6:8:ILE:HG21	2:J6:19:ALA:HB1	1.89	0.53
2:M6:19:ALA:HB2	2:M6:64:ALA:HB2	1.89	0.53
2:N3:5:LEU:O	2:N3:53:VAL:HG11	2.08	0.53
2:O6:23:MET:HG2	2:O6:56:ALA:O	2.08	0.53
2:P7:14:MET:HB2	2:P7:40:VAL:HG23	1.91	0.53
1:Q1:50:GLY:N	1:Q1:53:GLU:OE1	2.30	0.53
3:Q8:123:GLN:NE2	3:Q9:31:PRO:O	2.41	0.53
1:S1:30:CYS:HA	1:S1:36:PRO:HA	1.91	0.53
2:U7:49:ASP:OD1	2:U7:49:ASP:N	2.42	0.53
3:V8:35:GLN:HA	3:V8:80:PHE:HA	1.89	0.53
3:X8:9:ILE:HD12	3:X8:150:TYR:HA	1.90	0.53
2:17:53:VAL:HA	2:17:56:ALA:HB3	1.90	0.53
1:31:70:ASN:C	1:31:72:ARG:H	2.16	0.53
2:C4:47:ARG:HH22	2:C4:84:ASP:CG	2.16	0.53
3:C8:6:ARG:HA	3:C8:104:LEU:HG	1.91	0.53
3:C8:38:LEU:O	3:C8:76:GLU:HA	2.09	0.53
2:D4:62:ARG:NE	2:D5:66:ARG:NH1	2.57	0.53
2:G2:32:ILE:CD1	2:G2:90:GLY:HA3	2.38	0.53
2:G7:17:VAL:HG21	2:W3:7:MET:HE1	1.91	0.53
2:H2:13:PHE:CE2	2:Z5:35:GLU:HG2	2.44	0.53
2:H7:53:VAL:HA	2:H7:56:ALA:HB3	1.91	0.53
2:K2:16:MET:HG2	2:K2:44:ALA:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K8:112:GLN:CD	3:18:50:ARG:HE	2.15	0.53
2:L5:13:PHE:HD2	2:L6:43:THR:HG21	1.74	0.53
2:N5:13:PHE:HB2	2:N6:37:THR:HG21	1.90	0.53
3:N8:11:LEU:HB3	3:N8:14:LEU:HD21	1.89	0.53
3:O8:121:GLN:O	3:O8:125:ILE:HG13	2.09	0.53
3:Q8:59:THR:HB	3:Q8:61:VAL:HG23	1.91	0.53
2:S7:51:ALA:HB2	2:U3:51:ALA:HB2	1.91	0.53
2:T2:47:ARG:NH2	2:T2:84:ASP:OD2	2.42	0.53
2:T7:30:GLU:OE1	2:T7:91:ARG:NH2	2.39	0.53
2:U3:47:ARG:NH1	2:U3:84:ASP:OD1	2.42	0.53
3:U9:39:TRP:HA	3:U9:76:GLU:HA	1.91	0.53
2:V2:47:ARG:HD3	2:V2:91:ARG:HG2	1.91	0.53
2:V3:4:ALA:O	2:V3:47:ARG:HD2	2.09	0.53
2:V7:20:ALA:HB1	2:V7:31:LEU:HD22	1.91	0.53
2:W5:36:LYS:NZ	2:W6:35:GLU:OE2	2.40	0.53
2:X6:16:MET:HG3	2:X6:42:VAL:HG12	1.91	0.53
2:36:61:GLN:CD	2:36:73:VAL:HG21	2.33	0.53
3:49:37:SER:HA	3:49:78:HIS:HA	1.91	0.53
2:A2:16:MET:HG2	2:A2:44:ALA:HB2	1.90	0.53
2:D2:3:ASP:C	2:D2:47:ARG:HH12	2.16	0.53
2:F3:9:GLU:HB3	2:F3:43:THR:HG23	1.90	0.53
3:F8:106:PRO:HG3	3:F8:150:TYR:HE2	1.74	0.53
3:G8:183:SER:OG	3:G8:186:GLU:OE2	2.25	0.53
2:I5:13:PHE:CD2	2:I6:43:THR:HG21	2.44	0.53
1:K1:91:VAL:HG21	1:K1:94:ARG:NH2	2.24	0.53
3:K8:6:ARG:NH1	3:K8:72:TYR:OH	2.41	0.53
3:N8:126:ASN:O	3:N8:129:SER:HB3	2.09	0.53
3:O8:8:TYR:HA	3:O8:40:VAL:HG22	1.91	0.53
3:Q8:9:ILE:CD1	3:Q8:150:TYR:HA	2.33	0.53
2:S2:30:GLU:OE1	2:S2:91:ARG:NH1	2.37	0.53
3:V8:8:TYR:CE2	3:V8:93:LEU:HD23	2.43	0.53
2:Y2:37:THR:HG21	2:Y4:13:PHE:HB2	1.91	0.53
3:Z8:121:GLN:O	3:Z8:125:ILE:HG13	2.09	0.53
3:Z9:65:VAL:O	3:Z9:75:LEU:HA	2.09	0.53
2:23:45:VAL:CG1	2:23:89:LEU:HD12	2.39	0.53
1:31:6:VAL:HG12	1:31:27:VAL:HG12	1.91	0.53
3:38:21:PHE:CE2	3:38:169:VAL:HB	2.43	0.53
3:A8:50:ARG:HD2	3:A8:95:LYS:HD3	1.90	0.53
3:B8:29:PHE:HB2	3:B8:63:PRO:O	2.08	0.53
3:B8:128:ASN:O	3:B8:168:ASN:ND2	2.41	0.53
2:C5:36:LYS:NZ	2:C6:35:GLU:OE2	2.34	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D7:20:ALA:HB1	2:D7:31:LEU:HD22	1.90	0.53
2:E6:5:LEU:HD23	2:E6:76:ILE:HD12	1.91	0.53
2:F3:5:LEU:HB3	2:F3:76:ILE:HB	1.91	0.53
3:F8:64:ALA:HB3	3:F8:76:GLU:OE1	2.08	0.53
2:H4:66:ARG:NH1	2:H5:62:ARG:CZ	2.71	0.53
3:K8:121:GLN:O	3:K8:125:ILE:HG13	2.09	0.53
2:N2:30:GLU:OE1	2:N2:91:ARG:NH2	2.41	0.53
2:N2:54:LYS:HZ2	2:N5:55:ALA:HB2	1.73	0.53
3:N8:110:THR:O	3:N8:143:LEU:HA	2.09	0.53
2:O3:18:GLU:OE1	2:O4:74:HIS:NE2	2.37	0.53
3:P8:29:PHE:CD2	3:P8:63:PRO:HD2	2.44	0.53
3:P8:47:ALA:HB1	3:P8:50:ARG:HH12	1.74	0.53
3:R9:190:ALA:O	3:R9:194:ALA:N	2.38	0.53
1:S1:31:ASP:C	1:S1:33:ASP:H	2.17	0.53
3:S8:8:TYR:HA	3:S8:40:VAL:HG22	1.91	0.53
3:T8:135:LEU:CD2	3:T9:17:GLN:HA	2.39	0.53
3:T8:143:LEU:O	3:T8:177:ARG:HA	2.09	0.53
2:U2:16:MET:O	2:U2:20:ALA:N	2.29	0.53
1:V1:83:ASP:OD2	1:W1:13:SER:OG	2.06	0.53
1:Y1:31:ASP:OD1	1:Y1:35:THR:OG1	2.25	0.53
1:31:15:LYS:HE2	1:31:19:ILE:HD11	1.90	0.53
1:31:26:LEU:HD22	1:31:40:ALA:HB1	1.91	0.53
1:41:45:ASP:OD1	1:41:47:VAL:N	2.32	0.53
3:48:183:SER:OG	3:48:186:GLU:OE2	2.27	0.53
2:D3:53:ALA:O	2:D3:57:ALA:N	2.33	0.52
3:D8:70:ARG:HE	3:D8:173:GLY:HA2	1.73	0.52
3:F8:111:HIS:HA	3:F8:142:ILE:O	2.10	0.52
2:G3:11:ARG:NH1	2:G3:41:TYR:CZ	2.77	0.52
2:I4:78:ARG:NH1	3:I8:159:GLU:OE1	2.42	0.52
2:J4:16:MET:HG2	2:J4:44:ALA:HB2	1.90	0.52
2:J4:90:GLY:O	2:J4:91:ARG:NH1	2.40	0.52
2:M4:47:ARG:HH22	2:M4:84:ASP:CG	2.16	0.52
3:N9:45:GLY:N	3:N9:71:ALA:O	2.34	0.52
2:O5:13:PHE:HD2	2:O6:43:THR:HG21	1.74	0.52
3:O8:7:THR:OG1	3:O8:41:GLU:N	2.42	0.52
3:O8:9:ILE:HD11	3:O8:150:TYR:CD2	2.44	0.52
3:R8:142:ILE:HA	3:R8:178:LEU:O	2.09	0.52
3:S8:21:PHE:HE2	3:S8:169:VAL:HB	1.73	0.52
2:V2:11:ARG:HB3	2:V2:69:GLU:HG2	1.90	0.52
3:X8:63:PRO:HA	3:X8:77:VAL:HA	1.91	0.52
1:Y1:41:VAL:HG11	1:Y1:57:TYR:OH	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:22:29:VAL:HG11	2:22:46:VAL:HB	1.91	0.52
3:28:65:VAL:N	3:28:76:GLU:OE2	2.34	0.52
3:28:186:GLU:OE1	3:28:186:GLU:N	2.31	0.52
3:38:70:ARG:HG2	3:38:173:GLY:N	2.24	0.52
2:47:92:THR:O	2:47:94:GLY:N	2.41	0.52
3:48:8:TYR:CE2	3:48:93:LEU:HD23	2.44	0.52
2:A2:13:PHE:HD2	2:B5:37:THR:HG22	1.74	0.52
1:B1:22:LEU:HG	1:B1:44:ALA:HB1	1.91	0.52
2:B3:24:VAL:HG11	2:B4:82:ASN:HB3	1.90	0.52
2:B4:16:MET:HG3	2:B4:42:VAL:HG12	1.92	0.52
3:B8:3:ILE:HB	3:B8:96:LEU:HD22	1.91	0.52
3:B8:20:THR:HG21	3:B9:135:LEU:HA	1.91	0.52
3:D8:15:GLN:HG2	3:D8:156:ASN:OD1	2.09	0.52
3:D8:60:LYS:CG	2:P7:76:ARG:HD3	2.33	0.52
3:F8:6:ARG:HA	3:F8:104:LEU:HG	1.91	0.52
3:G8:63:PRO:HB3	3:G8:77:VAL:HG12	1.91	0.52
3:G9:113:ILE:HA	3:G9:141:PHE:HA	1.90	0.52
1:I1:64:ARG:HD3	1:J1:62:SER:HB2	1.91	0.52
2:I3:4:ALA:O	2:I3:47:ARG:HD2	2.10	0.52
3:I8:63:PRO:HA	3:I8:77:VAL:HA	1.91	0.52
3:I8:70:ARG:HG2	3:I8:172:TYR:HB2	1.91	0.52
3:K8:21:PHE:HE2	3:K8:169:VAL:HB	1.74	0.52
2:L2:84:ASP:O	2:L2:92:THR:HG22	2.09	0.52
3:R8:20:THR:O	3:R8:24:LYS:N	2.32	0.52
3:R8:29:PHE:CZ	3:U8:120:TYR:HD1	2.27	0.52
3:R8:88:ALA:O	3:R8:91:THR:OG1	2.27	0.52
2:S6:8:ILE:O	2:S6:43:THR:HA	2.10	0.52
2:S7:49:ASP:N	2:S7:49:ASP:OD1	2.42	0.52
2:V2:13:PHE:N	2:W5:9:GLU:OE2	2.42	0.52
2:V5:9:GLU:HG3	2:V5:43:THR:OG1	2.09	0.52
2:X3:47:ARG:NH1	2:X3:84:ASP:OD1	2.42	0.52
1:21:70:ASN:O	1:21:72:ARG:N	2.42	0.52
3:28:127:ARG:C	3:28:127:ARG:CD	2.83	0.52
3:28:140:LEU:HA	3:28:180:LEU:O	2.09	0.52
3:48:21:PHE:O	3:48:25:THR:OG1	2.15	0.52
3:A8:142:ILE:HB	3:G8:46:ILE:HG21	1.91	0.52
3:D8:112:GLN:OE1	3:N8:50:ARG:NE	2.42	0.52
2:E2:4:ALA:O	2:E2:47:ARG:HG2	2.09	0.52
2:F6:32:ILE:HG21	2:F6:90:GLY:CA	2.39	0.52
2:J2:3:ASP:O	2:J2:47:ARG:NH1	2.36	0.52
2:L5:32:ILE:HD12	2:L5:47:ARG:HG3	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M7:49:ASP:OD1	2:M7:49:ASP:N	2.42	0.52
2:N3:26:ALA:O	3:N8:12:ASP:HB3	2.08	0.52
3:N8:7:THR:HG23	3:N8:41:GLU:HB3	1.91	0.52
2:P7:14:MET:HB2	2:P7:40:VAL:CG2	2.39	0.52
2:Q5:21:ASP:OD2	2:Q5:25:LYS:NZ	2.39	0.52
2:S3:47:ARG:NH1	2:S3:79:PRO:HG2	2.22	0.52
3:T8:70:ARG:HG2	3:T8:172:TYR:HB2	1.90	0.52
3:T9:105:LYS:N	3:T9:204:VAL:O	2.38	0.52
2:X2:45:VAL:HG11	2:X2:89:LEU:HD12	1.91	0.52
2:X5:52:ALA:O	2:X5:56:ALA:N	2.42	0.52
3:X8:60:LYS:CG	2:47:78:ARG:HD3	2.32	0.52
2:32:4:ALA:HB3	2:32:53:VAL:HG21	1.91	0.52
2:45:31:LEU:O	2:45:32:ILE:HB	2.09	0.52
3:48:21:PHE:CE2	3:48:169:VAL:HB	2.45	0.52
2:B6:16:MET:HG3	2:B6:42:VAL:HG12	1.90	0.52
3:B8:177:ARG:HG2	3:J8:46:ILE:HD11	1.90	0.52
1:C1:62:SER:HB2	1:D1:64:ARG:HD3	1.90	0.52
2:D3:5:ALA:O	2:D3:48:ARG:HD2	2.09	0.52
3:F8:9:ILE:HG21	3:F8:153:LEU:HB2	1.92	0.52
3:G8:121:GLN:O	3:G8:125:ILE:HG13	2.09	0.52
2:J6:32:ILE:HD11	2:J6:47:ARG:HD2	1.91	0.52
2:K6:27:ALA:HA	3:K8:116:ALA:HB2	1.90	0.52
2:K7:52:ALA:O	2:K7:56:ALA:N	2.42	0.52
3:K8:183:SER:OG	3:K8:186:GLU:OE2	2.27	0.52
3:M8:76:GLU:OE2	3:M8:78:HIS:HB3	2.09	0.52
3:P8:9:ILE:HB	3:P8:39:TRP:HB2	1.91	0.52
1:Q1:16:GLU:C	1:Q1:16:GLU:OE1	2.53	0.52
1:R1:66:THR:O	1:R1:69:THR:OG1	2.20	0.52
3:R8:109:MET:HB2	3:R8:144:GLU:HB3	1.92	0.52
2:T2:3:ASP:OD2	2:T2:91:ARG:NH2	2.42	0.52
3:U9:88:ALA:O	3:U9:92:ILE:N	2.40	0.52
1:W1:19:ILE:O	1:W1:22:LEU:HB2	2.10	0.52
3:W8:70:ARG:HG2	3:W8:173:GLY:N	2.25	0.52
2:36:13:PHE:N	2:37:9:GLU:OE2	2.41	0.52
2:A2:18:GLU:OE1	2:B5:74:HIS:NE2	2.43	0.52
2:B2:43:THR:HG21	2:B4:13:PHE:HD2	1.75	0.52
2:B6:8:ILE:HD13	2:B6:19:ALA:HB1	1.90	0.52
3:C8:13:ALA:HA	3:C8:35:GLN:O	2.09	0.52
3:C8:59:THR:O	2:M7:78:ARG:NE	2.42	0.52
3:C8:127:ARG:NH1	3:28:67:VAL:HG12	2.22	0.52
1:D1:79:MET:HE1	1:E1:73:PRO:O	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G6:18:GLU:CD	2:G7:74:HIS:HE2	2.17	0.52
2:J2:45:VAL:HG11	2:J2:89:LEU:HD12	1.92	0.52
2:J6:27:ALA:HB1	2:J6:52:ALA:HB1	1.91	0.52
3:J8:60:LYS:HE2	3:J8:84:GLU:OE2	2.09	0.52
3:K8:118:GLU:HG2	3:18:56:LEU:HD13	1.91	0.52
2:L7:58:GLU:O	2:L7:62:ARG:HG3	2.10	0.52
3:L8:183:SER:O	3:L8:187:ILE:HG12	2.09	0.52
3:M8:128:ASN:O	3:M8:130:GLN:N	2.41	0.52
1:O1:64:ARG:HH11	1:P1:62:SER:CB	2.22	0.52
2:S2:29:VAL:HG11	2:S2:46:VAL:HB	1.91	0.52
2:S2:37:THR:OG1	2:S4:40:GLY:HA2	2.08	0.52
3:S8:128:ASN:O	3:S8:130:GLN:N	2.39	0.52
2:T2:54:LYS:HZ1	2:T5:55:ALA:CB	2.22	0.52
2:U2:3:ASP:OD2	2:U2:91:ARG:NE	2.36	0.52
2:U3:47:ARG:NH2	2:U3:79:PRO:HG2	2.24	0.52
1:V1:70:ASN:C	1:V1:72:ARG:H	2.16	0.52
3:V8:21:PHE:CE2	3:V8:169:VAL:HB	2.44	0.52
1:Y1:27:VAL:O	1:Y1:41:VAL:HG12	2.10	0.52
1:Z1:87:MET:HG2	1:11:7:VAL:HG12	1.91	0.52
2:A3:47:ARG:HH22	2:A3:79:PRO:HG2	1.74	0.52
3:A8:14:LEU:O	3:A8:34:GLY:HA3	2.09	0.52
2:B2:13:PHE:CE2	2:C5:35:GLU:HG2	2.44	0.52
3:C8:15:GLN:HG3	3:C8:160:LYS:HB2	1.90	0.52
2:F2:45:VAL:HG11	2:F2:89:LEU:HD12	1.92	0.52
2:H7:49:ASP:OD1	2:H7:49:ASP:N	2.43	0.52
3:J8:70:ARG:HG2	3:J8:173:GLY:N	2.25	0.52
2:L4:31:LEU:HA	2:L4:46:VAL:HG12	1.92	0.52
3:M8:9:ILE:HG21	3:M8:153:LEU:HB2	1.91	0.52
1:O1:31:ASP:C	1:O1:33:ASP:H	2.17	0.52
1:R1:65:GLN:C	1:V1:18:ARG:NH1	2.68	0.52
3:S8:21:PHE:CE2	3:S8:169:VAL:HB	2.45	0.52
2:U3:26:ALA:O	3:U8:12:ASP:HB3	2.09	0.52
2:U6:13:PHE:HB2	2:U7:37:THR:HG21	1.92	0.52
3:U8:143:LEU:O	3:U8:177:ARG:HA	2.09	0.52
2:V3:78:ARG:NH1	2:X7:28:LYS:HA	2.24	0.52
3:V8:16:PRO:HA	3:V8:33:PRO:HB3	1.91	0.52
2:X3:18:GLU:OE1	2:X4:74:HIS:NE2	2.40	0.52
3:Y9:195:GLU:O	3:Y9:199:ARG:N	2.35	0.52
2:Z2:16:MET:HG2	2:Z2:44:ALA:HB2	1.92	0.52
3:Z8:65:VAL:HG12	3:Z8:76:GLU:HB3	1.91	0.52
3:Z9:89:GLY:O	3:Z9:93:LEU:N	2.31	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:62:SER:HA	1:D1:64:ARG:NH1	2.25	0.52
2:E7:29:VAL:HG11	2:E7:46:VAL:HB	1.90	0.52
2:F3:54:LYS:O	2:F3:58:GLU:HG3	2.10	0.52
3:K8:79:HIS:CE1	3:K8:81:ASP:H	2.27	0.52
3:L9:10:PHE:HA	3:L9:38:LEU:HA	1.91	0.52
2:N5:92:THR:O	2:N5:94:GLY:N	2.43	0.52
2:N7:78:ARG:HD3	3:P8:60:LYS:HD3	1.92	0.52
3:O8:6:ARG:NH1	3:O8:72:TYR:OH	2.43	0.52
3:P8:61:VAL:HG11	3:P8:77:VAL:HB	1.91	0.52
1:S1:20:GLU:HG3	2:32:62:ARG:HH22	1.75	0.52
2:S5:3:ASP:HB3	2:S5:48:GLY:O	2.08	0.52
2:T2:35:GLU:HG2	2:T4:13:PHE:CE2	2.45	0.52
2:U3:32:ILE:HD13	2:U3:90:GLY:HA3	1.92	0.52
3:W8:141:PHE:CZ	3:W8:143:LEU:HB2	2.45	0.52
2:X2:47:ARG:HH22	2:X2:79:PRO:HG2	1.73	0.52
1:Y1:28:ARG:NH1	1:Y1:36:PRO:HB2	2.25	0.52
2:13:5:LEU:HD13	2:13:47:ARG:HD3	1.90	0.52
2:24:31:LEU:HA	2:24:46:VAL:HG12	1.91	0.52
2:33:13:PHE:HB2	2:34:37:THR:HG21	1.91	0.52
2:33:47:ARG:NH1	2:33:91:ARG:HB2	2.24	0.52
3:49:20:THR:O	3:49:24:LYS:N	2.41	0.52
3:C8:177:ARG:HG2	3:28:46:ILE:HD11	1.92	0.52
1:F1:47:VAL:CG1	1:R1:14:ARG:HG3	2.40	0.52
3:G8:128:ASN:O	3:G8:130:GLN:N	2.41	0.52
2:H3:32:ILE:HG12	2:H3:90:GLY:HA3	1.92	0.52
3:J8:128:ASN:O	3:J8:130:GLN:N	2.40	0.52
2:M3:5:LEU:O	2:M3:53:VAL:HG11	2.09	0.52
3:N8:8:TYR:HE2	3:N8:93:LEU:HD23	1.70	0.52
3:N8:49:ASN:HA	3:N8:66:GLN:HE22	1.75	0.52
2:P2:11:ARG:HB3	2:P2:69:GLU:HG2	1.90	0.52
3:P8:15:GLN:HG3	3:P8:160:LYS:HB2	1.92	0.52
1:S1:2:VAL:HG23	1:S1:57:TYR:CE1	2.45	0.52
2:W3:10:VAL:O	2:W3:12:GLY:N	2.42	0.52
2:W7:50:VAL:HG21	2:W7:77:PRO:HB3	1.92	0.52
2:X4:62:ARG:NE	2:X5:66:ARG:NH1	2.58	0.52
2:X6:13:PHE:HB2	2:X7:37:THR:HG21	1.91	0.52
2:Y3:47:ARG:NH2	2:Y3:79:PRO:HG2	2.24	0.52
1:Z1:66:THR:O	1:Z1:69:THR:OG1	2.19	0.52
1:11:63:ALA:HB1	1:11:77:THR:HG22	1.91	0.52
2:26:16:MET:HG2	2:26:44:ALA:HB2	1.92	0.52
3:48:167:VAL:HB	3:48:179:TYR:HB2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A1:2:VAL:HG23	1:A1:57:TYR:CE1	2.44	0.52
1:B1:41:VAL:HG11	1:B1:57:TYR:CZ	2.45	0.52
3:D8:70:ARG:HG2	3:D8:173:GLY:N	2.25	0.52
2:H3:36:LYS:O	2:Z7:36:LYS:NZ	2.38	0.52
3:I8:183:SER:OG	3:I8:186:GLU:OE2	2.28	0.52
3:J8:123:GLN:NE2	3:J9:23:GLY:O	2.43	0.52
3:P8:144:GLU:HA	3:P8:176:GLY:O	2.10	0.52
1:Q1:7:VAL:HG12	1:S1:87:MET:HG2	1.92	0.52
2:R2:92:THR:O	2:R2:94:GLY:N	2.42	0.52
2:T6:58:GLU:O	2:T6:62:ARG:HG3	2.10	0.52
2:U7:47:ARG:NH1	2:U7:89:LEU:O	2.41	0.52
2:V2:16:MET:O	2:V2:20:ALA:N	2.33	0.52
3:V8:140:LEU:HA	3:V8:180:LEU:O	2.08	0.52
3:W8:48:ILE:HG23	3:W8:75:LEU:HB2	1.92	0.52
2:X3:27:ALA:HB3	2:X3:56:ALA:HB2	1.90	0.52
3:28:93:LEU:O	3:28:97:GLU:N	2.43	0.52
2:43:4:ALA:O	2:43:47:ARG:HD2	2.10	0.52
2:A6:32:ILE:HD11	2:A6:47:ARG:HD2	1.91	0.52
2:B3:19:ALA:HB2	2:B3:64:ALA:HB2	1.91	0.52
3:B8:45:GLY:HA3	3:B8:73:GLY:H	1.75	0.52
3:B8:106:PRO:HG3	3:B8:150:TYR:CE2	2.45	0.52
2:D5:52:ALA:O	2:D5:56:ALA:N	2.42	0.52
1:E1:45:ASP:OD2	1:E1:49:ALA:N	2.35	0.52
2:E3:47:ARG:HH22	2:E3:79:PRO:HG2	1.74	0.52
1:F1:41:VAL:HG11	1:F1:57:TYR:CZ	2.45	0.52
2:I5:37:THR:HG21	2:J2:13:PHE:HB2	1.91	0.52
2:N2:16:MET:HE2	2:N2:42:VAL:HG11	1.91	0.52
1:O1:16:GLU:OE1	1:O1:17:PRO:CD	2.58	0.52
2:P6:27:ALA:HB3	2:P6:56:ALA:HB2	1.92	0.52
3:P9:67:VAL:N	3:P9:74:LEU:O	2.31	0.52
1:R1:86:GLU:HG2	1:R1:87:MET:N	2.25	0.52
2:U5:7:MET:HE1	2:42:17:VAL:HG21	1.91	0.52
2:X6:19:ALA:HB2	2:X6:64:ALA:HB2	1.92	0.52
3:X8:111:HIS:ND1	3:X8:195:GLU:OE2	2.42	0.52
2:Z3:9:GLU:HB3	2:Z3:43:THR:HG23	1.92	0.52
2:Z4:62:ARG:CZ	2:Z5:66:ARG:NH1	2.73	0.52
3:48:134:ILE:HG12	3:48:181:ALA:HB2	1.92	0.52
2:A3:18:GLU:CD	2:A4:74:HIS:HE2	2.16	0.51
2:A7:52:ALA:O	2:A7:56:ALA:N	2.43	0.51
2:B5:5:LEU:HD22	2:B5:89:LEU:HD13	1.91	0.51
3:B8:17:GLN:CD	3:B8:159:GLU:HG3	2.35	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D1:15:LYS:HE2	1:D1:19:ILE:HD11	1.92	0.51
3:D8:29:PHE:CD2	3:D8:63:PRO:HD2	2.45	0.51
1:F1:7:VAL:HG21	1:F1:28:ARG:HD3	1.92	0.51
2:I3:13:PHE:HB2	2:I4:37:THR:HG21	1.92	0.51
2:J5:16:MET:HG2	2:J5:44:ALA:HB2	1.92	0.51
2:J7:49:ASP:OD1	2:J7:49:ASP:N	2.43	0.51
3:J8:21:PHE:CE2	3:J8:169:VAL:HB	2.46	0.51
1:K1:45:ASP:OD1	1:K1:48:GLY:N	2.39	0.51
2:N6:16:MET:HG2	2:N6:44:ALA:HB2	1.92	0.51
3:U8:8:TYR:CE2	3:U8:93:LEU:HD23	2.45	0.51
2:V3:19:ALA:HB2	2:V3:64:ALA:HB2	1.92	0.51
2:Y3:10:VAL:HG11	2:Y3:15:GLY:HA3	1.91	0.51
2:Z3:13:PHE:N	2:Z4:9:GLU:OE2	2.41	0.51
2:24:20:ALA:HB1	2:24:31:LEU:HD22	1.92	0.51
3:38:88:ALA:O	3:38:91:THR:OG1	2.20	0.51
2:B3:7:MET:HE1	2:C7:17:VAL:HG11	1.92	0.51
2:D2:10:VAL:HG11	2:D2:15:GLY:HA3	1.92	0.51
2:F2:16:MET:HG2	2:F2:44:ALA:HB2	1.92	0.51
2:F6:47:ARG:HD3	2:F6:91:ARG:HG2	1.91	0.51
3:H9:20:THR:O	3:H9:24:LYS:N	2.44	0.51
3:I8:111:HIS:HA	3:I8:142:ILE:O	2.10	0.51
1:K1:66:THR:HG22	1:K1:67:GLU:O	2.10	0.51
2:K5:13:PHE:HD2	2:K6:43:THR:HG21	1.75	0.51
2:L5:37:THR:OG1	2:22:40:GLY:HA2	2.11	0.51
3:L8:20:THR:OG1	3:L8:21:PHE:N	2.44	0.51
1:M1:70:ASN:C	1:M1:72:ARG:H	2.18	0.51
3:M8:46:ILE:HD11	3:28:177:ARG:HB3	1.91	0.51
3:P8:29:PHE:HB2	3:P8:63:PRO:O	2.10	0.51
2:Q7:47:ARG:NH1	2:Q7:89:LEU:O	2.42	0.51
2:S5:24:VAL:HG11	2:S6:82:ASN:HB3	1.91	0.51
3:S8:123:GLN:HA	3:S8:126:ASN:HD22	1.75	0.51
1:T1:31:ASP:O	1:T1:33:ASP:N	2.40	0.51
2:T2:19:ALA:HB2	2:T2:64:ALA:HB2	1.92	0.51
2:T5:31:LEU:HA	2:T5:46:VAL:HG12	1.92	0.51
2:U5:9:GLU:HG3	2:U5:43:THR:OG1	2.11	0.51
2:W7:27:ALA:O	2:Y3:78:ARG:NH2	2.43	0.51
2:X4:5:LEU:HD23	2:X4:76:ILE:HD12	1.92	0.51
1:Z1:59:SER:N	1:11:75:ASP:OD2	2.27	0.51
2:Z6:56:ALA:O	2:Z6:60:GLY:N	2.42	0.51
3:Z8:93:LEU:HB2	3:Z8:98:VAL:O	2.10	0.51
2:16:32:ILE:HG21	2:16:90:GLY:CA	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:25:11:ARG:HG2	2:25:11:ARG:O	2.11	0.51
2:A7:28:LYS:HA	2:G3:78:ARG:NE	2.25	0.51
1:E1:81:ILE:HD12	2:E5:77:PRO:HG2	1.93	0.51
2:F2:84:ASP:O	2:F2:92:THR:OG1	2.24	0.51
3:G8:65:VAL:HG12	3:G8:76:GLU:HB3	1.91	0.51
3:G8:70:ARG:HG2	3:G8:173:GLY:N	2.25	0.51
3:G8:140:LEU:HA	3:G8:180:LEU:O	2.10	0.51
2:I6:30:GLU:OE1	2:I6:91:ARG:NH2	2.31	0.51
3:I8:21:PHE:HE2	3:I8:169:VAL:HB	1.75	0.51
1:J1:28:ARG:HH11	1:J1:36:PRO:HB2	1.74	0.51
2:J5:90:GLY:O	2:J5:91:ARG:HG2	2.10	0.51
3:K8:61:VAL:HG21	3:K8:88:ALA:HB2	1.92	0.51
3:L8:124:ILE:O	3:L8:127:ARG:HB2	2.09	0.51
2:M7:20:ALA:HB1	2:M7:31:LEU:HD22	1.92	0.51
1:N1:28:ARG:HH11	1:N1:36:PRO:HB2	1.75	0.51
2:N2:85:ALA:HA	2:N2:92:THR:HG23	1.93	0.51
3:N8:105:LYS:HG3	3:N8:203:GLY:C	2.36	0.51
2:U3:5:LEU:HD13	2:U3:47:ARG:HD3	1.91	0.51
3:U8:7:THR:HG23	3:U8:41:GLU:HB3	1.92	0.51
1:V1:47:VAL:HG12	1:W1:14:ARG:HG3	1.93	0.51
2:15:47:ARG:HH12	2:15:84:ASP:CG	2.16	0.51
2:17:58:GLU:O	2:17:62:ARG:HG3	2.11	0.51
2:25:57:THR:O	2:25:60:GLY:N	2.42	0.51
2:C2:32:ILE:CD1	2:C2:90:GLY:HA3	2.40	0.51
2:D2:6:GLY:O	2:D2:46:VAL:HG12	2.10	0.51
2:E4:62:ARG:NE	2:E5:66:ARG:NH1	2.59	0.51
1:F1:14:ARG:HG3	1:G1:47:VAL:HG12	1.93	0.51
2:F3:21:ASP:OD1	2:F4:83:VAL:HG21	2.11	0.51
1:G1:61:SER:HB2	1:W1:61:SER:HB3	1.93	0.51
2:G3:11:ARG:NH1	2:G3:41:TYR:CE1	2.79	0.51
1:I1:50:GLY:HA3	2:J2:25:LYS:HE2	1.91	0.51
3:K8:106:PRO:HB2	3:K8:198:ILE:HG22	1.93	0.51
3:L8:21:PHE:HE2	3:L8:169:VAL:HB	1.75	0.51
3:M8:126:ASN:O	3:M8:129:SER:HB3	2.11	0.51
2:N7:52:ALA:O	2:N7:56:ALA:N	2.43	0.51
2:Q3:9:GLU:HG3	2:Q3:71:VAL:HB	1.91	0.51
3:R9:39:TRP:HA	3:R9:76:GLU:HA	1.92	0.51
2:T3:5:LEU:HD23	2:T3:47:ARG:HD3	1.91	0.51
1:U1:50:GLY:N	1:U1:53:GLU:OE1	2.25	0.51
2:U4:5:LEU:HD23	2:U4:76:ILE:HD12	1.92	0.51
3:U8:170:THR:OG1	3:U8:177:ARG:N	2.28	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:V6:32:ILE:HD11	2:V6:47:ARG:HD2	1.93	0.51
2:W3:5:LEU:HD12	2:W3:6:GLY:H	1.75	0.51
2:X5:3:ASP:HB3	2:X5:48:GLY:C	2.34	0.51
2:X6:27:ALA:HA	3:X8:116:ALA:HB2	1.93	0.51
1:Z1:62:SER:HB2	1:11:64:ARG:HD3	1.92	0.51
2:Z3:47:ARG:HH12	2:Z3:84:ASP:CG	2.18	0.51
1:31:63:ALA:HB1	1:31:77:THR:HG22	1.92	0.51
3:C8:7:THR:OG1	3:C8:41:GLU:N	2.43	0.51
2:E4:16:MET:HG2	2:E4:44:ALA:HB2	1.91	0.51
1:F1:19:ILE:O	1:F1:22:LEU:HB2	2.10	0.51
2:H2:32:ILE:CD1	2:H2:90:GLY:HA3	2.41	0.51
3:I8:170:THR:OG1	3:I8:177:ARG:N	2.25	0.51
2:J2:47:ARG:NH2	2:J2:84:ASP:OD1	2.43	0.51
1:K1:94:ARG:HG2	1:K1:95:LYS:H	1.76	0.51
2:N7:19:ALA:HB2	2:N7:64:ALA:HB2	1.92	0.51
3:O8:31:PRO:HD3	3:O8:64:ALA:HB2	1.93	0.51
2:P2:92:THR:C	2:P2:94:GLY:H	2.19	0.51
2:P6:47:ARG:HH22	2:P6:79:PRO:HG3	1.75	0.51
2:P7:43:VAL:HG11	2:P7:87:LEU:HD12	1.92	0.51
3:Q8:45:GLY:HA2	3:Q8:48:ILE:HD13	1.92	0.51
3:S8:119:ALA:O	3:S8:122:THR:OG1	2.26	0.51
3:S8:143:LEU:O	3:S8:177:ARG:HA	2.10	0.51
1:T1:74:VAL:HG23	1:U1:1:MET:SD	2.50	0.51
2:V6:23:MET:HG2	2:V6:56:ALA:O	2.11	0.51
3:V8:9:ILE:O	3:V8:38:LEU:HD12	2.10	0.51
3:V8:29:PHE:CD2	3:V8:63:PRO:HD2	2.46	0.51
2:Z3:12:GLY:HA2	2:Z4:9:GLU:OE2	2.10	0.51
2:23:4:ALA:O	2:23:47:ARG:HD2	2.09	0.51
2:25:30:GLU:CD	2:25:91:ARG:HH22	2.18	0.51
3:28:29:PHE:CD2	3:28:63:PRO:HD2	2.46	0.51
3:48:169:VAL:HG12	3:48:171:PRO:HD3	1.92	0.51
2:A7:23:MET:HG2	2:A7:56:ALA:O	2.11	0.51
1:B1:32:PRO:HG3	1:B1:87:MET:HE1	1.93	0.51
1:D1:2:VAL:HG23	1:D1:57:TYR:CE1	2.45	0.51
2:E2:3:ASP:HB2	2:E2:47:ARG:NH1	2.26	0.51
1:F1:53:GLU:OE2	2:F5:78:ARG:HB3	2.10	0.51
2:H3:47:ARG:HH12	2:H3:84:ASP:CG	2.19	0.51
3:H8:183:SER:OG	3:H8:186:GLU:OE2	2.28	0.51
2:I4:47:ARG:NH1	2:I4:89:LEU:HB3	2.25	0.51
3:K8:143:LEU:O	3:K8:177:ARG:HA	2.11	0.51
1:M1:10:VAL:HG13	1:N1:82:VAL:HG13	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N8:128:ASN:O	3:N8:130:GLN:N	2.42	0.51
2:O4:53:VAL:O	2:O4:57:THR:OG1	2.21	0.51
1:P1:31:ASP:OD1	1:P1:35:THR:OG1	2.26	0.51
1:W1:31:ASP:O	1:W1:33:ASP:N	2.39	0.51
2:Z2:47:ARG:HH22	2:Z2:79:PRO:HG2	1.75	0.51
3:Z8:126:ASN:O	3:Z8:129:SER:HB3	2.11	0.51
2:22:32:ILE:HD13	2:22:90:GLY:HA3	1.93	0.51
2:26:47:ARG:HH22	2:26:79:PRO:HG3	1.76	0.51
1:31:68:VAL:HA	1:31:72:ARG:HH12	1.75	0.51
3:48:142:ILE:HA	3:48:178:LEU:O	2.10	0.51
2:C7:92:THR:C	2:C7:94:GLY:H	2.18	0.51
3:C8:8:TYR:HE2	3:C8:93:LEU:HB3	1.76	0.51
1:F1:64:ARG:HH11	1:G1:62:SER:CB	2.22	0.51
2:J6:57:THR:HG21	2:J6:75:VAL:HG22	1.93	0.51
2:K7:49:ASP:OD1	2:K7:49:ASP:N	2.44	0.51
3:K9:20:THR:O	3:K9:24:LYS:N	2.40	0.51
2:L5:27:ALA:HB1	2:L5:52:ALA:HB1	1.92	0.51
2:M2:3:ASP:OD2	2:M2:91:ARG:NH2	2.43	0.51
2:P2:47:ARG:HH22	2:P2:79:PRO:HG2	1.75	0.51
1:Q1:16:GLU:CD	1:Q1:17:PRO:HD2	2.36	0.51
2:Q2:16:MET:HE2	2:Q2:42:VAL:HG11	1.92	0.51
2:R7:47:ARG:NH1	2:R7:89:LEU:HB3	2.25	0.51
3:R8:3:ILE:HB	3:R8:96:LEU:HD22	1.92	0.51
3:R8:123:GLN:CG	3:R9:23:GLY:HA3	2.40	0.51
2:S6:32:ILE:HD11	2:S6:47:ARG:HD2	1.92	0.51
3:T8:133:MET:HE1	3:T9:132:MET:N	2.26	0.51
3:W8:24:LYS:HZ2	3:W8:131:GLY:HA2	1.75	0.51
2:Z3:47:ARG:NH1	2:Z3:84:ASP:OD1	2.44	0.51
3:38:20:THR:HG21	3:39:135:LEU:HA	1.92	0.51
1:A1:31:ASP:O	1:A1:33:ASP:N	2.43	0.51
3:B8:58:ALA:HA	2:L6:25:LYS:NZ	2.25	0.51
3:F8:38:LEU:O	3:F8:76:GLU:HA	2.10	0.51
3:G8:51:VAL:HG13	3:G8:92:ILE:HG12	1.91	0.51
2:I3:16:MET:HG2	2:I3:44:ALA:HB2	1.93	0.51
3:I8:169:VAL:HG12	3:I8:171:PRO:HD3	1.93	0.51
2:J3:10:VAL:O	2:J3:12:GLY:N	2.44	0.51
2:J5:57:THR:O	2:J5:60:GLY:N	2.44	0.51
1:K1:64:ARG:HD3	1:L1:62:SER:HB2	1.93	0.51
2:N2:32:ILE:HD11	2:N2:90:GLY:HA3	1.92	0.51
1:O1:31:ASP:O	1:O1:33:ASP:N	2.44	0.51
2:O2:16:MET:HG2	2:O2:44:ALA:HB2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P5:37:THR:HG21	2:Q2:13:PHE:HB2	1.92	0.51
3:P9:20:THR:O	3:P9:24:LYS:N	2.44	0.51
2:S7:78:ARG:NH2	3:U8:56:LEU:O	2.43	0.51
2:V6:5:LEU:HB3	2:V6:76:ILE:HB	1.93	0.51
2:W6:36:LYS:NZ	2:W7:35:GLU:OE1	2.41	0.51
2:Y5:9:VAL:HG13	2:Y5:68:GLU:O	2.11	0.51
1:Z1:86:GLU:HG2	1:Z1:87:MET:N	2.25	0.51
2:Z6:45:VAL:HG11	2:Z6:89:LEU:HD22	1.93	0.51
2:Z6:47:ARG:NH1	2:Z6:84:ASP:OD2	2.44	0.51
2:22:10:VAL:HG11	2:22:15:GLY:HA3	1.92	0.51
3:28:183:SER:OG	3:28:186:GLU:OE2	2.26	0.51
3:38:19:ALA:HB3	3:38:33:PRO:HG3	1.91	0.51
3:A8:7:THR:HG23	3:A8:41:GLU:HB3	1.92	0.51
3:A8:154:ALA:HB2	3:A8:198:ILE:HD11	1.92	0.51
2:C6:16:MET:HG2	2:C6:44:ALA:HB2	1.93	0.51
1:D1:70:ASN:C	1:D1:72:ARG:H	2.18	0.51
1:F1:7:VAL:HG11	1:G1:87:MET:HE2	1.92	0.51
2:F3:10:VAL:O	2:F3:12:GLY:N	2.44	0.51
3:F8:126:ASN:O	3:F8:129:SER:HB3	2.10	0.51
2:I3:10:VAL:HG11	2:I3:15:GLY:HA3	1.91	0.51
2:J2:32:ILE:HD13	2:J2:90:GLY:HA3	1.93	0.51
2:J3:61:GLN:HB2	2:J3:73:VAL:HG21	1.93	0.51
2:L3:32:ILE:CD1	2:L3:47:ARG:HG3	2.41	0.51
1:N1:31:ASP:O	1:N1:33:ASP:N	2.41	0.51
2:O3:13:PHE:HB2	2:O4:37:THR:CG2	2.41	0.51
3:R8:183:SER:OG	3:R8:186:GLU:OE2	2.29	0.51
3:R9:7:THR:N	3:R9:41:GLU:O	2.26	0.51
3:R9:55:ALA:HB1	3:R9:88:ALA:HB1	1.92	0.51
3:X8:183:SER:OG	3:X8:186:GLU:OE2	2.29	0.51
2:23:5:LEU:HD12	2:23:6:GLY:H	1.76	0.51
2:23:47:ARG:NH1	2:23:91:ARG:HB2	2.14	0.51
2:24:16:MET:HG3	2:24:42:VAL:HG12	1.92	0.51
2:26:30:GLU:OE1	2:26:91:ARG:NH2	2.39	0.51
2:35:12:GLY:HA2	2:36:9:GLU:OE2	2.11	0.51
3:38:79:HIS:CE1	3:38:81:ASP:H	2.28	0.51
3:48:8:TYR:HE2	3:48:93:LEU:HD23	1.76	0.51
3:B8:127:ARG:HD2	3:B8:127:ARG:O	2.11	0.51
3:C8:93:LEU:HD12	3:C8:94:ASP:N	2.26	0.51
3:C8:143:LEU:O	3:C8:177:ARG:HA	2.10	0.51
1:E1:53:GLU:HG2	2:E5:78:ARG:HD3	1.92	0.51
2:E2:35:GLU:HG2	2:E4:13:PHE:CE2	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F3:4:ALA:O	2:F3:47:ARG:HD2	2.11	0.51
2:I5:54:LYS:O	2:I5:58:GLU:HG2	2.11	0.51
3:I8:126:ASN:O	3:I8:129:SER:HB3	2.11	0.51
3:I8:144:GLU:HA	3:I8:176:GLY:O	2.11	0.51
2:K5:8:ILE:O	2:K5:44:ALA:N	2.36	0.51
1:M1:75:ASP:OD1	1:N1:1:MET:N	2.29	0.51
2:R7:49:ASP:OD1	2:R7:49:ASP:N	2.44	0.51
3:T8:183:SER:OG	3:T8:186:GLU:OE2	2.28	0.51
2:V7:53:VAL:HA	2:V7:56:ALA:HB3	1.92	0.51
3:V8:128:ASN:O	3:V8:130:GLN:N	2.42	0.51
2:X5:36:LYS:NZ	2:X6:35:GLU:OE2	2.36	0.51
2:23:61:GLN:HB2	2:23:73:VAL:HG21	1.92	0.51
3:28:126:ASN:O	3:28:129:SER:HB3	2.10	0.51
2:A3:5:LEU:HD11	2:A3:7:MET:CE	2.40	0.50
2:A6:45:VAL:HG11	2:A6:89:LEU:HD22	1.92	0.50
2:B6:16:MET:HG2	2:B6:44:ALA:HB2	1.93	0.50
1:E1:32:PRO:HG3	1:E1:87:MET:HE3	1.93	0.50
3:E8:11:LEU:HD21	3:E8:153:LEU:HA	1.93	0.50
3:E8:63:PRO:HA	3:E8:77:VAL:HA	1.93	0.50
2:F6:10:VAL:HG11	2:F6:15:GLY:HA3	1.93	0.50
2:F7:92:THR:C	2:F7:94:GLY:H	2.19	0.50
3:F8:9:ILE:HD12	3:F8:150:TYR:HA	1.92	0.50
3:F8:28:GLY:CA	3:Q8:124:ILE:HD11	2.42	0.50
2:G4:20:ALA:O	2:G4:24:VAL:HG22	2.10	0.50
1:H1:31:ASP:O	1:H1:33:ASP:N	2.42	0.50
1:H1:79:MET:HE1	1:Z1:73:PRO:O	2.10	0.50
2:H4:16:MET:HG3	2:H4:42:VAL:HG12	1.91	0.50
2:I3:47:ARG:HH11	2:I3:91:ARG:CB	2.17	0.50
3:I8:8:TYR:HE2	3:I8:93:LEU:HD23	1.74	0.50
1:J1:50:GLY:N	1:J1:53:GLU:OE1	2.26	0.50
3:J8:127:ARG:HD2	3:J8:127:ARG:O	2.12	0.50
3:K8:8:TYR:HB3	3:K8:103:ARG:HD2	1.93	0.50
2:M5:84:ASP:O	2:M5:92:THR:HG22	2.11	0.50
2:M7:79:PRO:HG2	2:M7:84:ASP:OD2	2.11	0.50
2:N7:49:ASP:OD1	2:N7:49:ASP:N	2.44	0.50
1:S1:32:PRO:HG3	1:S1:87:MET:HE1	1.93	0.50
2:U2:4:ALA:O	2:U2:47:ARG:HG2	2.11	0.50
2:U5:3:ASP:OD2	2:U5:91:ARG:NH2	2.27	0.50
2:V2:13:PHE:CE2	2:W5:35:GLU:HG2	2.46	0.50
1:W1:66:THR:HG22	1:W1:67:GLU:O	2.11	0.50
1:W1:86:GLU:HG2	1:W1:87:MET:N	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:W8:6:ARG:NH1	3:W8:72:TYR:OH	2.44	0.50
3:Y8:19:ALA:HB3	3:Y8:33:PRO:HG3	1.91	0.50
2:12:83:VAL:HG13	2:12:87:LEU:HD12	1.93	0.50
2:37:49:ASP:N	2:37:49:ASP:OD1	2.44	0.50
2:A3:8:ILE:HD11	2:A3:23:MET:HE2	1.93	0.50
2:D2:21:ASP:OD2	2:D2:25:LYS:HD2	2.11	0.50
3:I8:51:VAL:HG13	3:I8:92:ILE:HG12	1.93	0.50
1:L1:50:GLY:N	1:L1:53:GLU:OE1	2.21	0.50
1:L1:64:ARG:HH11	1:21:62:SER:HB3	1.75	0.50
2:L6:47:ARG:HD3	2:L6:91:ARG:HG2	1.93	0.50
2:P2:35:GLU:HG2	2:P4:13:PHE:CE2	2.46	0.50
2:Q4:31:LEU:HA	2:Q4:46:VAL:HG12	1.93	0.50
3:Q8:128:ASN:O	3:Q8:130:GLN:N	2.43	0.50
1:S1:31:ASP:O	1:S1:33:ASP:N	2.42	0.50
2:S4:78:ARG:NH2	3:S8:159:GLU:OE1	2.44	0.50
3:S8:142:ILE:HA	3:S8:178:LEU:O	2.11	0.50
2:W2:32:ILE:HD11	2:W2:90:GLY:HA3	1.91	0.50
3:X8:59:THR:O	2:47:78:ARG:NE	2.45	0.50
1:Z1:1:MET:SD	1:11:74:VAL:HG23	2.52	0.50
2:Z5:13:PHE:HD2	2:Z6:43:THR:HG21	1.76	0.50
1:21:66:THR:HG22	1:21:67:GLU:O	2.11	0.50
3:28:23:GLY:HA3	3:28:30:LEU:HG	1.93	0.50
2:A2:9:GLU:HB2	2:A4:14:VAL:HG23	1.92	0.50
2:A4:10:VAL:HG11	2:A4:15:GLY:HA3	1.92	0.50
2:A5:5:LEU:HB3	2:A5:76:ILE:HB	1.94	0.50
3:A8:27:ARG:HB2	3:I8:127:ARG:HE	1.76	0.50
3:C8:42:ILE:HD13	3:C8:96:LEU:HD11	1.93	0.50
2:F6:13:PHE:HB2	2:F7:37:THR:HG21	1.93	0.50
3:F8:27:ARG:HD2	3:Q8:127:ARG:NH1	2.25	0.50
3:F8:65:VAL:HG12	3:F8:76:GLU:HB3	1.92	0.50
3:G8:7:THR:OG1	3:G8:41:GLU:N	2.45	0.50
3:H8:45:GLY:HA3	3:H8:73:GLY:H	1.76	0.50
3:I8:31:PRO:HD3	3:I8:64:ALA:HB2	1.94	0.50
2:J5:39:GLY:HA3	2:12:39:GLY:HA2	1.91	0.50
2:L7:29:VAL:HB	2:L7:46:VAL:CG1	2.42	0.50
3:N8:106:PRO:HG2	3:N8:198:ILE:O	2.11	0.50
3:O8:8:TYR:O	3:O8:103:ARG:NH2	2.44	0.50
3:O8:45:GLY:CA	3:O8:73:GLY:H	2.24	0.50
2:R3:64:ALA:O	2:R3:68:GLY:N	2.44	0.50
2:S3:8:ILE:HG23	2:S3:73:VAL:HG22	1.92	0.50
3:T8:125:ILE:HD12	3:T8:134:ILE:HD12	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:U6:10:VAL:HG11	2:U6:15:GLY:HA3	1.94	0.50
3:U8:79:HIS:CE1	3:U8:81:ASP:H	2.30	0.50
2:V2:13:PHE:HB2	2:W5:37:THR:HG21	1.92	0.50
2:V5:31:LEU:HB3	2:V6:82:ASN:OD1	2.11	0.50
3:V8:57:LYS:O	2:X7:78:ARG:NH2	2.45	0.50
3:W8:21:PHE:HA	3:W8:24:LYS:HE3	1.92	0.50
1:X1:70:ASN:C	1:X1:72:ARG:H	2.19	0.50
3:Y8:21:PHE:CE2	3:Y8:169:VAL:HB	2.46	0.50
3:28:134:ILE:HG12	3:28:181:ALA:HB2	1.94	0.50
3:B8:186:GLU:O	3:B8:190:ALA:N	2.37	0.50
2:C4:16:MET:HG3	2:C4:42:VAL:HG12	1.92	0.50
1:I1:31:ASP:O	1:I1:33:ASP:N	2.44	0.50
3:M8:21:PHE:HE2	3:M8:169:VAL:HB	1.77	0.50
2:O2:9:GLU:HB2	2:O4:14:VAL:HG23	1.94	0.50
2:O3:26:ALA:O	3:O8:12:ASP:HB3	2.12	0.50
2:O6:27:ALA:HA	3:O8:116:ALA:HB2	1.92	0.50
1:P1:61:SER:HB2	1:Q1:61:SER:HB3	1.93	0.50
3:R8:127:ARG:HH21	3:S8:67:VAL:HG12	1.77	0.50
2:S2:45:VAL:HG11	2:S2:89:LEU:HD12	1.94	0.50
2:T7:53:VAL:HA	2:T7:56:ALA:HB3	1.93	0.50
3:U8:106:PRO:HG2	3:U8:198:ILE:O	2.12	0.50
1:V1:1:MET:N	1:W1:75:ASP:OD1	2.34	0.50
1:V1:19:ILE:O	1:V1:22:LEU:HB2	2.12	0.50
1:W1:66:THR:O	1:W1:69:THR:OG1	2.23	0.50
3:W9:10:PHE:HA	3:W9:38:LEU:HA	1.94	0.50
3:Z8:128:ASN:O	3:Z8:130:GLN:N	2.44	0.50
2:23:8:ILE:HG12	2:23:73:VAL:HG22	1.92	0.50
1:31:15:LYS:HZ3	1:31:19:ILE:HG13	1.76	0.50
3:38:8:TYR:HE2	3:38:93:LEU:HB3	1.77	0.50
2:A3:51:ALA:HB2	2:I7:51:ALA:HB2	1.92	0.50
2:B6:47:ARG:HH22	2:B6:79:PRO:HG3	1.76	0.50
3:B8:122:THR:HG22	3:B8:134:ILE:HG22	1.94	0.50
2:C3:34:TYR:OH	2:C4:35:GLU:OE2	2.23	0.50
1:D1:61:SER:HB3	1:E1:61:SER:HB2	1.93	0.50
2:E4:30:GLU:OE1	2:E4:91:ARG:NH2	2.33	0.50
3:F8:128:ASN:O	3:F8:130:GLN:N	2.43	0.50
3:H8:111:HIS:HB3	3:H8:143:LEU:HD13	1.92	0.50
2:I5:3:ASP:O	2:I5:47:ARG:NH2	2.40	0.50
3:I9:103:ARG:O	3:I9:204:VAL:N	2.45	0.50
2:J6:3:ASP:HB2	2:J6:47:ARG:NH1	2.26	0.50
2:J6:16:MET:HG2	2:J6:44:ALA:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L4:8:ILE:O	2:L4:43:THR:HA	2.12	0.50
2:L6:32:ILE:HG21	2:L6:90:GLY:CA	2.41	0.50
2:M3:10:VAL:O	2:M3:12:GLY:N	2.45	0.50
3:M8:106:PRO:HG3	3:M8:150:TYR:CE2	2.46	0.50
2:P5:47:ARG:NH1	2:P5:84:ASP:OD1	2.45	0.50
2:Q3:5:LEU:HD12	2:Q3:6:GLY:H	1.75	0.50
2:R4:10:VAL:HG11	2:R4:15:GLY:HA3	1.94	0.50
3:R8:63:PRO:HA	3:R8:77:VAL:HA	1.93	0.50
2:S4:66:ARG:NH1	2:S5:62:ARG:CZ	2.74	0.50
3:S8:126:ASN:O	3:S8:129:SER:HB3	2.10	0.50
2:T7:49:ASP:N	2:T7:49:ASP:OD1	2.43	0.50
3:T8:64:ALA:HB3	3:T8:76:GLU:OE1	2.11	0.50
2:U3:13:PHE:HD2	2:U4:43:THR:HG21	1.77	0.50
3:U8:29:PHE:CD2	3:U8:63:PRO:HD2	2.47	0.50
3:V8:36:ALA:N	3:V8:79:HIS:O	2.44	0.50
3:V8:143:LEU:O	3:V8:177:ARG:HA	2.12	0.50
3:W9:88:ALA:O	3:W9:92:ILE:N	2.39	0.50
1:Z1:45:ASP:OD1	1:Z1:46:ALA:N	2.45	0.50
2:13:4:ALA:O	2:13:47:ARG:HD2	2.12	0.50
3:18:183:SER:OG	3:18:186:GLU:OE2	2.29	0.50
2:24:5:LEU:HD23	2:24:76:ILE:HD12	1.93	0.50
2:44:16:MET:HG2	2:44:44:ALA:HB2	1.94	0.50
3:B8:21:PHE:CE2	3:B8:169:VAL:HB	2.47	0.50
2:D3:14:PHE:HB2	2:D4:37:THR:CG2	2.40	0.50
3:D9:4:THR:N	3:D9:43:ALA:O	2.33	0.50
2:E7:49:ASP:OD1	2:E7:49:ASP:N	2.44	0.50
2:E7:78:ARG:NH2	3:Q8:56:LEU:O	2.45	0.50
3:E8:9:ILE:O	3:E8:38:LEU:HD12	2.12	0.50
2:J5:9:GLU:HB2	2:12:14:VAL:HG23	1.94	0.50
3:L8:111:HIS:ND1	3:L8:195:GLU:OE2	2.45	0.50
3:M8:65:VAL:HG12	3:M8:76:GLU:HB3	1.94	0.50
3:P8:7:THR:OG1	3:P8:41:GLU:N	2.45	0.50
3:P8:169:VAL:HG22	3:P8:178:LEU:HD13	1.94	0.50
3:Q8:21:PHE:CE2	3:Q8:169:VAL:HB	2.46	0.50
3:Q8:64:ALA:HB3	3:Q8:76:GLU:OE2	2.10	0.50
2:T2:37:THR:HG21	2:T4:13:PHE:HB2	1.93	0.50
3:Z9:165:HIS:N	3:Z9:181:ALA:O	2.35	0.50
2:13:10:VAL:O	2:13:12:GLY:N	2.45	0.50
2:27:92:THR:C	2:27:94:GLY:H	2.19	0.50
3:A8:103:ARG:HH21	3:A8:201:VAL:HG13	1.77	0.50
3:C8:9:ILE:CD1	3:C8:150:TYR:HA	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D3:6:LEU:HD12	2:D3:7:GLY:H	1.76	0.50
1:E1:45:ASP:OD1	1:E1:47:VAL:N	2.32	0.50
3:E9:67:VAL:N	3:E9:74:LEU:O	2.44	0.50
1:H1:62:SER:CB	1:Z1:64:ARG:HH11	2.25	0.50
1:J1:31:ASP:C	1:J1:33:ASP:H	2.19	0.50
2:J5:35:GLU:OE2	2:12:36:LYS:NZ	2.33	0.50
2:N4:57:THR:HG22	2:N4:73:VAL:HG13	1.94	0.50
2:P6:10:VAL:HG11	2:P6:15:GLY:HA3	1.94	0.50
2:U2:10:VAL:HG11	2:U2:15:GLY:HA3	1.94	0.50
2:U4:62:ARG:NE	2:U5:66:ARG:NH1	2.60	0.50
3:V8:126:ASN:O	3:V8:129:SER:HB3	2.11	0.50
2:Z2:35:GLU:HG2	2:Z4:13:PHE:CE2	2.46	0.50
2:35:16:MET:HG2	2:35:44:ALA:HB2	1.94	0.50
1:41:70:ASN:C	1:41:72:ARG:H	2.20	0.50
2:43:24:VAL:HG11	2:44:82:ASN:HB3	1.93	0.50
3:48:12:ASP:O	3:48:82:GLN:NE2	2.45	0.50
3:C8:186:GLU:OE1	3:C8:186:GLU:N	2.31	0.50
1:F1:45:ASP:OD1	1:F1:47:VAL:N	2.30	0.50
2:G2:20:ALA:HA	2:G2:23:MET:HE3	1.94	0.50
3:G9:42:ILE:O	3:G9:73:GLY:N	2.24	0.50
2:H5:16:MET:HG2	2:H5:44:ALA:HB2	1.94	0.50
2:J2:4:ALA:O	2:J2:47:ARG:NH1	2.44	0.50
2:J3:5:LEU:HD12	2:J3:6:GLY:H	1.77	0.50
2:J3:47:ARG:HH12	2:J3:84:ASP:CG	2.16	0.50
3:J8:177:ARG:CG	3:L8:46:ILE:HD11	2.40	0.50
1:K1:32:PRO:HG3	1:K1:87:MET:CE	2.42	0.50
2:K4:8:ILE:HD12	2:K4:73:VAL:HG22	1.94	0.50
1:L1:66:THR:O	1:L1:69:THR:OG1	2.20	0.50
2:L3:5:LEU:HD12	2:L3:6:GLY:H	1.77	0.50
3:L8:6:ARG:HB2	3:L8:41:GLU:O	2.12	0.50
3:M8:21:PHE:CE2	3:M8:169:VAL:HB	2.47	0.50
2:N4:50:VAL:HG11	3:N8:186:GLU:HG3	1.94	0.50
2:O2:47:ARG:HH22	2:O2:79:PRO:HG2	1.76	0.50
2:Q2:3:ASP:OD2	2:Q2:91:ARG:NH2	2.45	0.50
2:S3:13:PHE:HB2	2:S4:37:THR:HG21	1.93	0.50
2:S7:47:ARG:NH1	2:S7:89:LEU:O	2.44	0.50
2:T2:4:ALA:O	2:T2:47:ARG:NH1	2.45	0.50
3:T8:126:ASN:O	3:T8:129:SER:HB3	2.12	0.50
3:U8:126:ASN:O	3:U8:129:SER:HB3	2.12	0.50
3:U9:119:ALA:O	3:U9:123:GLN:N	2.40	0.50
2:V7:49:ASP:N	2:V7:49:ASP:OD1	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X2:4:ALA:O	2:X2:47:ARG:NH1	2.44	0.50
2:X7:49:ASP:OD1	2:X7:49:ASP:N	2.42	0.50
3:X8:47:ALA:HB1	3:X8:50:ARG:HH12	1.75	0.50
1:Y1:31:ASP:C	1:Y1:33:ASP:H	2.20	0.50
2:Z5:16:MET:HG2	2:Z5:44:ALA:HB2	1.94	0.50
3:18:142:ILE:HA	3:18:178:LEU:O	2.12	0.50
2:44:8:ILE:HD12	2:44:73:VAL:HG22	1.94	0.50
2:B2:30:GLU:CD	2:B2:91:ARG:HH12	2.16	0.50
2:B3:16:MET:O	2:B3:20:ALA:N	2.35	0.50
1:C1:2:VAL:HG23	1:C1:57:TYR:CE1	2.47	0.50
1:E1:83:ASP:HA	1:E1:95:LYS:HG3	1.93	0.50
2:E3:12:GLY:HA2	2:E4:9:GLU:OE2	2.12	0.50
1:G1:31:ASP:C	1:G1:33:ASP:H	2.20	0.50
3:I8:15:GLN:HG2	3:I8:156:ASN:OD1	2.11	0.50
2:L2:5:LEU:HB3	2:L2:76:ILE:HB	1.93	0.50
1:M1:19:ILE:O	1:M1:22:LEU:HB2	2.12	0.50
3:O9:62:GLN:O	3:O9:78:HIS:N	2.39	0.50
1:S1:50:GLY:N	2:32:25:LYS:HZ2	2.10	0.50
3:T9:132:MET:N	3:T9:166:LEU:O	2.39	0.50
2:U6:16:MET:HG2	2:U6:44:ALA:HB2	1.93	0.50
3:U8:42:ILE:HD11	3:U8:96:LEU:HD11	1.93	0.50
3:X8:29:PHE:HB2	3:X8:63:PRO:O	2.12	0.50
2:27:87:LEU:HB3	2:27:89:LEU:HD13	1.93	0.50
1:C1:3:LEU:HD22	1:C1:56:LEU:HD21	1.94	0.49
2:C3:16:MET:HG2	2:C3:44:ALA:HB2	1.94	0.49
2:C6:55:ALA:HB1	3:C8:115:ARG:HD2	1.94	0.49
2:E3:19:ALA:HB2	2:E3:64:ALA:HB2	1.94	0.49
2:E5:9:GLU:HG3	2:E5:43:THR:OG1	2.12	0.49
3:E9:65:VAL:O	3:E9:76:GLU:N	2.41	0.49
2:F4:62:ARG:CZ	2:F5:66:ARG:NH1	2.75	0.49
3:F8:35:GLN:HE22	3:F8:78:HIS:CE1	2.30	0.49
3:F8:50:ARG:HD2	3:F8:95:LYS:HD3	1.94	0.49
2:G7:52:ALA:O	2:G7:56:ALA:N	2.44	0.49
3:H8:170:THR:HG1	3:H8:177:ARG:H	1.55	0.49
3:I8:23:GLY:HA3	3:I8:30:LEU:HG	1.93	0.49
3:I8:117:VAL:HG12	3:I8:121:GLN:HB3	1.94	0.49
3:I8:123:GLN:HA	3:I8:126:ASN:HD22	1.77	0.49
2:J3:30:GLU:CD	2:J3:91:ARG:HH12	2.19	0.49
3:J9:39:TRP:HA	3:J9:76:GLU:HA	1.92	0.49
3:K8:109:MET:HB2	3:K8:144:GLU:HB3	1.94	0.49
2:L3:47:ARG:HH11	2:L3:91:ARG:CB	2.14	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M1:61:SER:HB2	1:N1:61:SER:HB3	1.93	0.49
2:N7:47:ARG:NH1	2:N7:89:LEU:O	2.45	0.49
1:O1:64:ARG:HH11	1:P1:62:SER:HB3	1.76	0.49
2:O6:3:ASP:O	2:O6:47:ARG:NH1	2.43	0.49
2:O7:58:GLU:O	2:O7:62:ARG:HG3	2.12	0.49
2:Q2:54:LYS:NZ	2:Q5:55:ALA:HB2	2.27	0.49
3:Q8:11:LEU:HD22	3:Q8:156:ASN:HD22	1.77	0.49
2:T7:2:ALA:N	2:T7:78:ARG:HG3	2.27	0.49
1:U1:31:ASP:O	1:U1:33:ASP:N	2.43	0.49
2:U3:5:LEU:O	2:U3:53:VAL:HG11	2.12	0.49
3:U8:35:GLN:HG2	3:U8:80:PHE:CG	2.47	0.49
3:U9:105:LYS:N	3:U9:204:VAL:O	2.34	0.49
1:V1:31:ASP:O	1:V1:33:ASP:N	2.42	0.49
2:W3:18:GLU:OE1	2:W4:74:HIS:NE2	2.34	0.49
3:W8:79:HIS:CE1	3:W8:81:ASP:H	2.30	0.49
2:X3:47:ARG:NH2	2:X3:79:PRO:HG2	2.23	0.49
3:X8:8:TYR:O	3:X8:103:ARG:NH2	2.45	0.49
3:X8:45:GLY:HA3	3:X8:73:GLY:H	1.77	0.49
3:Y8:147:PRO:HD2	3:Y8:150:TYR:CD2	2.47	0.49
3:Z8:143:LEU:O	3:Z8:177:ARG:HA	2.12	0.49
2:42:32:ILE:CD1	2:42:90:GLY:HA3	2.42	0.49
2:43:18:GLU:OE1	2:44:74:HIS:NE2	2.24	0.49
2:B2:47:ARG:HD3	2:B2:91:ARG:HG2	1.94	0.49
2:B3:78:ARG:NH1	2:L7:24:VAL:O	2.44	0.49
3:C8:70:ARG:HH22	3:28:71:ALA:HA	1.77	0.49
2:D3:22:ASP:OD2	2:D4:76:ILE:HG21	2.11	0.49
2:E2:4:ALA:O	2:E2:47:ARG:NH1	2.44	0.49
2:E2:47:ARG:HD3	2:E2:91:ARG:HG2	1.93	0.49
3:E8:118:GLU:HG3	3:E8:119:ALA:N	2.27	0.49
3:F8:7:THR:OG1	3:F8:41:GLU:N	2.44	0.49
3:F8:29:PHE:HB2	3:F8:63:PRO:O	2.11	0.49
1:H1:62:SER:HB3	1:Z1:64:ARG:HH11	1.77	0.49
2:J3:3:ASP:OD2	2:J3:91:ARG:NH2	2.42	0.49
2:J7:78:ARG:NH2	3:L8:57:LYS:O	2.45	0.49
2:K4:78:ARG:NH2	3:K8:159:GLU:OE1	2.45	0.49
2:K7:21:ASP:OD1	2:K7:25:LYS:HE3	2.12	0.49
3:L8:126:ASN:O	3:L8:129:SER:HB3	2.12	0.49
2:M6:16:MET:HG2	2:M6:44:ALA:HB2	1.94	0.49
3:M8:109:MET:HB2	3:M8:144:GLU:HB3	1.94	0.49
2:O5:13:PHE:HB2	2:O6:37:THR:HG21	1.93	0.49
3:Q8:169:VAL:HG12	3:Q8:171:PRO:HD3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R1:63:ALA:HB1	1:R1:77:THR:HG22	1.95	0.49
2:R7:29:VAL:H	2:S3:78:ARG:HH12	1.60	0.49
2:S4:52:ALA:O	2:S4:56:ALA:N	2.32	0.49
3:S8:15:GLN:HG2	3:S8:156:ASN:OD1	2.11	0.49
2:T3:5:LEU:HD12	2:T3:76:ILE:HB	1.94	0.49
3:U8:16:PRO:HA	3:U8:33:PRO:CB	2.36	0.49
3:V8:51:VAL:HG13	3:V8:92:ILE:HG12	1.94	0.49
1:W1:31:ASP:C	1:W1:33:ASP:H	2.21	0.49
2:W6:16:MET:HG2	2:W6:44:ALA:HB2	1.94	0.49
3:W8:29:PHE:HB2	3:W8:63:PRO:O	2.11	0.49
2:X4:16:MET:HG3	2:X4:42:VAL:HG12	1.94	0.49
2:X6:47:ARG:NH2	2:X6:84:ASP:OD1	2.45	0.49
3:Y8:6:ARG:NH1	3:Y8:72:TYR:OH	2.43	0.49
2:Z7:32:ILE:HD13	2:Z7:90:GLY:N	2.27	0.49
3:19:121:GLN:O	3:19:125:ILE:N	2.40	0.49
3:38:7:THR:HG22	3:38:150:TYR:CE1	2.47	0.49
3:A8:24:LYS:NZ	3:A9:122:THR:O	2.45	0.49
3:B8:9:ILE:CD1	3:B8:150:TYR:HA	2.41	0.49
2:H2:17:VAL:HG21	2:Z5:7:MET:HE1	1.93	0.49
2:H3:5:LEU:HD12	2:H3:6:GLY:H	1.78	0.49
2:H5:12:GLY:HA2	2:H6:9:GLU:OE2	2.12	0.49
3:H8:143:LEU:O	3:H8:177:ARG:HA	2.12	0.49
1:I1:31:ASP:C	1:I1:33:ASP:H	2.20	0.49
2:I2:47:ARG:HD3	2:I2:91:ARG:HG2	1.95	0.49
2:I4:3:ASP:CG	2:I4:91:ARG:HH21	2.19	0.49
1:L1:66:THR:HG22	1:L1:67:GLU:O	2.12	0.49
2:Q2:32:ILE:HD11	2:Q2:90:GLY:HA3	1.93	0.49
3:Q8:123:GLN:HG3	3:Q9:23:GLY:HA3	1.93	0.49
2:Z3:5:LEU:HD13	2:Z3:47:ARG:HD3	1.94	0.49
2:34:78:ARG:NH2	3:38:159:GLU:OE1	2.46	0.49
3:38:143:LEU:O	3:38:177:ARG:HA	2.12	0.49
3:48:47:ALA:HB1	3:48:50:ARG:HH12	1.78	0.49
2:A3:21:ASP:OD2	2:A4:76:ILE:HG21	2.13	0.49
3:A8:142:ILE:HA	3:A8:178:LEU:O	2.12	0.49
3:C8:64:ALA:HB3	3:C8:76:GLU:OE1	2.13	0.49
1:F1:86:GLU:HG2	1:F1:87:MET:N	2.27	0.49
3:F8:119:ALA:O	3:F8:122:THR:OG1	2.30	0.49
2:G3:5:LEU:O	2:G3:53:VAL:HG11	2.11	0.49
2:H4:16:MET:HG2	2:H4:44:ALA:HB2	1.95	0.49
2:K5:82:ASN:OD1	2:L2:31:LEU:HB3	2.13	0.49
3:L8:110:THR:O	3:L8:143:LEU:HA	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L8:128:ASN:O	3:L8:168:ASN:ND2	2.46	0.49
3:L9:37:SER:HA	3:L9:78:HIS:HA	1.94	0.49
2:N5:47:ARG:HH12	2:N5:84:ASP:CG	2.10	0.49
2:N6:55:ALA:HB1	3:N8:115:ARG:HD2	1.93	0.49
2:Q5:16:MET:HG2	2:Q5:44:ALA:HB2	1.93	0.49
3:R8:140:LEU:HA	3:R8:180:LEU:O	2.12	0.49
2:S2:47:ARG:HH22	2:S2:79:PRO:HG2	1.76	0.49
3:S8:110:THR:O	3:S8:143:LEU:HA	2.12	0.49
3:S8:140:LEU:HA	3:S8:180:LEU:O	2.13	0.49
2:V4:47:ARG:HH22	2:V4:84:ASP:CG	2.21	0.49
2:V4:78:ARG:NH2	3:V8:159:GLU:OE1	2.45	0.49
2:V5:5:LEU:HB3	2:V5:76:ILE:HB	1.94	0.49
2:W3:8:ILE:HD12	2:W3:19:ALA:HB1	1.94	0.49
3:Y8:24:LYS:HE2	3:Y9:122:THR:O	2.11	0.49
2:Z2:17:VAL:HG21	2:15:7:MET:HE1	1.94	0.49
2:13:47:ARG:HH22	2:13:84:ASP:CG	2.20	0.49
1:31:66:THR:HG22	1:31:67:GLU:O	2.13	0.49
3:38:6:ARG:NH2	3:38:72:TYR:OH	2.45	0.49
2:45:92:THR:O	2:45:94:GLY:N	2.45	0.49
3:48:13:ALA:HA	3:48:35:GLN:O	2.12	0.49
3:A8:3:ILE:HD13	3:A8:47:ALA:HB1	1.93	0.49
3:A8:143:LEU:O	3:A8:177:ARG:HA	2.11	0.49
3:B9:6:ARG:O	3:B9:104:LEU:N	2.33	0.49
3:C8:42:ILE:CD1	3:C8:96:LEU:HD11	2.42	0.49
1:G1:31:ASP:O	1:G1:33:ASP:N	2.42	0.49
2:G4:16:MET:HG3	2:G4:42:VAL:HG12	1.95	0.49
2:G4:16:MET:HG2	2:G4:44:ALA:HB2	1.95	0.49
3:G8:126:ASN:O	3:G8:129:SER:HB3	2.11	0.49
2:H6:16:MET:HG2	2:H6:44:ALA:HB2	1.93	0.49
3:H8:148:ALA:O	3:H8:171:PRO:HA	2.12	0.49
3:I8:7:THR:HG22	3:I8:150:TYR:CE1	2.47	0.49
3:I8:45:GLY:HA3	3:I8:73:GLY:H	1.77	0.49
3:J8:111:HIS:HA	3:J8:142:ILE:O	2.13	0.49
3:K8:128:ASN:O	3:K8:168:ASN:ND2	2.45	0.49
3:M8:3:ILE:HD13	3:M8:47:ALA:HB1	1.94	0.49
3:N8:93:LEU:HD12	3:N8:94:ASP:N	2.27	0.49
2:Q2:32:ILE:CD1	2:Q2:90:GLY:HA3	2.43	0.49
2:Q2:43:THR:HG21	2:Q4:13:PHE:HD2	1.77	0.49
2:S4:66:ARG:NH1	2:S5:62:ARG:NE	2.59	0.49
3:T9:139:SER:N	3:T9:182:GLY:O	2.40	0.49
2:V2:9:GLU:HB2	2:V4:14:VAL:HG23	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:V8:20:THR:OG1	3:V8:21:PHE:N	2.45	0.49
3:V8:56:LEU:O	2:X7:78:ARG:NH2	2.46	0.49
2:X3:77:PRO:HB2	2:47:27:ALA:HA	1.94	0.49
3:X8:7:THR:HG23	3:X8:41:GLU:HB3	1.94	0.49
1:Z1:66:THR:HG22	1:Z1:67:GLU:O	2.12	0.49
2:13:5:LEU:HD12	2:13:6:GLY:H	1.78	0.49
1:21:32:PRO:HG3	1:21:87:MET:CE	2.42	0.49
3:29:7:THR:O	3:29:41:GLU:N	2.29	0.49
2:C5:57:THR:O	2:C5:60:GLY:N	2.46	0.49
3:C8:142:ILE:HA	3:C8:178:LEU:O	2.13	0.49
3:D8:186:GLU:O	3:D8:190:ALA:N	2.36	0.49
2:E3:26:ALA:O	3:E8:12:ASP:HB3	2.13	0.49
1:F1:10:VAL:HG13	1:G1:82:VAL:HG13	1.95	0.49
2:G5:18:GLU:CD	2:G6:74:HIS:HE2	2.19	0.49
3:G8:63:PRO:HA	3:G8:77:VAL:HA	1.95	0.49
2:H3:5:LEU:HD13	2:H3:47:ARG:HD3	1.93	0.49
2:I2:45:VAL:HG11	2:I2:89:LEU:HD12	1.93	0.49
3:I8:128:ASN:O	3:I8:130:GLN:N	2.43	0.49
3:K8:42:ILE:CD1	3:K8:96:LEU:HD11	2.42	0.49
3:K8:115:ARG:HA	3:K8:139:SER:OG	2.12	0.49
3:K8:120:TYR:HD1	3:18:29:PHE:CZ	2.31	0.49
3:L8:76:GLU:OE1	3:L8:78:HIS:HB3	2.12	0.49
2:M3:47:ARG:NH1	2:M3:84:ASP:OD1	2.45	0.49
1:N1:82:VAL:O	1:N1:95:LYS:NZ	2.38	0.49
2:O2:3:ASP:C	2:O2:47:ARG:HH12	2.15	0.49
3:O8:126:ASN:O	3:O8:129:SER:HB3	2.11	0.49
3:O9:45:GLY:N	3:O9:71:ALA:O	2.46	0.49
1:P1:45:ASP:OD1	1:P1:48:GLY:N	2.38	0.49
1:Q1:31:ASP:C	1:Q1:33:ASP:H	2.20	0.49
2:Q6:32:ILE:HD13	2:Q6:90:GLY:HA3	1.94	0.49
2:R3:16:MET:HG2	2:R3:44:ALA:HB2	1.95	0.49
3:R8:141:PHE:HE2	3:R8:178:LEU:HD23	1.78	0.49
3:S8:29:PHE:HB2	3:S8:63:PRO:O	2.12	0.49
2:U7:17:VAL:HG11	2:43:7:MET:HE1	1.95	0.49
2:V6:47:ARG:NH2	2:V6:84:ASP:OD1	2.46	0.49
2:W7:51:ALA:HB2	2:Y3:51:ALA:HB2	1.94	0.49
3:X8:134:ILE:HG12	3:X8:181:ALA:HB2	1.95	0.49
2:Y6:32:ILE:HD13	2:Y6:90:GLY:HA3	1.95	0.49
3:Y8:20:THR:HG21	3:Y9:135:LEU:HA	1.94	0.49
1:Z1:79:MET:HE1	1:11:73:PRO:HB2	1.95	0.49
1:31:19:ILE:HG22	1:31:73:PRO:HD2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:48:147:PRO:HD2	3:48:150:TYR:HE2	1.77	0.49
1:B1:22:LEU:HD21	1:B1:69:THR:HG22	1.95	0.49
3:B8:38:LEU:O	3:B8:76:GLU:HA	2.12	0.49
3:D8:55:ALA:O	3:D8:59:THR:OG1	2.30	0.49
3:D8:126:ASN:O	3:D8:129:SER:HB3	2.13	0.49
1:E1:64:ARG:HD2	1:E1:72:ARG:O	2.13	0.49
2:E3:5:LEU:HD12	2:E3:6:GLY:H	1.78	0.49
3:G8:18:LEU:CD1	3:G8:156:ASN:HA	2.43	0.49
2:H6:29:VAL:CG1	2:H6:46:VAL:HB	2.43	0.49
3:H8:17:GLN:O	3:H8:20:THR:OG1	2.26	0.49
2:L5:31:LEU:HA	2:L5:46:VAL:HG12	1.94	0.49
3:L8:186:GLU:OE1	3:L8:186:GLU:N	2.36	0.49
2:M3:47:ARG:NH2	2:M3:79:PRO:HG2	2.24	0.49
3:M8:7:THR:OG1	3:M8:41:GLU:N	2.46	0.49
3:N8:31:PRO:HA	3:N8:78:HIS:CE1	2.48	0.49
1:O1:16:GLU:O	1:O1:19:ILE:HG22	2.11	0.49
1:Q1:10:VAL:HG22	1:S1:85:VAL:HG22	1.94	0.49
2:Q3:4:ALA:O	2:Q3:47:ARG:HD2	2.12	0.49
3:R8:7:THR:HA	3:R8:150:TYR:HE1	1.77	0.49
3:R8:123:GLN:HG2	3:R9:23:GLY:HA3	1.93	0.49
3:S8:170:THR:OG1	3:S8:177:ARG:N	2.22	0.49
1:U1:73:PRO:O	1:41:79:MET:HE1	2.12	0.49
1:W1:22:LEU:HG	1:W1:44:ALA:HB1	1.93	0.49
3:W8:67:VAL:O	3:W8:73:GLY:HA2	2.12	0.49
2:Y2:74:HIS:NE2	2:Y4:18:GLU:OE1	2.43	0.49
2:Y5:3:ALA:O	2:Y5:46:ARG:NE	2.41	0.49
2:Y5:18:ALA:HB2	2:Y5:63:ALA:HB2	1.95	0.49
2:Y7:49:ASP:N	2:Y7:49:ASP:OD1	2.45	0.49
2:Z3:5:LEU:HD12	2:Z3:6:GLY:H	1.78	0.49
3:Z8:106:PRO:HG3	3:Z8:150:TYR:CE2	2.48	0.49
2:34:9:GLU:O	2:34:10:VAL:HB	2.13	0.49
2:45:8:ILE:HG12	2:45:73:VAL:HG22	1.95	0.49
2:A2:19:ALA:HB2	2:A2:64:ALA:HB2	1.93	0.49
2:B4:16:MET:HG2	2:B4:44:ALA:HB2	1.94	0.49
3:B8:51:VAL:HG13	3:B8:92:ILE:HG12	1.95	0.49
1:D1:22:LEU:HG	1:D1:44:ALA:HB1	1.94	0.49
2:D4:10:VAL:HG11	2:D4:15:GLY:HA3	1.95	0.49
1:E1:31:ASP:O	1:E1:33:ASP:N	2.44	0.49
1:F1:33:ASP:HB2	1:F1:35:THR:HG23	1.95	0.49
1:H1:2:VAL:HB	1:H1:57:TYR:CE1	2.47	0.49
2:H3:13:PHE:N	2:H4:9:GLU:OE2	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H6:27:ALA:HA	3:H8:116:ALA:HB2	1.95	0.49
3:I9:22:ILE:O	3:I9:26:ALA:N	2.46	0.49
2:J6:14:VAL:HG23	2:J7:9:GLU:HB2	1.95	0.49
2:K7:28:LYS:HA	2:13:78:ARG:NH1	2.28	0.49
2:O2:47:ARG:NH2	2:O2:79:PRO:HG2	2.27	0.49
3:O8:93:LEU:HB2	3:O8:98:VAL:O	2.12	0.49
3:P9:39:TRP:HA	3:P9:76:GLU:HA	1.94	0.49
3:Q8:60:LYS:HE2	3:Q8:84:GLU:CD	2.37	0.49
2:R2:10:VAL:HG11	2:R2:15:GLY:HA3	1.95	0.49
2:R5:52:ALA:O	2:R5:56:ALA:N	2.44	0.49
2:T7:47:ARG:HH22	2:T7:84:ASP:CG	2.20	0.49
2:U5:57:THR:O	2:U5:60:GLY:N	2.45	0.49
1:V1:85:VAL:HG22	1:W1:10:VAL:HG22	1.94	0.49
2:V3:51:ALA:HB2	2:X7:51:ALA:HB2	1.95	0.49
2:Y7:30:GLU:OE1	2:Y7:91:ARG:NH2	2.34	0.49
3:Y8:35:GLN:HE22	3:Y8:78:HIS:CE1	2.30	0.49
2:15:18:GLU:CD	2:16:74:HIS:HE2	2.21	0.49
3:18:70:ARG:HE	3:18:173:GLY:HA2	1.77	0.49
3:18:105:LYS:HG3	3:18:203:GLY:C	2.38	0.49
2:22:45:VAL:HG11	2:22:89:LEU:HD12	1.94	0.49
2:23:5:LEU:O	2:23:53:VAL:HG11	2.13	0.49
3:38:20:THR:OG1	3:38:21:PHE:N	2.46	0.49
3:38:24:LYS:NZ	3:39:134:ILE:O	2.46	0.49
2:44:53:VAL:O	2:44:57:THR:OG1	2.25	0.49
2:A4:16:MET:HG2	2:A4:44:ALA:HB2	1.94	0.49
2:B6:30:GLU:OE1	2:B6:91:ARG:NH2	2.40	0.49
3:B8:33:PRO:HG2	3:B9:136:PRO:CB	2.43	0.49
3:B8:183:SER:OG	3:B8:186:GLU:OE2	2.29	0.49
2:C7:19:ALA:HB2	2:C7:64:ALA:HB2	1.95	0.49
3:C9:52:THR:O	3:C9:56:LEU:N	2.36	0.49
1:G1:10:VAL:HG13	1:W1:82:VAL:HG13	1.94	0.49
3:G8:18:LEU:O	3:G8:22:ILE:N	2.30	0.49
3:I8:167:VAL:HB	3:I8:179:TYR:HB2	1.94	0.49
2:J4:31:LEU:HA	2:J4:46:VAL:HG12	1.94	0.49
3:M8:17:GLN:CD	3:M8:159:GLU:HG3	2.37	0.49
2:P3:5:LEU:HD12	2:P3:6:GLY:H	1.78	0.49
2:Q5:13:PHE:HD2	2:Q6:43:THR:HG21	1.78	0.49
2:Q6:32:ILE:HD11	2:Q6:47:ARG:HD2	1.95	0.49
3:Q9:5:LEU:O	3:Q9:103:ARG:HA	2.13	0.49
2:R3:13:PHE:HB2	2:R4:37:THR:CG2	2.38	0.49
2:T2:11:ARG:HB3	2:T2:69:GLU:HG2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T5:39:GLY:HA3	2:U2:39:GLY:HA2	1.95	0.49
2:T7:50:VAL:HG21	2:T7:77:PRO:HB3	1.95	0.49
2:V2:47:ARG:NH2	2:V2:84:ASP:OD2	2.46	0.49
2:X3:5:LEU:O	2:X3:53:VAL:HG11	2.13	0.49
2:Z7:61:GLN:O	2:Z7:65:GLU:HB2	2.13	0.49
1:A1:31:ASP:C	1:A1:33:ASP:H	2.20	0.49
3:A8:126:ASN:O	3:A8:129:SER:HB3	2.13	0.49
1:C1:44:ALA:HB3	1:C1:77:THR:HG22	1.95	0.49
2:C6:32:ILE:HG13	2:C6:33:GLY:N	2.28	0.49
1:D1:87:MET:HG2	1:E1:7:VAL:HG12	1.95	0.49
2:D3:62:GLN:HB2	2:D3:74:VAL:HG21	1.95	0.49
3:D8:143:LEU:O	3:D8:177:ARG:HA	2.12	0.49
2:F2:2:ALA:N	2:F2:78:ARG:NH1	2.61	0.49
2:F3:12:GLY:HA2	2:F4:9:GLU:OE2	2.13	0.49
2:F5:13:PHE:HB2	2:F6:37:THR:HG21	1.95	0.49
2:G2:29:VAL:HG11	2:G2:46:VAL:HB	1.94	0.49
2:G5:18:GLU:OE1	2:G6:74:HIS:NE2	2.45	0.49
1:I1:54:VAL:HG21	1:I1:93:PHE:CZ	2.47	0.49
3:I9:7:THR:O	3:I9:41:GLU:N	2.24	0.49
1:N1:32:PRO:HG3	1:N1:87:MET:HE3	1.94	0.49
1:N1:63:ALA:HB1	1:N1:77:THR:HG22	1.94	0.49
1:N1:70:ASN:O	1:N1:72:ARG:N	2.45	0.49
2:O6:4:ALA:O	2:O6:47:ARG:HG2	2.13	0.49
3:P9:42:ILE:O	3:P9:73:GLY:N	2.38	0.49
1:Q1:74:VAL:HG23	1:S1:1:MET:SD	2.53	0.49
2:R4:57:THR:HG22	2:R4:73:VAL:HG13	1.95	0.49
2:S3:10:VAL:O	2:S3:12:GLY:N	2.45	0.49
1:U1:61:SER:HB2	1:41:61:SER:HB3	1.94	0.49
3:V8:50:ARG:HB2	3:X8:114:ILE:HD11	1.94	0.49
2:W6:21:ASP:OD1	2:W6:25:LYS:HE3	2.13	0.49
2:W7:53:VAL:HA	2:W7:56:ALA:HB3	1.95	0.49
1:X1:66:THR:HG22	1:X1:67:GLU:O	2.13	0.49
1:X1:86:GLU:HG2	1:X1:87:MET:N	2.26	0.49
2:X5:90:GLY:O	2:X5:91:ARG:HG2	2.13	0.49
3:X8:50:ARG:NE	3:48:112:GLN:OE1	2.46	0.49
3:Y8:20:THR:OG1	3:Y8:21:PHE:N	2.46	0.49
2:12:47:ARG:HD2	2:12:89:LEU:O	2.13	0.49
1:21:27:VAL:O	1:21:41:VAL:HG12	2.12	0.49
1:A1:7:VAL:HG12	1:E1:87:MET:HG2	1.94	0.48
3:A8:62:GLN:O	3:A8:78:HIS:N	2.34	0.48
3:B8:39:TRP:CD2	3:B8:76:GLU:HB2	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C7:7:MET:O	2:C7:8:ILE:HD12	2.13	0.48
2:D2:32:ILE:CD1	2:D2:90:GLY:HA3	2.43	0.48
3:D8:23:GLY:HA3	3:D8:30:LEU:HG	1.95	0.48
3:E8:48:ILE:O	3:E8:52:THR:OG1	2.28	0.48
2:F3:87:LEU:HD13	2:R7:17:VAL:HG22	1.95	0.48
2:H3:10:VAL:O	2:H3:12:GLY:N	2.45	0.48
3:H9:4:THR:O	3:H9:43:ALA:N	2.32	0.48
2:I3:59:ALA:HA	2:I3:62:ARG:HG2	1.95	0.48
2:I4:78:ARG:NH1	3:I8:159:GLU:OE2	2.46	0.48
2:I6:14:VAL:HG23	2:I7:9:GLU:HB2	1.95	0.48
2:J2:47:ARG:HD3	2:J2:91:ARG:HG2	1.95	0.48
1:K1:31:ASP:O	1:K1:33:ASP:N	2.46	0.48
2:L5:24:VAL:HG11	2:L6:82:ASN:HB3	1.94	0.48
3:L8:24:LYS:HD3	3:L9:126:ASN:O	2.13	0.48
3:M9:35:GLN:HA	3:M9:80:PHE:HA	1.93	0.48
3:O8:12:ASP:O	3:O8:82:GLN:NE2	2.45	0.48
1:Q1:86:GLU:HG2	1:Q1:87:MET:N	2.27	0.48
2:Q7:17:VAL:CG1	2:S3:7:MET:HE1	2.43	0.48
3:Q8:65:VAL:HG12	3:Q8:76:GLU:HB3	1.95	0.48
3:R8:50:ARG:HD3	3:R8:95:LYS:HD3	1.95	0.48
3:R8:120:TYR:HD1	3:S8:29:PHE:CE2	2.31	0.48
2:S3:5:LEU:HD12	2:S3:6:GLY:H	1.79	0.48
2:S6:14:VAL:HG23	2:S7:9:GLU:HB2	1.95	0.48
3:T8:141:PHE:O	3:T8:179:TYR:HA	2.13	0.48
3:T9:109:MET:H	3:T9:145:THR:HA	1.78	0.48
2:V2:65:GLU:HG3	2:V2:70:VAL:HG21	1.93	0.48
2:V3:32:ILE:CD1	2:V3:47:ARG:HG3	2.43	0.48
3:X8:106:PRO:HG3	3:X8:150:TYR:CE2	2.48	0.48
3:Z9:10:PHE:HA	3:Z9:38:LEU:HA	1.95	0.48
2:12:37:THR:HG21	2:14:13:PHE:HB2	1.95	0.48
3:28:19:ALA:HB3	3:28:33:PRO:HG3	1.95	0.48
2:37:47:ARG:NH1	2:37:89:LEU:HB3	2.28	0.48
3:38:183:SER:OG	3:38:186:GLU:OE2	2.26	0.48
3:48:6:ARG:NH1	3:48:72:TYR:OH	2.46	0.48
3:48:93:LEU:HD12	3:48:94:ASP:N	2.28	0.48
3:C8:7:THR:HG21	3:C8:149:GLY:HA3	1.94	0.48
2:E2:9:GLU:HB2	2:E4:14:VAL:HG23	1.94	0.48
2:E7:50:VAL:HG21	2:E7:77:PRO:HB3	1.93	0.48
2:F3:7:MET:HE1	2:R7:17:VAL:CG1	2.37	0.48
2:F3:13:PHE:N	2:F4:9:GLU:OE2	2.44	0.48
2:F3:13:PHE:HD2	2:F4:43:THR:HG21	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H2:20:ALA:HA	2:H2:23:MET:HE3	1.94	0.48
2:I5:9:GLU:HG3	2:I5:43:THR:OG1	2.13	0.48
1:J1:68:VAL:HA	1:J1:72:ARG:HH12	1.77	0.48
2:J6:13:PHE:HB2	2:J7:37:THR:HG21	1.95	0.48
2:K2:9:GLU:HB2	2:K4:14:VAL:HG23	1.95	0.48
3:L8:39:TRP:CZ2	3:L8:76:GLU:HG3	2.47	0.48
1:M1:31:ASP:O	1:M1:33:ASP:N	2.45	0.48
3:M8:118:GLU:HG3	3:M8:119:ALA:N	2.29	0.48
2:N2:32:ILE:CD1	2:N2:90:GLY:HA3	2.43	0.48
2:N2:37:THR:OG1	2:N4:40:GLY:HA2	2.12	0.48
2:P7:34:LYS:NZ	2:Q3:35:GLU:OE2	2.36	0.48
3:P9:41:GLU:HA	3:P9:74:LEU:HA	1.95	0.48
2:S7:3:ASP:OD2	2:S7:91:ARG:NE	2.36	0.48
1:T1:86:GLU:HG2	1:T1:87:MET:N	2.28	0.48
2:X3:5:LEU:HD12	2:X3:6:GLY:H	1.78	0.48
2:X3:51:ALA:HB2	2:47:51:ALA:HB2	1.95	0.48
3:X8:6:ARG:HG2	3:X8:104:LEU:HD11	1.94	0.48
3:Y8:64:ALA:HB3	3:Y8:76:GLU:OE1	2.14	0.48
1:Z1:22:LEU:HG	1:Z1:44:ALA:HB1	1.95	0.48
2:Z3:10:VAL:O	2:Z3:12:GLY:N	2.46	0.48
2:Z4:66:ARG:HD2	2:Z5:62:ARG:HD2	1.95	0.48
2:Z6:13:PHE:N	2:Z7:9:GLU:OE2	2.40	0.48
1:11:66:THR:HG22	1:11:67:GLU:O	2.13	0.48
2:35:31:LEU:HD21	2:36:87:LEU:HD11	1.94	0.48
3:A8:110:THR:O	3:A8:143:LEU:HA	2.13	0.48
3:B8:35:GLN:HE22	3:B8:78:HIS:CE1	2.30	0.48
3:B8:48:ILE:HG22	3:B8:66:GLN:NE2	2.28	0.48
3:B8:142:ILE:HG22	3:B8:179:TYR:CD1	2.48	0.48
3:C9:105:LYS:N	3:C9:204:VAL:O	2.25	0.48
1:D1:63:ALA:HB1	1:D1:77:THR:HG22	1.95	0.48
2:D5:47:ARG:HH12	2:D5:84:ASP:CG	2.21	0.48
2:E7:60:GLY:O	2:E7:64:ALA:N	2.42	0.48
3:E8:29:PHE:HB2	3:E8:63:PRO:O	2.13	0.48
1:F1:70:ASN:O	1:F1:72:ARG:N	2.47	0.48
2:F4:8:ILE:O	2:F4:43:THR:HA	2.13	0.48
1:G1:19:ILE:O	1:G1:22:LEU:HB2	2.13	0.48
3:G8:120:TYR:HD1	3:I8:29:PHE:CZ	2.30	0.48
3:G8:170:THR:OG1	3:G8:177:ARG:N	2.31	0.48
2:I5:57:THR:O	2:I5:60:GLY:N	2.46	0.48
2:J6:3:ASP:OD2	2:J6:91:ARG:NE	2.35	0.48
2:L6:10:VAL:HG23	2:L6:12:GLY:H	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O5:47:ARG:NH1	2:O5:84:ASP:OD1	2.47	0.48
3:P8:9:ILE:O	3:P8:38:LEU:HD12	2.13	0.48
3:P9:38:LEU:N	3:P9:77:VAL:O	2.43	0.48
2:Q4:47:ARG:HH22	2:Q4:84:ASP:CG	2.21	0.48
3:U8:121:GLN:O	3:U8:125:ILE:HG13	2.14	0.48
2:V5:13:PHE:HD2	2:V6:43:THR:HG21	1.78	0.48
2:W6:16:MET:HG3	2:W6:42:VAL:HG12	1.95	0.48
3:W9:29:PHE:N	3:W9:63:PRO:O	2.46	0.48
3:X8:23:GLY:HA3	3:X8:30:LEU:HG	1.95	0.48
3:X8:64:ALA:HB3	3:X8:76:GLU:OE1	2.13	0.48
2:Y6:47:ARG:NH2	2:Y6:79:PRO:HG3	2.24	0.48
3:Z8:7:THR:HG23	3:Z8:41:GLU:HB3	1.94	0.48
1:21:31:ASP:C	1:21:33:ASP:H	2.21	0.48
2:22:37:THR:OG1	2:24:40:GLY:HA2	2.12	0.48
3:28:42:ILE:CD1	3:28:96:LEU:HD11	2.44	0.48
2:33:84:ASP:HB3	2:33:91:ARG:O	2.14	0.48
2:A3:90:GLY:O	2:A3:92:THR:N	2.45	0.48
2:A5:58:GLU:O	2:A5:62:ARG:NH2	2.47	0.48
2:A7:28:LYS:HA	2:G3:78:ARG:HE	1.78	0.48
3:B8:144:GLU:HA	3:B8:176:GLY:O	2.13	0.48
3:B8:171:PRO:HD2	3:B8:172:TYR:CD2	2.49	0.48
2:C2:23:MET:HG2	2:C2:56:ALA:C	2.39	0.48
2:C2:65:GLU:HG3	2:C2:70:VAL:HG21	1.96	0.48
2:C4:62:ARG:CZ	2:C4:62:ARG:HB2	2.42	0.48
2:C7:20:ALA:HB1	2:C7:31:LEU:HD22	1.95	0.48
2:E4:16:MET:HG3	2:E4:42:VAL:HG12	1.94	0.48
2:F2:47:ARG:HD2	2:F2:89:LEU:O	2.13	0.48
2:F4:66:ARG:HD2	2:F5:62:ARG:HD2	1.95	0.48
2:J3:5:LEU:HD13	2:J3:47:ARG:HD3	1.94	0.48
2:L2:4:ALA:O	2:L2:47:ARG:NH1	2.47	0.48
3:N8:19:ALA:HB3	3:N8:33:PRO:HG3	1.95	0.48
2:P3:9:GLU:HG3	2:P3:71:VAL:HB	1.95	0.48
3:Q8:169:VAL:HG22	3:Q8:178:LEU:HD13	1.95	0.48
3:R8:29:PHE:HB2	3:R8:63:PRO:O	2.13	0.48
3:R8:110:THR:O	3:R8:143:LEU:HA	2.13	0.48
1:S1:2:VAL:CG2	1:S1:57:TYR:CE1	2.96	0.48
3:S8:9:ILE:HD11	3:S8:150:TYR:CD2	2.48	0.48
2:T5:90:GLY:O	2:T5:91:ARG:NH1	2.44	0.48
3:V9:121:GLN:O	3:V9:125:ILE:N	2.45	0.48
3:Y8:17:GLN:O	3:Y8:20:THR:OG1	2.27	0.48
3:18:167:VAL:HB	3:18:179:TYR:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:24:16:MET:HG2	2:24:44:ALA:HB2	1.95	0.48
2:25:16:MET:HG2	2:25:44:ALA:HB2	1.95	0.48
3:28:9:ILE:HD11	3:28:150:TYR:CD2	2.48	0.48
2:43:26:ALA:O	3:48:12:ASP:HB3	2.13	0.48
2:A5:41:TYR:N	2:A5:41:TYR:CD1	2.81	0.48
3:A8:53:ASP:O	3:A8:56:LEU:N	2.46	0.48
3:A8:105:LYS:HG3	3:A8:203:GLY:C	2.38	0.48
1:B1:31:ASP:C	1:B1:33:ASP:H	2.20	0.48
2:B7:78:ARG:HD3	3:J8:60:LYS:CG	2.35	0.48
3:B8:20:THR:OG1	3:B8:21:PHE:N	2.46	0.48
2:C3:78:ARG:O	2:D7:25:LYS:NZ	2.41	0.48
2:G5:54:LYS:HD2	2:G5:75:VAL:HG21	1.95	0.48
1:H1:82:VAL:HG13	1:Z1:10:VAL:HG13	1.95	0.48
2:H5:28:LYS:NZ	2:H5:49:ASP:OD2	2.47	0.48
1:J1:19:ILE:O	1:J1:22:LEU:HB2	2.13	0.48
3:J8:143:LEU:O	3:J8:177:ARG:HA	2.12	0.48
1:K1:28:ARG:NH2	1:K1:38:GLY:O	2.47	0.48
3:M8:121:GLN:O	3:M8:125:ILE:HG13	2.14	0.48
3:O8:9:ILE:CD1	3:O8:150:TYR:HA	2.44	0.48
1:P1:32:PRO:HG3	1:P1:87:MET:HE2	1.95	0.48
1:Q1:64:ARG:HH11	1:S1:62:SER:CB	2.27	0.48
2:S5:43:THR:HG21	2:32:13:PHE:HD2	1.78	0.48
3:S8:6:ARG:NH1	3:S8:72:TYR:OH	2.46	0.48
3:U8:9:ILE:O	3:U8:38:LEU:HD12	2.13	0.48
2:V6:16:MET:HG3	2:V6:42:VAL:HG12	1.94	0.48
3:W8:150:TYR:HE2	3:W8:201:VAL:HG11	1.78	0.48
3:X8:121:GLN:O	3:X8:125:ILE:HG13	2.13	0.48
3:Y8:76:GLU:OE2	3:Y8:78:HIS:HB3	2.13	0.48
2:12:32:ILE:HD13	2:12:90:GLY:HA3	1.95	0.48
2:15:12:GLY:HA2	2:16:9:GLU:OE2	2.14	0.48
3:18:44:PRO:O	3:18:46:ILE:N	2.46	0.48
2:27:49:ASP:OD1	2:27:49:ASP:N	2.44	0.48
3:28:141:PHE:HD2	3:28:180:LEU:HD12	1.79	0.48
3:28:171:PRO:HD2	3:28:172:TYR:CD2	2.49	0.48
3:29:88:ALA:O	3:29:92:ILE:N	2.40	0.48
2:32:47:ARG:NH2	2:32:84:ASP:OD1	2.45	0.48
2:37:10:VAL:HG11	2:37:15:GLY:HA3	1.96	0.48
3:38:59:THR:HG21	3:38:88:ALA:HB2	1.94	0.48
3:A8:7:THR:HG22	3:A8:150:TYR:CE1	2.49	0.48
2:B3:5:LEU:HD12	2:B3:6:GLY:H	1.79	0.48
2:D3:11:VAL:O	2:D3:13:GLY:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D3:22:ASP:OD1	2:D4:83:VAL:HG21	2.14	0.48
1:E1:32:PRO:HG3	1:E1:87:MET:CE	2.43	0.48
2:E5:20:ALA:O	2:E5:24:VAL:HG23	2.14	0.48
2:E6:16:MET:HG2	2:E6:44:ALA:HB2	1.95	0.48
2:F3:21:ASP:OD2	2:F4:76:ILE:HG21	2.13	0.48
2:F3:45:VAL:HG11	2:F3:89:LEU:HD22	1.95	0.48
2:F7:49:ASP:N	2:F7:49:ASP:OD1	2.43	0.48
3:G8:119:ALA:O	3:G8:122:THR:OG1	2.31	0.48
3:H8:169:VAL:HG12	3:H8:171:PRO:HD3	1.95	0.48
3:J8:38:LEU:O	3:J8:76:GLU:HA	2.12	0.48
2:L6:13:PHE:HB2	2:L7:37:THR:HG21	1.95	0.48
3:L8:50:ARG:HD2	3:L8:95:LYS:HD3	1.94	0.48
2:M3:10:VAL:HG11	2:M3:15:GLY:HA3	1.95	0.48
2:M5:74:HIS:NE2	2:N2:18:GLU:OE1	2.47	0.48
2:N2:78:ARG:NH1	2:N5:28:LYS:HD3	2.29	0.48
1:O1:45:ASP:OD1	1:O1:47:VAL:N	2.32	0.48
2:Q2:92:THR:O	2:Q2:94:GLY:N	2.46	0.48
2:Q5:9:GLU:HG3	2:Q5:43:THR:OG1	2.13	0.48
2:S2:4:ALA:O	2:S2:47:ARG:NH1	2.47	0.48
2:W6:27:ALA:HA	3:W8:116:ALA:HB2	1.95	0.48
3:W8:42:ILE:HB	3:W8:48:ILE:HD11	1.95	0.48
3:W8:93:LEU:O	3:W8:97:GLU:N	2.46	0.48
2:X4:78:ARG:HD3	3:X8:163:ASN:CG	2.39	0.48
3:X8:48:ILE:HG23	3:X8:75:LEU:HB2	1.95	0.48
1:Y1:50:GLY:N	1:Y1:53:GLU:OE1	2.31	0.48
2:14:5:LEU:HD21	2:14:45:VAL:HG13	1.94	0.48
2:37:21:ASP:OD1	2:37:25:LYS:HE3	2.14	0.48
2:A7:60:GLY:O	2:A7:64:ALA:N	2.42	0.48
2:D3:6:LEU:O	2:D3:76:VAL:HG13	2.13	0.48
3:D8:67:VAL:HG12	3:P8:127:ARG:HH21	1.79	0.48
3:F8:27:ARG:HD2	3:Q8:127:ARG:HH11	1.77	0.48
1:G1:45:ASP:OD1	1:G1:48:GLY:N	2.39	0.48
2:G7:87:LEU:HB3	2:G7:89:LEU:HD13	1.95	0.48
3:H8:134:ILE:HG12	3:H8:181:ALA:HB2	1.95	0.48
1:J1:64:ARG:HH11	1:11:62:SER:HB3	1.79	0.48
2:L5:21:ASP:OD1	2:L5:25:LYS:HD2	2.14	0.48
3:L8:93:LEU:HD12	3:L8:94:ASP:N	2.29	0.48
2:N7:57:THR:HG21	2:N7:75:VAL:HG22	1.95	0.48
3:N8:106:PRO:HG3	3:N8:150:TYR:HE2	1.77	0.48
2:O3:30:GLU:OE1	2:O3:91:ARG:NH1	2.37	0.48
3:P8:13:ALA:HA	3:P8:35:GLN:O	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S8:45:GLY:HA3	3:S8:73:GLY:H	1.79	0.48
2:U2:3:ASP:C	2:U2:47:ARG:HH12	2.21	0.48
3:U8:29:PHE:HB2	3:U8:63:PRO:O	2.14	0.48
3:V8:11:LEU:HA	3:V8:11:LEU:HD23	1.67	0.48
2:W3:26:ALA:O	3:W8:12:ASP:HB3	2.13	0.48
2:W7:49:ASP:N	2:W7:49:ASP:OD1	2.43	0.48
2:X2:16:MET:HE2	2:X2:42:VAL:HG11	1.96	0.48
2:X4:47:ARG:HH22	2:X4:84:ASP:CG	2.21	0.48
2:X7:53:VAL:HA	2:X7:56:ALA:HB3	1.96	0.48
2:16:47:ARG:HH12	2:16:79:PRO:HG3	1.78	0.48
2:16:57:THR:HG21	2:16:75:VAL:HG22	1.95	0.48
2:23:27:ALA:HB3	2:23:56:ALA:HB2	1.95	0.48
1:31:31:ASP:C	1:31:33:ASP:H	2.21	0.48
2:34:66:ARG:HD2	2:35:62:ARG:HD2	1.95	0.48
3:38:29:PHE:HB2	3:38:63:PRO:O	2.14	0.48
2:B2:2:ALA:N	2:B2:78:ARG:NH1	2.61	0.48
2:B2:40:GLY:HA2	2:C5:37:THR:OG1	2.14	0.48
3:D8:127:ARG:NE	3:N8:27:ARG:HD2	2.29	0.48
3:D8:169:VAL:HG22	3:D8:178:LEU:CD1	2.44	0.48
2:E7:19:ALA:HB2	2:E7:64:ALA:HB2	1.94	0.48
3:E8:45:GLY:HA2	3:E8:48:ILE:HD13	1.95	0.48
3:F8:12:ASP:O	3:F8:82:GLN:NE2	2.47	0.48
3:G8:139:SER:HB2	3:G8:187:ILE:HG13	1.95	0.48
1:H1:86:GLU:HG2	1:H1:87:MET:N	2.29	0.48
2:I7:10:VAL:HG11	2:I7:15:GLY:HA3	1.95	0.48
3:J9:37:SER:HA	3:J9:78:HIS:HA	1.96	0.48
1:L1:28:ARG:HH11	1:L1:36:PRO:HB2	1.77	0.48
1:M1:31:ASP:C	1:M1:33:ASP:H	2.21	0.48
3:O8:142:ILE:HA	3:O8:178:LEU:O	2.14	0.48
2:Q5:90:GLY:O	2:Q5:91:ARG:HG2	2.14	0.48
3:R8:44:PRO:C	3:R8:46:ILE:H	2.21	0.48
1:S1:66:THR:O	1:S1:69:THR:OG1	2.22	0.48
2:U5:11:ARG:HG2	2:U5:11:ARG:O	2.14	0.48
2:V7:12:GLY:N	2:V7:40:GLY:O	2.46	0.48
2:V7:28:LYS:NZ	2:43:3:ASP:OD1	2.33	0.48
3:W8:124:ILE:HG21	3:Y8:66:GLN:HB3	1.95	0.48
2:23:45:VAL:HG11	2:23:89:LEU:CD1	2.44	0.48
2:46:31:LEU:HD12	2:46:45:VAL:O	2.14	0.48
2:B3:47:ARG:NH1	2:B3:84:ASP:CG	2.70	0.48
3:B8:23:GLY:CA	3:B8:30:LEU:HG	2.43	0.48
3:B8:93:LEU:HD12	3:B8:94:ASP:N	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C1:82:VAL:HG13	1:D1:10:VAL:HG13	1.96	0.48
3:E8:44:PRO:C	3:E8:46:ILE:H	2.22	0.48
3:E9:29:PHE:O	3:E9:64:ALA:HA	2.13	0.48
2:F2:47:ARG:NH2	2:F2:79:PRO:HG2	2.29	0.48
2:F6:13:PHE:N	2:F7:9:GLU:OE2	2.41	0.48
3:F9:52:THR:O	3:F9:56:LEU:N	2.35	0.48
3:G8:183:SER:O	3:G8:187:ILE:HG12	2.14	0.48
3:H8:8:TYR:CE2	3:H8:93:LEU:HD23	2.48	0.48
2:K7:50:VAL:HG21	2:K7:77:PRO:HB3	1.96	0.48
2:L2:78:ARG:HG3	2:L5:27:ALA:HA	1.95	0.48
2:L3:10:VAL:O	2:L3:12:GLY:N	2.47	0.48
2:L4:62:ARG:CZ	2:L5:66:ARG:NH1	2.77	0.48
3:L8:88:ALA:O	3:L8:91:THR:OG1	2.29	0.48
1:N1:50:GLY:N	1:N1:53:GLU:OE1	2.28	0.48
3:N8:49:ASN:HA	3:N8:66:GLN:NE2	2.29	0.48
3:O8:13:ALA:HA	3:O8:35:GLN:O	2.13	0.48
3:O8:124:ILE:O	3:O8:127:ARG:HB2	2.14	0.48
1:P1:31:ASP:O	1:P1:33:ASP:N	2.45	0.48
1:S1:64:ARG:NH2	1:31:62:SER:HA	2.28	0.48
2:S3:18:GLU:OE1	2:S4:74:HIS:NE2	2.44	0.48
3:S8:8:TYR:CE2	3:S8:93:LEU:HB3	2.37	0.48
2:T5:47:ARG:NH1	2:T5:84:ASP:OD1	2.46	0.48
3:T8:127:ARG:HH21	3:38:67:VAL:HG12	1.79	0.48
2:V6:55:ALA:HB1	3:V8:115:ARG:HD2	1.95	0.48
3:V8:110:THR:O	3:V8:143:LEU:HA	2.14	0.48
3:W8:17:GLN:NE2	3:W8:166:LEU:HB2	2.29	0.48
2:X3:19:ALA:HB2	2:X3:64:ALA:HB2	1.96	0.48
2:Y6:32:ILE:HG21	2:Y6:90:GLY:CA	2.43	0.48
2:Z4:16:MET:HG2	2:Z4:44:ALA:HB2	1.95	0.48
2:A3:78:ARG:HH12	2:I7:29:VAL:H	1.62	0.48
2:B4:50:VAL:HG11	3:B8:186:GLU:HG3	1.96	0.48
1:C1:66:THR:HG22	1:C1:67:GLU:O	2.14	0.48
2:C7:7:MET:C	2:C7:8:ILE:HD12	2.38	0.48
3:C8:11:LEU:HD13	3:C8:14:LEU:HD21	1.96	0.48
3:E8:20:THR:HG21	3:E9:135:LEU:HA	1.95	0.48
2:F7:13:PHE:CB	2:G3:43:THR:HG21	2.44	0.48
2:G4:20:ALA:HB1	2:G4:31:LEU:HD22	1.96	0.48
3:G8:42:ILE:CD1	3:G8:96:LEU:HD11	2.44	0.48
1:H1:70:ASN:C	1:H1:72:ARG:H	2.22	0.48
3:I8:171:PRO:HD2	3:I8:172:TYR:CD2	2.49	0.48
3:J8:29:PHE:HB2	3:J8:63:PRO:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J8:169:VAL:HG12	3:J8:171:PRO:HD3	1.96	0.48
3:J9:44:PRO:HA	3:J9:71:ALA:O	2.14	0.48
3:K8:20:THR:OG1	3:K8:21:PHE:N	2.46	0.48
1:M1:2:VAL:CG2	1:M1:57:TYR:CE1	2.97	0.48
1:O1:45:ASP:OD1	1:O1:46:ALA:N	2.47	0.48
3:P8:11:LEU:HD22	3:P8:156:ASN:HD22	1.79	0.48
1:T1:2:VAL:HG23	1:T1:57:TYR:CE1	2.49	0.48
2:T5:5:LEU:O	2:T5:53:VAL:HG11	2.13	0.48
3:U8:169:VAL:HG12	3:U8:171:PRO:HD3	1.95	0.48
3:V8:27:ARG:HD3	3:X8:127:ARG:HD3	1.96	0.48
2:W6:30:GLU:OE1	2:W6:91:ARG:NH2	2.46	0.48
2:X7:50:VAL:HG21	2:X7:77:PRO:HB3	1.94	0.48
3:Y9:158:ALA:O	3:Y9:162:ALA:N	2.42	0.48
2:Z3:52:ALA:O	2:Z3:56:ALA:N	2.38	0.48
3:Z9:7:THR:CB	3:Z9:149:GLY:HA3	2.44	0.48
3:28:167:VAL:HB	3:28:179:TYR:HB2	1.94	0.48
3:38:135:LEU:HD12	3:38:138:GLU:OE1	2.14	0.48
3:48:7:THR:OG1	3:48:41:GLU:N	2.47	0.48
3:B8:42:ILE:CD1	3:B8:96:LEU:HD11	2.44	0.47
2:D3:79:ARG:HH11	2:P7:26:LYS:HA	1.78	0.47
2:D6:4:ALA:HB2	2:D6:50:VAL:HA	1.95	0.47
2:D6:47:ARG:NH2	2:D6:84:ASP:OD1	2.47	0.47
3:D8:134:ILE:HG12	3:D8:181:ALA:HB2	1.95	0.47
2:F3:26:ALA:O	3:F8:12:ASP:HB3	2.12	0.47
2:G7:50:VAL:HG21	2:G7:77:PRO:HB3	1.95	0.47
3:G8:186:GLU:OE1	3:G8:186:GLU:N	2.32	0.47
2:I2:4:ALA:N	2:I2:48:GLY:O	2.45	0.47
2:J4:16:MET:HG3	2:J4:42:VAL:HG12	1.95	0.47
1:K1:70:ASN:C	1:K1:72:ARG:H	2.21	0.47
1:L1:70:ASN:O	1:L1:72:ARG:N	2.46	0.47
2:L6:61:GLN:O	2:L6:65:GLU:HG3	2.14	0.47
2:N3:34:TYR:OH	2:N4:35:GLU:OE2	2.23	0.47
2:N6:25:LYS:HZ1	3:P8:58:ALA:HA	1.75	0.47
2:N6:57:THR:HG21	2:N6:75:VAL:HG22	1.96	0.47
3:N8:142:ILE:HA	3:N8:178:LEU:O	2.13	0.47
3:Q8:183:SER:OG	3:Q8:186:GLU:OE2	2.32	0.47
1:S1:86:GLU:HG2	1:S1:87:MET:N	2.29	0.47
3:S8:11:LEU:HD21	3:S8:153:LEU:HA	1.96	0.47
2:T5:13:PHE:CE2	2:T6:35:GLU:HG2	2.49	0.47
3:V8:76:GLU:OE1	3:V8:78:HIS:HB3	2.13	0.47
2:W5:90:GLY:O	2:W5:91:ARG:HG2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:W6:47:ARG:HD3	2:W6:91:ARG:HG2	1.95	0.47
3:W8:24:LYS:NZ	3:W8:131:GLY:HA2	2.29	0.47
1:X1:61:SER:HB2	1:Y1:61:SER:HB3	1.95	0.47
3:X9:158:ALA:O	3:X9:162:ALA:N	2.44	0.47
2:26:16:MET:HG3	2:26:42:VAL:HG12	1.96	0.47
3:29:42:ILE:O	3:29:73:GLY:N	2.42	0.47
2:35:18:GLU:OE1	2:36:74:HIS:NE2	2.45	0.47
1:41:66:THR:HG22	1:41:67:GLU:O	2.14	0.47
3:A8:27:ARG:HD2	3:I8:127:ARG:NH2	2.27	0.47
3:C8:128:ASN:O	3:C8:168:ASN:ND2	2.47	0.47
2:F4:4:ALA:O	2:F4:47:ARG:NE	2.46	0.47
3:F8:7:THR:HG22	3:F8:147:PRO:HG2	1.96	0.47
3:F8:93:LEU:HB2	3:F8:98:VAL:O	2.14	0.47
3:G8:45:GLY:HA2	3:G8:48:ILE:HD13	1.96	0.47
3:K8:169:VAL:HG22	3:K8:178:LEU:HD13	1.95	0.47
1:L1:68:VAL:C	1:L1:72:ARG:NH1	2.72	0.47
2:M5:57:THR:O	2:M5:60:GLY:N	2.44	0.47
1:O1:73:PRO:O	1:P1:79:MET:HE1	2.14	0.47
3:P8:50:ARG:HD3	3:P8:95:LYS:HD3	1.96	0.47
3:R8:66:GLN:HB3	3:U8:124:ILE:HG21	1.96	0.47
2:S3:64:ALA:O	2:S3:68:GLY:N	2.47	0.47
2:S4:66:ARG:HD2	2:S5:62:ARG:HD2	1.96	0.47
2:S7:20:ALA:HB1	2:S7:31:LEU:HD22	1.96	0.47
1:W1:45:ASP:OD1	1:W1:47:VAL:N	2.36	0.47
3:X8:134:ILE:HG12	3:X8:181:ALA:CB	2.45	0.47
3:Y8:119:ALA:O	3:Y8:122:THR:OG1	2.31	0.47
3:Y8:123:GLN:HG2	3:Y9:23:GLY:HA3	1.96	0.47
2:Z2:9:GLU:HB2	2:Z4:14:VAL:HG23	1.96	0.47
3:Z8:41:GLU:HB2	3:Z8:74:LEU:HD13	1.97	0.47
1:21:2:VAL:HG23	1:21:57:TYR:CE1	2.49	0.47
3:28:8:TYR:HE2	3:28:93:LEU:HD23	1.79	0.47
2:35:18:GLU:CD	2:36:74:HIS:HE2	2.21	0.47
2:45:13:PHE:HD2	2:46:43:THR:HG21	1.77	0.47
2:C3:5:LEU:HD21	2:C3:89:LEU:HD13	1.95	0.47
2:C7:49:ASP:N	2:C7:49:ASP:OD1	2.46	0.47
2:D3:78:PRO:HB2	2:P7:25:ALA:HA	1.94	0.47
3:E8:124:ILE:O	3:E8:127:ARG:HB2	2.14	0.47
2:I4:57:THR:HG22	2:I4:73:VAL:HG13	1.96	0.47
1:J1:68:VAL:CA	1:J1:72:ARG:HH12	2.28	0.47
3:J8:15:GLN:HG2	3:J8:156:ASN:OD1	2.15	0.47
3:J8:111:HIS:ND1	3:J8:195:GLU:OE2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J8:127:ARG:HD3	3:L8:27:ARG:HD2	1.95	0.47
3:N8:32:VAL:N	3:N8:35:GLN:OE1	2.30	0.47
2:O7:49:ASP:OD1	2:O7:49:ASP:N	2.46	0.47
3:O8:106:PRO:HA	3:O8:146:GLN:O	2.15	0.47
2:T3:32:ILE:CD1	2:T3:47:ARG:HG3	2.44	0.47
1:V1:62:SER:CB	1:W1:64:ARG:HH11	2.26	0.47
2:V3:8:ILE:HG23	2:V3:73:VAL:HG22	1.96	0.47
2:X5:7:MET:HE1	2:Y2:17:VAL:HG21	1.96	0.47
3:Y8:9:ILE:O	3:Y8:39:TRP:N	2.46	0.47
1:Z1:62:SER:HA	1:11:64:ARG:NH2	2.28	0.47
2:15:92:THR:O	2:15:94:GLY:N	2.47	0.47
3:19:88:ALA:O	3:19:92:ILE:N	2.43	0.47
2:34:53:VAL:O	2:34:57:THR:OG1	2.22	0.47
2:A5:90:GLY:O	2:A5:91:ARG:HG2	2.14	0.47
2:B4:62:ARG:CZ	2:B5:66:ARG:NH1	2.77	0.47
3:B8:127:ARG:NH2	3:J8:67:VAL:HG12	2.29	0.47
3:B8:128:ASN:O	3:B8:130:GLN:N	2.47	0.47
2:D2:13:PHE:CE2	2:E5:35:GLU:HG2	2.49	0.47
2:D5:10:VAL:HG11	2:D5:15:GLY:HA3	1.96	0.47
3:D8:20:THR:OG1	3:D8:21:PHE:N	2.47	0.47
3:D8:23:GLY:CA	3:D8:30:LEU:HG	2.44	0.47
2:F4:16:MET:HG3	2:F4:42:VAL:HG12	1.97	0.47
3:F8:28:GLY:HA2	3:Q8:124:ILE:HD11	1.96	0.47
3:F8:93:LEU:HD12	3:F8:94:ASP:N	2.30	0.47
3:H8:13:ALA:HA	3:H8:35:GLN:O	2.14	0.47
3:H8:46:ILE:HD11	3:Y8:144:GLU:HB2	1.96	0.47
2:I2:5:LEU:HD11	2:I2:7:MET:HE2	1.95	0.47
3:I8:7:THR:OG1	3:I8:41:GLU:N	2.47	0.47
1:K1:61:SER:HB2	1:L1:61:SER:HB3	1.94	0.47
3:K8:121:GLN:OE1	3:18:52:THR:HB	2.15	0.47
3:L8:31:PRO:HD3	3:L8:64:ALA:HB2	1.95	0.47
3:L8:38:LEU:O	3:L8:76:GLU:HA	2.14	0.47
2:N4:47:ARG:HH22	2:N4:84:ASP:CG	2.22	0.47
1:O1:26:LEU:HD23	1:P1:87:MET:HE3	1.96	0.47
3:P8:127:ARG:HD2	3:P8:127:ARG:O	2.14	0.47
2:Q2:5:LEU:HD23	2:Q2:76:ILE:HD12	1.96	0.47
3:R8:118:GLU:HG3	3:R8:120:TYR:H	1.79	0.47
3:R8:186:GLU:OE1	3:R8:186:GLU:N	2.37	0.47
3:S8:124:ILE:O	3:S8:127:ARG:HB2	2.14	0.47
2:T6:32:ILE:HD11	2:T6:47:ARG:HD2	1.96	0.47
1:X1:94:ARG:HG2	1:X1:95:LYS:H	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X6:55:ALA:HB1	3:X8:115:ARG:HD2	1.96	0.47
3:X8:50:ARG:HB2	3:48:114:ILE:HD11	1.97	0.47
2:Z5:90:GLY:O	2:Z5:91:ARG:HG2	2.14	0.47
2:12:3:ASP:O	2:12:47:ARG:NH2	2.43	0.47
2:12:16:MET:O	2:12:20:ALA:N	2.34	0.47
2:25:2:ALA:O	2:25:78:ARG:NH1	2.47	0.47
2:43:12:GLY:HA2	2:44:9:GLU:OE2	2.14	0.47
2:A5:35:GLU:HG2	2:E2:13:PHE:HE2	1.77	0.47
2:A5:82:ASN:OD1	2:E2:31:LEU:HB3	2.14	0.47
2:A7:29:VAL:H	2:G3:78:ARG:NH2	2.11	0.47
2:B7:53:VAL:HG23	2:B7:54:LYS:N	2.30	0.47
3:B8:115:ARG:HA	3:B8:139:SER:OG	2.13	0.47
1:C1:86:GLU:HG2	1:C1:87:MET:N	2.28	0.47
2:D3:5:ALA:HB3	2:D3:49:GLY:O	2.13	0.47
2:D3:52:ALA:HB2	2:P7:49:ALA:HB2	1.95	0.47
2:E6:53:VAL:O	2:E6:57:THR:HG23	2.15	0.47
3:E8:143:LEU:O	3:E8:177:ARG:HA	2.15	0.47
2:G2:32:ILE:HD13	2:G2:90:GLY:HA3	1.96	0.47
3:H8:7:THR:OG1	3:H8:41:GLU:N	2.46	0.47
2:I6:32:ILE:HG21	2:I6:90:GLY:HA3	1.95	0.47
2:J7:31:LEU:HB3	2:13:82:ASN:OD1	2.13	0.47
3:K8:39:TRP:CZ2	3:K8:76:GLU:HG3	2.49	0.47
1:L1:48:GLY:O	2:22:25:LYS:NZ	2.39	0.47
3:M8:8:TYR:HE2	3:M8:93:LEU:HD23	1.78	0.47
2:N7:78:ARG:NH2	3:P8:60:LYS:HD3	2.30	0.47
3:O8:59:THR:HB	3:O8:61:VAL:HG23	1.95	0.47
3:P8:141:PHE:CZ	3:P8:143:LEU:HB2	2.50	0.47
3:Q8:154:ALA:HB2	3:Q8:198:ILE:HD11	1.95	0.47
3:S8:111:HIS:O	3:S8:111:HIS:CG	2.67	0.47
2:T7:47:ARG:NH1	2:T7:89:LEU:HB3	2.30	0.47
3:W8:37:SER:HA	3:W8:78:HIS:HA	1.96	0.47
3:W9:11:LEU:N	3:W9:37:SER:O	2.46	0.47
2:X7:23:MET:HG2	2:X7:56:ALA:O	2.14	0.47
2:Z3:4:ALA:O	2:Z3:47:ARG:HD2	2.15	0.47
3:18:20:THR:HG21	3:19:135:LEU:HA	1.95	0.47
3:39:107:GLN:N	3:39:146:GLN:O	2.47	0.47
3:49:62:GLN:O	3:49:77:VAL:HA	2.14	0.47
2:A4:62:ARG:CZ	2:A5:66:ARG:NH1	2.77	0.47
3:A8:111:HIS:HB3	3:A8:143:LEU:HD13	1.97	0.47
1:C1:68:VAL:C	1:C1:72:ARG:NH1	2.73	0.47
2:C4:50:VAL:O	2:C4:54:LYS:HB2	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D3:91:GLY:O	2:D3:93:THR:N	2.47	0.47
2:E6:31:LEU:HD12	2:E6:45:VAL:O	2.15	0.47
1:F1:45:ASP:OD1	1:F1:46:ALA:N	2.47	0.47
2:F2:9:GLU:HB2	2:F4:14:VAL:HG23	1.96	0.47
2:F5:27:ALA:HB1	2:F5:52:ALA:HB1	1.96	0.47
3:F8:118:GLU:HG3	3:F8:119:ALA:N	2.29	0.47
2:G3:18:GLU:OE1	2:G4:74:HIS:NE2	2.44	0.47
2:G3:31:LEU:HB3	2:G4:82:ASN:OD1	2.14	0.47
2:G4:78:ARG:NH2	3:G8:159:GLU:OE1	2.47	0.47
2:G6:32:ILE:HG21	2:G6:90:GLY:CA	2.44	0.47
2:H2:47:ARG:HD2	2:H2:89:LEU:O	2.15	0.47
3:H8:41:GLU:HA	3:H8:74:LEU:HD11	1.96	0.47
1:I1:63:ALA:HB1	1:I1:77:THR:HG22	1.97	0.47
2:I2:29:VAL:HG11	2:I2:46:VAL:HB	1.97	0.47
1:J1:45:ASP:OD1	1:J1:46:ALA:N	2.47	0.47
2:J7:51:ALA:HB2	2:L3:51:ALA:HB2	1.97	0.47
2:K3:10:VAL:O	2:K3:12:GLY:N	2.48	0.47
3:K8:142:ILE:HA	3:K8:178:LEU:O	2.14	0.47
2:L2:47:ARG:NH2	2:L2:84:ASP:OD1	2.47	0.47
2:L6:32:ILE:HD11	2:L6:47:ARG:HD2	1.96	0.47
3:M8:21:PHE:O	3:M8:25:THR:OG1	2.28	0.47
2:O4:9:GLU:HB3	2:O4:71:VAL:HB	1.97	0.47
2:O5:36:LYS:NZ	2:O6:35:GLU:OE2	2.38	0.47
2:P3:31:LEU:HB3	2:P4:82:ASN:OD1	2.15	0.47
3:P8:64:ALA:HB3	3:P8:76:GLU:OE2	2.14	0.47
2:Q2:5:LEU:HB3	2:Q2:76:ILE:HB	1.96	0.47
2:Q4:31:LEU:HD12	2:Q4:45:VAL:O	2.15	0.47
1:R1:22:LEU:HG	1:R1:44:ALA:HB1	1.97	0.47
2:R6:32:ILE:HG21	2:R6:90:GLY:CA	2.44	0.47
3:R8:9:ILE:HG21	3:R8:153:LEU:HB2	1.95	0.47
3:T8:9:ILE:O	3:T8:38:LEU:HD12	2.15	0.47
2:W3:16:MET:HG2	2:W3:44:ALA:HB2	1.97	0.47
3:W8:183:SER:OG	3:W8:186:GLU:OE2	2.33	0.47
2:X2:23:MET:HG2	2:X2:56:ALA:C	2.40	0.47
2:X3:10:VAL:O	2:X3:12:GLY:N	2.48	0.47
3:X9:67:VAL:N	3:X9:74:LEU:O	2.41	0.47
2:Z4:20:ALA:HB1	2:Z4:31:LEU:HD22	1.96	0.47
2:Z4:92:THR:O	2:Z4:94:GLY:N	2.48	0.47
2:36:16:MET:HG2	2:36:44:ALA:HB2	1.96	0.47
2:46:50:VAL:HG13	2:46:77:PRO:HB3	1.95	0.47
3:48:140:LEU:HA	3:48:180:LEU:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A1:47:VAL:HG12	1:B1:14:ARG:HG3	1.97	0.47
2:A5:34:TYR:CE2	2:A5:36:LYS:HD2	2.49	0.47
2:B6:3:ASP:OD2	2:B6:91:ARG:NE	2.43	0.47
2:B6:4:ALA:O	2:B6:47:ARG:HG2	2.15	0.47
2:B6:27:ALA:HA	3:B8:116:ALA:HB2	1.97	0.47
3:B8:132:MET:HE2	3:B8:165:HIS:ND1	2.29	0.47
2:C2:23:MET:HG2	2:C2:56:ALA:O	2.15	0.47
3:C8:79:HIS:CE1	3:C8:81:ASP:H	2.32	0.47
2:D6:4:ALA:HA	2:D6:77:PRO:O	2.14	0.47
3:D8:67:VAL:CG1	3:P8:127:ARG:HH21	2.28	0.47
3:E8:110:THR:O	3:E8:143:LEU:HA	2.15	0.47
3:E8:170:THR:HG1	3:E8:177:ARG:H	1.59	0.47
2:G6:13:PHE:HB2	2:G7:37:THR:HG21	1.96	0.47
2:G7:5:LEU:HD23	2:G7:47:ARG:HD3	1.96	0.47
3:G8:13:ALA:HA	3:G8:35:GLN:O	2.14	0.47
3:G8:186:GLU:O	3:G8:190:ALA:N	2.47	0.47
2:H2:13:PHE:HE2	2:Z5:35:GLU:HG2	1.78	0.47
2:H4:8:ILE:HD12	2:H4:73:VAL:HG22	1.97	0.47
3:H8:19:ALA:HB3	3:H8:33:PRO:HG3	1.97	0.47
1:I1:89:GLY:O	2:I2:28:LYS:HE3	2.14	0.47
2:I2:87:LEU:HD13	2:I4:16:MET:HE1	1.96	0.47
2:I3:12:GLY:HA2	2:I4:9:GLU:OE2	2.14	0.47
2:I7:49:ASP:OD1	2:I7:49:ASP:N	2.46	0.47
3:J8:118:GLU:HG3	3:J8:119:ALA:N	2.30	0.47
1:K1:68:VAL:C	1:K1:72:ARG:HH12	2.23	0.47
2:K2:74:HIS:HE2	2:K4:18:GLU:CD	2.23	0.47
2:K7:27:ALA:O	2:13:78:ARG:NH1	2.44	0.47
3:K8:51:VAL:HG13	3:K8:92:ILE:HG12	1.97	0.47
1:L1:22:LEU:HG	1:L1:44:ALA:HB1	1.97	0.47
3:L8:9:ILE:O	3:L8:38:LEU:HD12	2.15	0.47
3:L8:13:ALA:HA	3:L8:35:GLN:O	2.14	0.47
3:L8:29:PHE:HB2	3:L8:63:PRO:O	2.14	0.47
3:L8:45:GLY:CA	3:L8:73:GLY:H	2.26	0.47
3:L8:79:HIS:CE1	3:L8:81:ASP:HB2	2.50	0.47
2:N2:9:GLU:HB2	2:N4:14:VAL:HG23	1.97	0.47
3:N8:21:PHE:HA	3:N8:24:LYS:HE3	1.96	0.47
3:N8:29:PHE:HB2	3:N8:63:PRO:O	2.14	0.47
1:O1:22:LEU:HD12	1:O1:22:LEU:HA	1.70	0.47
2:O3:10:VAL:O	2:O3:12:GLY:N	2.47	0.47
3:O8:140:LEU:HD11	3:O8:179:TYR:HD2	1.80	0.47
3:Q8:13:ALA:HA	3:Q8:35:GLN:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Q8:23:GLY:HA3	3:Q8:30:LEU:HG	1.97	0.47
3:R8:106:PRO:HG2	3:R8:198:ILE:O	2.15	0.47
1:S1:66:THR:HG22	1:S1:67:GLU:O	2.14	0.47
2:S5:9:GLU:HG3	2:S5:43:THR:OG1	2.14	0.47
2:T7:8:ILE:HG12	2:T7:73:VAL:HG22	1.95	0.47
3:T8:111:HIS:HB2	3:T8:195:GLU:OE2	2.15	0.47
3:V8:7:THR:OG1	3:V8:41:GLU:N	2.48	0.47
3:V8:31:PRO:HA	3:V8:78:HIS:CE1	2.50	0.47
3:V8:70:ARG:HG2	3:V8:173:GLY:N	2.29	0.47
2:W5:2:ALA:HB1	2:W5:78:ARG:NH2	2.29	0.47
3:W8:106:PRO:HB2	3:W8:198:ILE:HG22	1.97	0.47
3:X8:93:LEU:HD12	3:X8:94:ASP:N	2.30	0.47
3:Z8:6:ARG:HA	3:Z8:104:LEU:HG	1.97	0.47
3:Z9:39:TRP:HA	3:Z9:76:GLU:HA	1.96	0.47
3:18:24:LYS:NZ	3:19:134:ILE:O	2.47	0.47
3:18:154:ALA:HB2	3:18:198:ILE:HD11	1.96	0.47
2:22:65:GLU:HG3	2:22:70:VAL:HG21	1.97	0.47
3:28:93:LEU:HD12	3:28:94:ASP:N	2.29	0.47
2:35:2:ALA:HA	2:35:78:ARG:CZ	2.45	0.47
2:42:5:LEU:HD23	2:42:76:ILE:HD12	1.95	0.47
3:48:122:THR:HG22	3:48:134:ILE:HG22	1.97	0.47
2:A2:78:ARG:NH1	2:A5:28:LYS:HD3	2.30	0.47
2:B3:27:ALA:HB3	2:B3:56:ALA:HB2	1.96	0.47
3:B8:46:ILE:CD1	3:L8:144:GLU:HB2	2.45	0.47
3:B8:142:ILE:HG22	3:B8:179:TYR:HD1	1.79	0.47
3:C8:7:THR:HG23	3:C8:41:GLU:HB3	1.97	0.47
3:D8:17:GLN:O	3:D8:20:THR:OG1	2.22	0.47
3:D8:21:PHE:O	3:D8:25:THR:OG1	2.12	0.47
3:D9:10:PHE:HA	3:D9:38:LEU:HA	1.96	0.47
3:I8:70:ARG:HG2	3:I8:173:GLY:N	2.29	0.47
3:I8:162:ALA:HB3	3:I8:190:ALA:HB2	1.97	0.47
3:J8:8:TYR:HE2	3:J8:93:LEU:HD23	1.78	0.47
3:J8:45:GLY:HA2	3:J8:48:ILE:HD13	1.97	0.47
3:J8:127:ARG:NH1	3:L8:27:ARG:HD2	2.25	0.47
3:K8:9:ILE:O	3:K8:39:TRP:N	2.46	0.47
2:M5:9:GLU:OE2	2:N2:13:PHE:N	2.47	0.47
2:N3:27:ALA:HB3	2:N3:56:ALA:HB2	1.96	0.47
2:N6:12:GLY:HA2	2:N7:9:GLU:OE2	2.15	0.47
3:N9:51:VAL:O	3:N9:55:ALA:N	2.47	0.47
2:P2:4:ALA:O	2:P2:47:ARG:NH1	2.47	0.47
3:P9:144:GLU:HA	3:P9:176:GLY:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R4:31:LEU:HD12	2:R4:45:VAL:O	2.15	0.47
2:R6:84:ASP:O	2:R6:92:THR:HG23	2.15	0.47
3:R8:24:LYS:NZ	3:R9:134:ILE:O	2.47	0.47
2:S4:10:VAL:HG22	2:S4:70:VAL:HG12	1.97	0.47
1:U1:45:ASP:OD1	1:U1:46:ALA:N	2.48	0.47
2:V2:16:MET:HG2	2:V2:44:ALA:HB2	1.96	0.47
3:W8:144:GLU:OE1	3:Y8:44:PRO:HG3	2.15	0.47
2:X6:47:ARG:HH22	2:X6:79:PRO:HG3	1.79	0.47
2:Y6:45:VAL:HG11	2:Y6:89:LEU:HD22	1.96	0.47
3:Z8:170:THR:HG1	3:Z8:177:ARG:H	1.56	0.47
2:15:9:GLU:HG3	2:15:43:THR:OG1	2.14	0.47
3:18:20:THR:OG1	3:18:21:PHE:N	2.46	0.47
1:41:2:VAL:HG23	1:41:57:TYR:CE1	2.49	0.47
2:44:62:ARG:NE	2:45:66:ARG:NH1	2.62	0.47
2:A7:49:ASP:N	2:A7:49:ASP:OD1	2.47	0.47
3:A8:124:ILE:HG21	3:G8:66:GLN:HB3	1.97	0.47
2:C7:57:THR:O	2:C7:60:GLY:N	2.48	0.47
3:C8:111:HIS:O	3:C8:111:HIS:CG	2.67	0.47
2:D5:9:GLU:HG3	2:D5:43:THR:OG1	2.15	0.47
2:F3:77:PRO:HB2	2:Q7:27:ALA:HA	1.97	0.47
2:H6:29:VAL:HG11	2:H6:46:VAL:HB	1.97	0.47
3:H8:57:LYS:O	2:Y7:78:ARG:NH2	2.48	0.47
3:J8:29:PHE:CD2	3:J8:63:PRO:HD2	2.50	0.47
3:J8:134:ILE:HG12	3:J8:181:ALA:HB2	1.96	0.47
3:K8:125:ILE:CD1	3:18:49:ASN:HD21	2.28	0.47
2:N5:90:GLY:O	2:N5:91:ARG:HG2	2.15	0.47
2:N7:51:ALA:HB2	2:P3:51:ALA:HB2	1.96	0.47
2:O5:86:ALA:HB3	2:P2:31:LEU:HD12	1.97	0.47
3:O8:144:GLU:HA	3:O8:176:GLY:O	2.15	0.47
2:Q3:21:ASP:OD1	2:Q3:25:LYS:HE3	2.15	0.47
2:R3:9:GLU:HA	2:R3:42:VAL:O	2.15	0.47
2:S5:8:ILE:HG12	2:S5:73:VAL:HG22	1.97	0.47
3:U8:110:THR:O	3:U8:143:LEU:HA	2.14	0.47
3:V8:93:LEU:HD12	3:V8:94:ASP:N	2.29	0.47
2:W2:85:ALA:HA	2:W2:92:THR:HG23	1.97	0.47
2:W5:3:ASP:HB3	2:W5:48:GLY:C	2.40	0.47
3:18:13:ALA:HA	3:18:35:GLN:O	2.14	0.47
2:33:47:ARG:NH1	2:33:84:ASP:OD1	2.37	0.47
2:36:47:ARG:HH22	2:36:79:PRO:CG	2.28	0.47
3:38:186:GLU:O	3:38:190:ALA:N	2.44	0.47
3:A8:51:VAL:HA	3:A8:95:LYS:HD2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B3:18:GLU:OE1	2:B4:74:HIS:NE2	2.49	0.47
2:B5:47:ARG:HH12	2:B5:84:ASP:CG	2.23	0.47
2:D4:8:ILE:HD12	2:D4:73:VAL:HG22	1.97	0.47
2:D4:19:ALA:O	2:D4:23:MET:HG3	2.15	0.47
3:D9:39:TRP:HA	3:D9:76:GLU:HA	1.96	0.47
2:E4:78:ARG:NH2	3:E8:159:GLU:OE2	2.48	0.47
3:F8:143:LEU:O	3:F8:177:ARG:HA	2.15	0.47
2:G2:16:MET:HG2	2:G2:44:ALA:HB2	1.96	0.47
2:G7:19:ALA:HB2	2:G7:64:ALA:HB2	1.97	0.47
3:G8:127:ARG:HH12	3:I8:67:VAL:CG1	2.21	0.47
3:H8:124:ILE:CG2	3:W8:66:GLN:HB3	2.45	0.47
1:J1:10:VAL:HG11	1:I1:56:LEU:HD11	1.97	0.47
1:J1:33:ASP:HB3	1:J1:35:THR:HG23	1.95	0.47
2:J2:4:ALA:O	2:J2:47:ARG:HG2	2.14	0.47
2:J7:17:VAL:CG1	2:I3:7:MET:HE1	2.45	0.47
1:K1:2:VAL:HG23	1:K1:57:TYR:CE1	2.49	0.47
3:L8:144:GLU:HA	3:L8:176:GLY:O	2.15	0.47
3:M8:64:ALA:HB3	3:M8:76:GLU:OE1	2.15	0.47
2:N2:16:MET:O	2:N2:20:ALA:N	2.34	0.47
3:N8:6:ARG:NH2	3:N8:72:TYR:OH	2.48	0.47
2:O5:37:THR:HG21	2:P2:13:PHE:HB2	1.97	0.47
3:P8:142:ILE:HA	3:P8:178:LEU:O	2.14	0.47
2:R3:39:GLY:HA3	2:V7:39:GLY:HA2	1.97	0.47
3:R9:87:ALA:O	3:R9:91:THR:N	2.39	0.47
2:T4:51:ALA:HB2	3:T8:185:ALA:CB	2.45	0.47
3:T8:119:ALA:O	3:T8:122:THR:OG1	2.32	0.47
1:V1:86:GLU:HG2	1:V1:87:MET:N	2.30	0.47
3:W8:126:ASN:O	3:W8:129:SER:HB3	2.15	0.47
1:X1:31:ASP:O	1:X1:33:ASP:N	2.46	0.47
2:X6:32:ILE:HD11	2:X6:47:ARG:HD2	1.96	0.47
3:Y8:3:ILE:HB	3:Y8:96:LEU:HD22	1.96	0.47
3:Y8:134:ILE:HD13	3:Y8:140:LEU:HB2	1.98	0.47
3:28:169:VAL:HG22	3:28:178:LEU:HD13	1.96	0.47
3:38:141:PHE:CZ	3:38:143:LEU:HB2	2.50	0.47
3:A8:17:GLN:O	3:A8:20:THR:OG1	2.24	0.46
2:B2:45:VAL:HG11	2:B2:89:LEU:HD22	1.97	0.46
3:B8:144:GLU:HB2	3:J8:46:ILE:HD11	1.97	0.46
2:C5:90:GLY:O	2:C5:91:ARG:HG2	2.15	0.46
2:D6:16:MET:HG2	2:D6:44:ALA:HB2	1.97	0.46
1:F1:2:VAL:CG2	1:F1:57:TYR:CE1	2.98	0.46
1:G1:63:ALA:HB1	1:G1:77:THR:HG22	1.95	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H8:54:ALA:HB2	3:H8:95:LYS:NZ	2.30	0.46
2:K5:37:THR:HG21	2:L2:13:PHE:HB2	1.96	0.46
3:K8:79:HIS:CE1	3:K8:81:ASP:HB2	2.50	0.46
3:K8:177:ARG:CG	3:18:46:ILE:HD11	2.45	0.46
3:M8:20:THR:OG1	3:M8:21:PHE:N	2.48	0.46
2:P2:16:MET:HG2	2:P2:44:ALA:HB2	1.95	0.46
2:P6:16:MET:HG2	2:P6:44:ALA:HB2	1.97	0.46
2:Q3:13:PHE:HB2	2:Q4:37:THR:HG21	1.97	0.46
3:Q9:165:HIS:N	3:Q9:181:ALA:O	2.33	0.46
1:S1:26:LEU:HD12	1:S1:26:LEU:HA	1.76	0.46
3:S8:141:PHE:CZ	3:S8:143:LEU:HB2	2.49	0.46
2:T6:57:THR:HG21	2:T6:75:VAL:HG22	1.95	0.46
3:T8:35:GLN:HE22	3:T8:78:HIS:CE1	2.33	0.46
2:U7:21:ASP:OD1	2:U7:25:LYS:HE3	2.16	0.46
3:U8:183:SER:OG	3:U8:186:GLU:OE2	2.32	0.46
2:V4:66:ARG:NH1	2:V5:62:ARG:NE	2.64	0.46
2:W4:16:MET:HG3	2:W4:42:VAL:HG12	1.98	0.46
3:W8:183:SER:O	3:W8:187:ILE:HG12	2.15	0.46
2:X2:47:ARG:HD2	2:X2:89:LEU:O	2.15	0.46
2:X5:23:MET:HG2	2:X5:56:ALA:O	2.14	0.46
2:Y2:23:MET:HG2	2:Y2:56:ALA:C	2.40	0.46
2:Y4:30:GLU:OE1	2:Y4:91:ARG:NH2	2.48	0.46
2:Z2:19:ALA:HB2	2:Z2:64:ALA:HB2	1.97	0.46
2:Z3:21:ASP:OD1	2:Z3:25:LYS:HE3	2.15	0.46
3:Z8:8:TYR:HA	3:Z8:40:VAL:HG22	1.96	0.46
1:11:64:ARG:C	1:11:66:THR:H	2.22	0.46
2:16:32:ILE:HD13	2:16:90:GLY:HA3	1.96	0.46
2:43:54:LYS:O	2:43:58:GLU:HG3	2.15	0.46
3:48:103:ARG:HH21	3:48:201:VAL:HG13	1.80	0.46
2:A3:21:ASP:OD2	2:A4:76:ILE:HD13	2.15	0.46
2:A4:47:ARG:NH1	2:A4:89:LEU:O	2.48	0.46
1:C1:31:ASP:O	1:C1:33:ASP:N	2.45	0.46
1:C1:45:ASP:OD1	1:C1:46:ALA:N	2.49	0.46
2:C5:29:VAL:HG11	2:C5:46:VAL:HB	1.97	0.46
2:D2:84:ASP:O	2:D2:92:THR:OG1	2.30	0.46
1:E1:22:LEU:HD12	1:E1:22:LEU:HA	1.67	0.46
2:E4:31:LEU:HD12	2:E4:45:VAL:O	2.15	0.46
2:G7:60:GLY:O	2:G7:64:ALA:N	2.42	0.46
3:H8:142:ILE:HB	3:W8:46:ILE:HG21	1.98	0.46
3:K8:197:ALA:O	3:K8:200:SER:OG	2.33	0.46
2:L2:90:GLY:O	2:L2:92:THR:HG23	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L8:61:VAL:CG1	3:L8:77:VAL:HB	2.44	0.46
3:L9:144:GLU:HA	3:L9:176:GLY:O	2.15	0.46
2:N3:10:VAL:O	2:N3:12:GLY:N	2.49	0.46
2:N3:47:ARG:HE	2:N3:91:ARG:HG2	1.80	0.46
2:N5:13:PHE:HD2	2:N6:43:THR:HG21	1.80	0.46
3:N8:9:ILE:HG21	3:N8:153:LEU:HB2	1.97	0.46
3:N8:186:GLU:O	3:N8:190:ALA:N	2.39	0.46
1:O1:16:GLU:OE1	1:O1:16:GLU:C	2.58	0.46
3:O8:18:LEU:O	3:O8:22:ILE:N	2.29	0.46
2:P7:47:ASP:OD1	2:P7:47:ASP:N	2.48	0.46
3:P9:42:ILE:N	3:P9:73:GLY:O	2.41	0.46
3:Q8:118:GLU:HG3	3:Q8:119:ALA:N	2.29	0.46
1:R1:66:THR:HG22	1:R1:67:GLU:O	2.15	0.46
2:S6:27:ALA:HB1	2:S6:52:ALA:HB1	1.96	0.46
3:T8:24:LYS:NZ	3:T9:134:ILE:O	2.47	0.46
1:U1:31:ASP:C	1:U1:33:ASP:H	2.21	0.46
2:V3:47:ARG:NH1	2:V3:91:ARG:HB2	2.22	0.46
2:V7:78:ARG:NH1	3:48:57:LYS:O	2.47	0.46
1:W1:45:ASP:OD1	1:W1:48:GLY:N	2.42	0.46
3:W9:45:GLY:N	3:W9:71:ALA:O	2.47	0.46
2:Z7:49:ASP:OD1	2:Z7:49:ASP:N	2.48	0.46
3:18:65:VAL:HG12	3:18:76:GLU:HB3	1.97	0.46
2:25:24:VAL:HG11	2:26:82:ASN:HB3	1.97	0.46
2:25:31:LEU:HD12	2:26:86:ALA:HB3	1.97	0.46
2:25:47:ARG:HH12	2:25:84:ASP:CG	2.23	0.46
2:26:31:LEU:HD12	2:26:45:VAL:O	2.15	0.46
3:38:118:GLU:HG3	3:38:119:ALA:N	2.30	0.46
1:41:50:GLY:N	1:41:53:GLU:OE1	2.27	0.46
2:46:84:ASP:O	2:46:92:THR:HG22	2.15	0.46
1:A1:22:LEU:HG	1:A1:44:ALA:HB1	1.96	0.46
1:A1:79:MET:HE1	1:B1:73:PRO:O	2.15	0.46
3:A8:117:VAL:HG12	3:A8:121:GLN:HB3	1.97	0.46
2:B7:21:ASP:OD1	2:B7:25:LYS:HE3	2.16	0.46
2:C3:10:VAL:O	2:C3:12:GLY:N	2.48	0.46
2:C4:62:ARG:HD2	2:C5:66:ARG:NH1	2.30	0.46
2:C6:61:GLN:O	2:C6:65:GLU:HG3	2.16	0.46
3:D8:9:ILE:HB	3:D8:39:TRP:HB2	1.98	0.46
1:F1:42:VAL:HG11	1:G1:56:LEU:HD21	1.97	0.46
3:F8:105:LYS:HG3	3:F8:203:GLY:C	2.41	0.46
3:G8:20:THR:OG1	3:G8:21:PHE:N	2.48	0.46
1:H1:32:PRO:HG3	1:H1:87:MET:HE2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H4:5:LEU:HD11	2:H4:45:VAL:HG13	1.98	0.46
1:J1:86:GLU:HG2	1:J1:87:MET:N	2.31	0.46
2:J3:21:ASP:OD1	2:J4:83:VAL:HG21	2.16	0.46
3:J8:45:GLY:HA3	3:J8:73:GLY:H	1.81	0.46
2:K4:10:VAL:HG11	2:K4:15:GLY:HA3	1.97	0.46
3:O8:38:LEU:O	3:O8:76:GLU:HA	2.16	0.46
3:O8:122:THR:HG21	3:O8:136:PRO:CA	2.43	0.46
3:O8:183:SER:OG	3:O8:186:GLU:OE2	2.32	0.46
2:Q4:20:ALA:HB1	2:Q4:31:LEU:HD22	1.98	0.46
3:Q8:117:VAL:HG12	3:Q8:121:GLN:HB3	1.97	0.46
2:R4:78:ARG:HD3	3:R8:163:ASN:CG	2.40	0.46
3:R8:20:THR:OG1	3:R8:21:PHE:N	2.48	0.46
2:T3:5:LEU:HD11	2:T3:7:MET:CE	2.41	0.46
3:T8:29:PHE:HB2	3:T8:63:PRO:O	2.16	0.46
2:U4:21:ASP:OD2	2:U4:25:LYS:NZ	2.38	0.46
3:U8:8:TYR:HE2	3:U8:93:LEU:HD23	1.79	0.46
3:U8:13:ALA:HA	3:U8:35:GLN:O	2.16	0.46
2:V4:47:ARG:NH1	2:V4:89:LEU:HB3	2.30	0.46
3:W8:21:PHE:CE2	3:W8:169:VAL:HB	2.50	0.46
3:18:93:LEU:HD12	3:18:94:ASP:N	2.30	0.46
2:23:5:LEU:HD21	2:23:7:MET:HE2	1.97	0.46
3:28:142:ILE:HA	3:28:178:LEU:O	2.15	0.46
3:48:183:SER:O	3:48:187:ILE:HG12	2.16	0.46
2:A4:25:LYS:O	2:A5:25:LYS:HE3	2.16	0.46
2:B2:32:ILE:CD1	2:B2:90:GLY:HA3	2.45	0.46
2:B5:90:GLY:O	2:B5:91:ARG:HG2	2.15	0.46
2:C2:20:ALA:O	2:C2:24:VAL:HG23	2.16	0.46
2:C2:30:GLU:OE1	2:C2:91:ARG:NH2	2.39	0.46
2:C3:21:ASP:OD1	2:C3:25:LYS:HE3	2.16	0.46
1:D1:2:VAL:CG2	1:D1:57:TYR:CE1	2.98	0.46
2:D2:29:VAL:HG11	2:D2:46:VAL:CG2	2.43	0.46
2:D2:32:ILE:HD11	2:D2:90:GLY:HA3	1.98	0.46
2:F6:32:ILE:HD11	2:F6:47:ARG:HD2	1.97	0.46
2:G5:34:TYR:OH	2:G6:35:GLU:OE2	2.17	0.46
2:G6:61:GLN:OE1	2:G6:73:VAL:HG21	2.15	0.46
3:G8:111:HIS:HB3	3:G8:143:LEU:HD13	1.96	0.46
3:H8:134:ILE:HD11	3:H8:140:LEU:HD13	1.97	0.46
3:J8:17:GLN:HE21	3:J8:166:LEU:HB2	1.81	0.46
3:J8:126:ASN:O	3:J8:129:SER:HB3	2.15	0.46
3:K8:7:THR:OG1	3:K8:41:GLU:N	2.49	0.46
1:L1:64:ARG:HH11	1:21:62:SER:CB	2.28	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M9:65:VAL:O	3:M9:75:LEU:HA	2.15	0.46
2:N4:16:MET:HG3	2:N4:42:VAL:HG12	1.96	0.46
2:N7:92:THR:O	2:N7:94:GLY:N	2.49	0.46
2:O6:14:VAL:HG23	2:O7:9:GLU:HB2	1.96	0.46
2:P7:2:ALA:O	2:P7:45:ARG:NE	2.42	0.46
2:Q2:16:MET:HG2	2:Q2:44:ALA:HB2	1.97	0.46
2:R3:26:ALA:O	3:R8:12:ASP:HB3	2.15	0.46
3:R8:112:GLN:CD	3:S8:50:ARG:HE	2.14	0.46
3:U8:21:PHE:CE2	3:U8:169:VAL:HB	2.50	0.46
3:U8:21:PHE:HE2	3:U8:169:VAL:HB	1.80	0.46
3:U9:87:ALA:O	3:U9:91:THR:N	2.38	0.46
1:V1:47:VAL:CG1	1:W1:14:ARG:HG3	2.46	0.46
2:W4:16:MET:HG2	2:W4:44:ALA:HB2	1.97	0.46
2:W7:92:THR:O	2:W7:94:GLY:N	2.48	0.46
2:X3:13:PHE:HD2	2:X4:43:THR:HG21	1.79	0.46
2:X3:49:ASP:N	2:X3:49:ASP:OD1	2.49	0.46
1:Y1:66:THR:O	1:Y1:69:THR:OG1	2.24	0.46
2:Y4:53:VAL:O	2:Y4:57:THR:OG1	2.25	0.46
3:Y8:93:LEU:HD12	3:Y8:94:ASP:N	2.30	0.46
1:Z1:32:PRO:HG3	1:Z1:87:MET:CE	2.46	0.46
3:Z9:96:LEU:C	3:Z9:98:VAL:H	2.24	0.46
3:18:11:LEU:HD23	3:18:11:LEU:HA	1.67	0.46
3:18:21:PHE:CE2	3:18:169:VAL:HB	2.47	0.46
3:28:38:LEU:O	3:28:76:GLU:HA	2.15	0.46
3:38:65:VAL:HG12	3:38:76:GLU:HB3	1.98	0.46
3:38:127:ARG:O	3:38:127:ARG:HD2	2.16	0.46
3:39:6:ARG:N	3:39:41:GLU:O	2.43	0.46
1:41:63:ALA:HB1	1:41:77:THR:HG22	1.96	0.46
2:C2:16:MET:HG2	2:C2:44:ALA:HB2	1.97	0.46
2:C6:4:ALA:O	2:C6:47:ARG:HG2	2.16	0.46
2:C6:57:THR:HG21	2:C6:75:VAL:HG22	1.96	0.46
1:D1:86:GLU:HG2	1:D1:87:MET:N	2.29	0.46
3:E8:31:PRO:HA	3:E8:78:HIS:CE1	2.50	0.46
3:F8:66:GLN:HG2	3:Q8:124:ILE:HG23	1.97	0.46
3:F9:66:GLN:HA	3:F9:74:LEU:O	2.14	0.46
2:G2:90:GLY:C	2:G2:92:THR:H	2.16	0.46
2:G7:51:ALA:HB2	2:I3:51:ALA:HB2	1.96	0.46
3:G8:167:VAL:HB	3:G8:179:TYR:HB2	1.96	0.46
3:G9:105:LYS:N	3:G9:204:VAL:O	2.36	0.46
2:J3:5:LEU:O	2:J3:53:VAL:HG11	2.15	0.46
2:K3:8:ILE:HG23	2:K3:73:VAL:HG22	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K8:8:TYR:CE2	3:K8:93:LEU:HD23	2.51	0.46
2:L4:20:ALA:HB1	2:L4:31:LEU:HD22	1.97	0.46
2:L4:78:ARG:HD3	3:L8:163:ASN:CG	2.41	0.46
2:L5:9:GLU:HG3	2:L5:43:THR:OG1	2.16	0.46
3:M8:9:ILE:HD13	3:M8:153:LEU:HB2	1.97	0.46
3:M8:15:GLN:HG2	3:M8:156:ASN:OD1	2.16	0.46
1:N1:66:THR:HG22	1:N1:67:GLU:O	2.16	0.46
1:N1:86:GLU:HG2	1:N1:87:MET:N	2.31	0.46
2:N7:21:ASP:OD1	2:N7:25:LYS:HE3	2.15	0.46
3:N8:116:ALA:HA	3:N8:137:GLY:HA2	1.96	0.46
2:O7:53:VAL:HA	2:O7:56:ALA:HB3	1.95	0.46
2:Q6:13:PHE:N	2:Q7:9:GLU:OE2	2.38	0.46
3:R8:118:GLU:HG3	3:R8:119:ALA:N	2.30	0.46
3:R8:164:VAL:HG21	3:R8:190:ALA:HB2	1.97	0.46
3:S9:87:ALA:O	3:S9:91:THR:N	2.40	0.46
2:U2:68:GLY:O	2:U2:70:VAL:HG23	2.16	0.46
3:Y8:7:THR:OG1	3:Y8:41:GLU:N	2.49	0.46
3:Y8:150:TYR:O	3:Y8:153:LEU:HB3	2.14	0.46
3:Z8:7:THR:HG21	3:Z8:149:GLY:HA3	1.96	0.46
1:11:2:VAL:HG23	1:11:57:TYR:CE1	2.51	0.46
3:19:5:LEU:O	3:19:103:ARG:HA	2.15	0.46
1:31:31:ASP:CG	1:31:32:PRO:HD2	2.41	0.46
2:32:5:LEU:HD23	2:32:76:ILE:HD12	1.96	0.46
3:38:170:THR:HG1	3:38:177:ARG:H	1.58	0.46
1:41:45:ASP:OD1	1:41:46:ALA:N	2.48	0.46
2:45:34:TYR:CE2	2:45:36:LYS:HE3	2.50	0.46
2:A5:60:GLY:O	2:A5:64:ALA:N	2.47	0.46
3:C8:20:THR:OG1	3:C8:21:PHE:N	2.49	0.46
3:C8:29:PHE:HB2	3:C8:63:PRO:O	2.16	0.46
2:E2:32:ILE:HD13	2:E2:90:GLY:HA3	1.97	0.46
3:E8:20:THR:OG1	3:E8:21:PHE:N	2.49	0.46
3:E8:38:LEU:O	3:E8:76:GLU:HA	2.15	0.46
2:G5:90:GLY:O	2:G5:91:ARG:HG2	2.15	0.46
1:H1:1:MET:SD	1:Z1:74:VAL:HG23	2.56	0.46
2:I6:3:ASP:O	2:I6:47:ARG:NH1	2.42	0.46
2:J6:3:ASP:HB2	2:J6:47:ARG:HH11	1.81	0.46
3:J8:121:GLN:O	3:J8:125:ILE:HG13	2.16	0.46
2:K2:74:HIS:NE2	2:K4:18:GLU:OE1	2.44	0.46
2:K6:57:THR:HG21	2:K6:75:VAL:HG22	1.98	0.46
2:M5:9:GLU:HG3	2:M5:43:THR:OG1	2.16	0.46
3:M8:53:ASP:O	3:M8:57:LYS:N	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N1:45:ASP:OD1	1:N1:46:ALA:N	2.48	0.46
2:N6:32:ILE:CD1	2:N6:47:ARG:HD2	2.44	0.46
1:O1:50:GLY:N	1:O1:53:GLU:OE1	2.28	0.46
2:O3:47:ARG:NH1	2:O3:79:PRO:HG2	2.23	0.46
2:P4:16:MET:HG3	2:P4:42:VAL:HG12	1.96	0.46
3:Q8:152:VAL:CG2	3:Q8:171:PRO:HG3	2.45	0.46
1:R1:81:ILE:HD12	2:R5:77:PRO:HG2	1.98	0.46
2:S5:10:VAL:HG13	2:S5:69:GLU:O	2.16	0.46
2:S5:90:GLY:O	2:S5:91:ARG:HG2	2.16	0.46
2:T2:90:GLY:C	2:T2:92:THR:H	2.17	0.46
2:T2:92:THR:O	2:T2:94:GLY:N	2.43	0.46
3:T8:24:LYS:HE2	3:T9:122:THR:O	2.15	0.46
2:U3:13:PHE:HB2	2:U4:37:THR:HG21	1.98	0.46
2:V6:47:ARG:HH22	2:V6:79:PRO:HG3	1.80	0.46
3:V8:169:VAL:HG12	3:V8:171:PRO:HD3	1.96	0.46
2:W2:32:ILE:HD13	2:W2:89:LEU:O	2.16	0.46
2:W3:5:LEU:HD21	2:W3:7:MET:HE2	1.97	0.46
2:W6:55:ALA:HB1	3:W8:115:ARG:HD2	1.98	0.46
3:W8:125:ILE:HD12	3:W8:134:ILE:HD12	1.98	0.46
3:X8:27:ARG:CD	3:48:127:ARG:HD3	2.45	0.46
2:Y3:26:ALA:O	3:Y8:12:ASP:HB3	2.15	0.46
3:Y8:169:VAL:HG22	3:Y8:178:LEU:HD13	1.98	0.46
3:Z8:63:PRO:HA	3:Z8:77:VAL:HA	1.98	0.46
3:19:126:ASN:CB	3:19:134:ILE:H	2.28	0.46
1:21:28:ARG:NH1	1:21:36:PRO:HB2	2.31	0.46
3:28:127:ARG:HD3	3:28:127:ARG:C	2.40	0.46
3:28:141:PHE:HB3	3:28:180:LEU:HB2	1.96	0.46
1:31:45:ASP:OD1	1:31:48:GLY:N	2.41	0.46
3:48:107:GLN:O	3:48:145:THR:HA	2.16	0.46
1:A1:10:VAL:HG13	1:E1:82:VAL:HG13	1.98	0.46
3:B8:127:ARG:HD2	3:B8:127:ARG:C	2.41	0.46
2:C5:46:VAL:O	2:C5:47:ARG:HG2	2.15	0.46
3:C8:11:LEU:HD23	3:C8:11:LEU:HA	1.76	0.46
1:D1:31:ASP:C	1:D1:33:ASP:H	2.24	0.46
3:D8:61:VAL:HA	3:D8:79:HIS:HB2	1.98	0.46
2:H3:7:MET:HE1	2:Z7:17:VAL:HG11	1.97	0.46
2:H5:11:ARG:O	2:H5:11:ARG:HG2	2.16	0.46
3:H8:70:ARG:HG2	3:H8:173:GLY:N	2.31	0.46
1:I1:71:ASN:O	1:J1:65:GLN:HB3	2.16	0.46
2:I2:16:MET:HG2	2:I2:44:ALA:HB2	1.97	0.46
2:I3:5:LEU:O	2:I3:53:VAL:HG11	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J1:7:VAL:HG11	1:11:87:MET:HE2	1.97	0.46
2:J2:82:ASN:OD1	2:J4:31:LEU:N	2.40	0.46
2:J6:4:ALA:O	2:J6:47:ARG:NH1	2.49	0.46
2:K6:47:ARG:HH22	2:K6:79:PRO:HG3	1.81	0.46
3:M8:93:LEU:HD12	3:M8:94:ASP:N	2.31	0.46
1:N1:64:ARG:C	1:N1:66:THR:H	2.24	0.46
3:O8:60:LYS:HE2	3:O8:84:GLU:OE2	2.16	0.46
2:P2:20:ALA:O	2:P2:24:VAL:HG23	2.16	0.46
2:P4:47:ARG:HH22	2:P4:84:ASP:CG	2.24	0.46
3:P8:140:LEU:HA	3:P8:180:LEU:O	2.15	0.46
3:Q8:124:ILE:HD12	3:Q8:124:ILE:HA	1.79	0.46
3:Q8:148:ALA:O	3:Q8:171:PRO:HA	2.16	0.46
3:Q8:164:VAL:HG21	3:Q8:190:ALA:HB2	1.98	0.46
2:R2:17:VAL:HG21	2:V5:7:MET:HE1	1.98	0.46
2:R7:21:ASP:OD1	2:R7:25:LYS:HE3	2.15	0.46
3:R8:152:VAL:CG2	3:R8:171:PRO:HG3	2.45	0.46
1:T1:58:ALA:HB2	1:T1:79:MET:HE3	1.96	0.46
3:T8:50:ARG:HD2	3:T8:95:LYS:HD3	1.98	0.46
3:T8:93:LEU:O	3:T8:97:GLU:N	2.48	0.46
1:V1:62:SER:HB2	1:W1:64:ARG:HD3	1.98	0.46
2:V3:47:ARG:HH11	2:V3:91:ARG:CB	2.22	0.46
2:V5:60:GLY:O	2:V5:64:ALA:N	2.48	0.46
3:V9:52:THR:O	3:V9:56:LEU:N	2.37	0.46
2:W3:30:GLU:OE1	2:W3:91:ARG:NH2	2.42	0.46
2:W6:14:VAL:HG23	2:W7:9:GLU:HB2	1.97	0.46
1:X1:3:LEU:HB3	1:X1:4:GLY:H	1.50	0.46
1:Y1:45:ASP:OD1	1:Y1:46:ALA:N	2.49	0.46
1:11:31:ASP:C	1:11:33:ASP:H	2.24	0.46
2:33:8:ILE:HG23	2:33:73:VAL:HG22	1.97	0.46
2:33:26:ALA:O	3:38:12:ASP:HB3	2.16	0.46
3:A8:23:GLY:HA3	3:A8:30:LEU:HG	1.98	0.46
2:B6:36:LYS:NZ	2:B7:35:GLU:OE1	2.43	0.46
3:B8:123:GLN:CG	3:B9:23:GLY:HA3	2.46	0.46
3:D8:111:HIS:HA	3:D8:142:ILE:O	2.16	0.46
3:E8:165:HIS:N	3:E8:181:ALA:O	2.38	0.46
2:F7:5:LEU:HD22	2:F7:89:LEU:HD23	1.98	0.46
2:F7:19:ALA:HB2	2:F7:64:ALA:HB2	1.97	0.46
2:G3:21:ASP:OD2	2:G4:76:ILE:HG21	2.15	0.46
2:H5:57:THR:O	2:H5:60:GLY:N	2.48	0.46
2:H6:39:GLY:HA2	2:H7:39:GLY:HA3	1.97	0.46
3:H8:29:PHE:CZ	3:Y8:120:TYR:HD1	2.34	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H8:93:LEU:HD12	3:H8:94:ASP:N	2.31	0.46
3:I8:61:VAL:HA	3:I8:79:HIS:HB2	1.97	0.46
3:I8:147:PRO:HD2	3:I8:150:TYR:CD1	2.51	0.46
2:J5:4:ALA:HB2	2:J5:50:VAL:HA	1.98	0.46
2:K4:78:ARG:HD3	3:K8:163:ASN:CG	2.41	0.46
2:K6:16:MET:O	2:K6:20:ALA:N	2.34	0.46
2:L7:49:ASP:OD1	2:L7:49:ASP:N	2.48	0.46
1:O1:8:GLY:HA3	1:P1:86:GLU:O	2.15	0.46
2:O5:19:ALA:HB2	2:O5:64:ALA:HB2	1.98	0.46
3:O8:7:THR:HG23	3:O8:41:GLU:HB3	1.96	0.46
3:O9:148:ALA:HA	3:O9:176:GLY:N	2.30	0.46
3:Q8:20:THR:OG1	3:Q8:21:PHE:N	2.47	0.46
3:Q8:70:ARG:HE	3:Q8:173:GLY:HA2	1.80	0.46
3:R8:64:ALA:HB3	3:R8:76:GLU:OE1	2.15	0.46
3:S9:148:ALA:HA	3:S9:176:GLY:H	1.80	0.46
2:T5:90:GLY:O	2:T5:91:ARG:HG2	2.16	0.46
2:U6:27:ALA:HA	3:U8:116:ALA:HB2	1.97	0.46
2:V3:9:GLU:OE1	2:W7:13:PHE:N	2.45	0.46
2:V6:19:ALA:HB2	2:V6:64:ALA:HB2	1.97	0.46
3:W8:20:THR:OG1	3:W8:21:PHE:N	2.49	0.46
3:X8:66:GLN:HB3	3:48:124:ILE:HG21	1.98	0.46
2:Z6:55:ALA:HB1	3:Z8:115:ARG:HD2	1.98	0.46
3:Z8:35:GLN:HE22	3:Z8:78:HIS:CE1	2.33	0.46
1:11:32:PRO:HG3	1:11:87:MET:HE3	1.98	0.46
2:16:10:VAL:HG11	2:16:15:GLY:HA3	1.96	0.46
2:16:16:MET:HG2	2:16:44:ALA:HB2	1.98	0.46
1:31:31:ASP:O	1:31:33:ASP:N	2.48	0.46
3:38:21:PHE:O	3:38:25:THR:OG1	2.27	0.46
3:39:8:TYR:HA	3:39:39:TRP:O	2.16	0.46
2:43:5:LEU:HD12	2:43:6:GLY:H	1.80	0.46
3:A8:21:PHE:CE2	3:A8:169:VAL:HB	2.47	0.46
2:C3:4:ALA:HB3	2:C3:48:GLY:O	2.16	0.46
3:E8:60:LYS:CG	2:F7:78:ARG:HD3	2.40	0.46
3:E8:169:VAL:HG22	3:E8:178:LEU:HD13	1.97	0.46
3:F8:8:TYR:HB3	3:F8:103:ARG:HD2	1.96	0.46
3:H8:168:ASN:O	3:H8:178:LEU:HD12	2.16	0.46
2:I5:18:GLU:CD	2:I6:74:HIS:HE2	2.24	0.46
3:I8:93:LEU:HD12	3:I8:94:ASP:N	2.30	0.46
1:J1:63:ALA:HB1	1:J1:77:THR:HG22	1.98	0.46
2:J3:31:LEU:HD12	2:J3:45:VAL:O	2.16	0.46
1:K1:2:VAL:CG2	1:K1:57:TYR:CE1	2.99	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K6:16:MET:HG2	2:K6:44:ALA:HB2	1.97	0.46
3:K8:53:ASP:O	3:K8:57:LYS:N	2.29	0.46
1:L1:68:VAL:HA	1:L1:72:ARG:NH1	2.29	0.46
2:M6:61:GLN:CD	2:M6:73:VAL:HG21	2.41	0.46
2:N5:57:THR:O	2:N5:60:GLY:N	2.44	0.46
3:N8:18:LEU:HD11	3:N8:156:ASN:HA	1.98	0.46
3:N8:127:ARG:HH21	3:P8:67:VAL:HG12	1.79	0.46
3:N8:165:HIS:N	3:N8:181:ALA:O	2.38	0.46
1:O1:2:VAL:HG23	1:O1:57:TYR:CE1	2.51	0.46
1:O1:61:SER:HB2	1:P1:61:SER:HB3	1.97	0.46
1:P1:31:ASP:C	1:P1:33:ASP:H	2.24	0.46
2:T5:4:ALA:O	2:T5:47:ARG:NE	2.49	0.46
2:U2:9:GLU:HB2	2:U4:14:VAL:HG23	1.97	0.46
2:U3:5:LEU:HD12	2:U3:6:GLY:H	1.81	0.46
3:U8:12:ASP:O	3:U8:82:GLN:NE2	2.49	0.46
3:W8:11:LEU:HD23	3:W8:11:LEU:HA	1.77	0.46
3:W9:151:ALA:HB2	3:W9:176:GLY:HA3	1.96	0.46
3:Y8:38:LEU:O	3:Y8:76:GLU:HA	2.15	0.46
3:Z8:20:THR:OG1	3:Z8:21:PHE:N	2.48	0.46
3:18:62:GLN:O	3:18:78:HIS:N	2.42	0.46
2:24:78:ARG:NH2	3:28:159:GLU:OE2	2.49	0.46
2:25:9:GLU:HG3	2:25:43:THR:OG1	2.16	0.46
2:25:52:ALA:O	2:25:56:ALA:N	2.49	0.46
3:28:74:LEU:CD2	3:28:171:PRO:HB2	2.46	0.46
2:D7:27:ALA:HB1	2:D7:52:ALA:HB1	1.98	0.46
1:E1:45:ASP:OD1	1:E1:46:ALA:N	2.49	0.46
2:E6:61:GLN:CD	2:E6:73:VAL:HG21	2.41	0.46
3:E8:21:PHE:HE2	3:E8:169:VAL:HB	1.80	0.46
2:F4:78:ARG:HD3	3:F8:163:ASN:CG	2.41	0.46
1:G1:10:VAL:HG22	1:W1:85:VAL:HG22	1.97	0.46
2:G5:37:THR:OG1	2:W2:40:GLY:HA2	2.16	0.46
2:H2:58:GLU:HB3	1:Z1:21:GLY:HA2	1.97	0.46
2:I2:37:THR:OG1	2:I4:40:GLY:HA2	2.15	0.46
2:I3:5:LEU:HD12	2:I3:6:GLY:H	1.80	0.46
2:I4:8:ILE:HD12	2:I4:73:VAL:HG22	1.97	0.46
3:J8:18:LEU:HD11	3:J8:156:ASN:HA	1.96	0.46
1:L1:73:PRO:O	1:21:79:MET:HE1	2.16	0.46
2:L3:47:ARG:NH2	2:L3:79:PRO:HG2	2.27	0.46
2:L7:17:VAL:CG1	2:23:7:MET:HE1	2.46	0.46
3:L8:19:ALA:HB3	3:L8:33:PRO:HG3	1.96	0.46
3:L8:23:GLY:HA2	3:L8:30:LEU:HG	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M8:29:PHE:CZ	3:28:120:TYR:HD1	2.34	0.46
1:O1:10:VAL:HG13	1:P1:82:VAL:HG13	1.97	0.46
1:O1:80:ALA:HA	1:31:14:ARG:O	2.15	0.46
2:P4:20:ALA:O	2:P4:24:VAL:HG22	2.16	0.46
1:Q1:70:ASN:C	1:Q1:72:ARG:H	2.23	0.46
2:T5:14:VAL:HG13	2:T6:7:MET:HE3	1.97	0.46
2:T5:21:ASP:OD1	2:T5:25:LYS:HD2	2.16	0.46
2:W7:47:ARG:NH1	2:W7:89:LEU:O	2.47	0.46
1:X1:16:GLU:OE1	1:X1:17:PRO:N	2.49	0.46
1:Z1:27:VAL:O	1:Z1:41:VAL:HG12	2.16	0.46
2:15:10:VAL:HG13	2:15:69:GLU:O	2.16	0.46
2:16:55:ALA:HB1	3:18:115:ARG:HD2	1.97	0.46
3:18:9:ILE:O	3:18:38:LEU:HD12	2.15	0.46
3:18:128:ASN:O	3:18:130:GLN:N	2.47	0.46
3:28:123:GLN:HE22	3:29:30:LEU:CB	2.29	0.46
2:42:47:ARG:NH2	2:42:84:ASP:OD1	2.48	0.46
2:44:16:MET:HE3	2:44:16:MET:HB3	1.91	0.46
3:48:53:ASP:O	3:48:57:LYS:N	2.22	0.46
2:A4:54:LYS:HD2	2:A4:75:VAL:HG21	1.98	0.45
3:A9:145:THR:O	3:A9:176:GLY:N	2.49	0.45
3:C8:20:THR:HG21	3:C9:135:LEU:HA	1.98	0.45
3:C8:27:ARG:HB2	3:M8:127:ARG:HE	1.81	0.45
2:D2:29:VAL:CG1	2:D2:46:VAL:CG2	2.93	0.45
3:D8:64:ALA:HB3	3:D8:76:GLU:OE1	2.16	0.45
1:E1:63:ALA:HB1	1:E1:77:THR:HG22	1.97	0.45
3:F8:20:THR:O	3:F8:23:GLY:N	2.50	0.45
3:G8:20:THR:HB	3:G8:24:LYS:HZ1	1.81	0.45
3:I9:8:TYR:HA	3:I9:40:VAL:HA	1.97	0.45
2:J7:17:VAL:HG11	2:13:7:MET:HE1	1.98	0.45
2:K5:57:THR:O	2:K5:60:GLY:N	2.49	0.45
1:M1:86:GLU:HG2	1:M1:87:MET:N	2.31	0.45
2:M7:2:ALA:N	2:M7:84:ASP:OD2	2.49	0.45
2:N7:50:VAL:HG21	2:N7:77:PRO:HB3	1.97	0.45
3:N8:21:PHE:CE2	3:N8:169:VAL:HB	2.50	0.45
3:N8:123:GLN:HG3	3:N9:23:GLY:HA3	1.97	0.45
3:O9:145:THR:O	3:O9:176:GLY:N	2.37	0.45
2:Q4:78:ARG:HD3	3:Q8:163:ASN:OD1	2.16	0.45
2:R7:74:HIS:CG	2:R7:75:VAL:H	2.33	0.45
3:R8:31:PRO:HB3	3:R8:78:HIS:CG	2.51	0.45
3:R8:145:THR:HG21	3:R8:198:ILE:HG21	1.98	0.45
2:S5:57:THR:O	2:S5:60:GLY:N	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S7:10:VAL:HG11	2:S7:15:GLY:HA3	1.98	0.45
2:T5:37:THR:OG1	2:U2:40:GLY:HA2	2.16	0.45
2:U6:45:VAL:HG11	2:U6:89:LEU:HD22	1.97	0.45
2:U7:20:ALA:HB1	2:U7:31:LEU:HD22	1.96	0.45
2:V7:28:LYS:HA	2:43:78:ARG:HH11	1.76	0.45
3:V8:17:GLN:O	3:V8:20:THR:OG1	2.26	0.45
1:Z1:19:ILE:O	1:Z1:22:LEU:HB2	2.15	0.45
2:Z6:32:ILE:CD1	2:Z6:47:ARG:HD2	2.46	0.45
2:14:3:ASP:OD2	2:14:91:ARG:NE	2.49	0.45
2:32:85:ALA:HA	2:32:92:THR:HG23	1.96	0.45
2:35:9:GLU:HG3	2:35:43:THR:OG1	2.16	0.45
3:48:41:GLU:OE1	3:48:147:PRO:HB2	2.17	0.45
3:A8:6:ARG:NH1	3:A8:72:TYR:OH	2.47	0.45
3:B8:126:ASN:O	3:B8:129:SER:HB3	2.16	0.45
2:C2:13:PHE:CE2	2:D5:35:GLU:HG2	2.50	0.45
2:D3:17:MET:HG2	2:D3:45:ALA:HB2	1.97	0.45
2:F3:13:PHE:HB2	2:F4:37:THR:CG2	2.41	0.45
3:F8:41:GLU:OE1	3:F8:147:PRO:HB2	2.16	0.45
1:H1:19:ILE:O	1:H1:22:LEU:HB2	2.16	0.45
1:I1:45:ASP:OD1	1:I1:48:GLY:N	2.44	0.45
2:I3:30:GLU:OE1	2:I3:91:ARG:NH2	2.46	0.45
2:I5:14:VAL:HG13	2:I6:7:MET:HE3	1.99	0.45
1:J1:2:VAL:HG23	1:J1:57:TYR:CE1	2.51	0.45
2:K5:90:GLY:O	2:K5:91:ARG:HG2	2.15	0.45
3:K8:18:LEU:O	3:K8:22:ILE:N	2.34	0.45
3:L8:11:LEU:HD23	3:L8:11:LEU:HA	1.79	0.45
2:M7:60:GLY:O	2:M7:64:ALA:N	2.43	0.45
3:M8:9:ILE:CD1	3:M8:150:TYR:HA	2.46	0.45
2:N4:30:GLU:OE1	2:N4:91:ARG:NH1	2.49	0.45
2:N5:2:ALA:HB3	2:N5:78:ARG:NH1	2.31	0.45
2:O3:5:LEU:HD21	2:O3:7:MET:HE2	1.98	0.45
2:O7:54:LYS:O	2:O7:58:GLU:HG2	2.16	0.45
2:P5:90:GLY:O	2:P5:91:ARG:HG2	2.17	0.45
3:P8:42:ILE:CD1	3:P8:96:LEU:HD11	2.46	0.45
2:T6:56:ALA:O	2:T6:60:GLY:N	2.47	0.45
2:U2:8:ILE:HG12	2:U2:73:VAL:HG22	1.97	0.45
2:U5:83:VAL:HG13	2:U5:87:LEU:HD12	1.97	0.45
2:X7:57:THR:HG21	2:X7:75:VAL:HG22	1.98	0.45
3:Y8:79:HIS:CE1	3:Y8:81:ASP:H	2.34	0.45
3:18:11:LEU:HD13	3:18:14:LEU:HD21	1.99	0.45
2:26:4:ALA:O	2:26:47:ARG:NH1	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:26:13:PHE:N	2:27:9:GLU:OE2	2.40	0.45
3:28:15:GLN:HG2	3:28:156:ASN:OD1	2.17	0.45
3:28:29:PHE:HB2	3:28:63:PRO:O	2.16	0.45
1:31:86:GLU:HG2	1:31:87:MET:N	2.31	0.45
2:35:61:GLN:HG3	2:35:70:VAL:HG11	1.98	0.45
2:36:16:MET:HG3	2:36:42:VAL:HG12	1.98	0.45
3:38:35:GLN:HA	3:38:80:PHE:HA	1.98	0.45
3:48:11:LEU:HD21	3:48:153:LEU:HA	1.99	0.45
3:48:121:GLN:O	3:48:125:ILE:HG13	2.16	0.45
1:A1:70:ASN:C	1:A1:72:ARG:H	2.24	0.45
3:A9:39:TRP:HA	3:A9:76:GLU:HA	1.98	0.45
1:B1:45:ASP:OD1	1:B1:47:VAL:N	2.39	0.45
3:B8:58:ALA:HA	2:L6:25:LYS:HZ3	1.81	0.45
3:C8:23:GLY:HA2	3:C8:30:LEU:HG	1.98	0.45
1:D1:32:PRO:HG3	1:D1:87:MET:HE1	1.99	0.45
3:D8:93:LEU:HD12	3:D8:94:ASP:N	2.31	0.45
2:G7:29:VAL:HG11	2:G7:46:VAL:HB	1.98	0.45
3:G8:106:PRO:HG3	3:G8:150:TYR:CE2	2.51	0.45
2:H3:61:GLN:HB2	2:H3:73:VAL:HG21	1.98	0.45
2:I4:21:ASP:OD1	2:I4:25:LYS:HD2	2.17	0.45
3:I8:123:GLN:HG3	3:I9:23:GLY:HA3	1.99	0.45
3:M8:45:GLY:HA2	3:M8:48:ILE:HD13	1.99	0.45
3:O8:42:ILE:CD1	3:O8:96:LEU:HD11	2.46	0.45
1:P1:86:GLU:HG2	1:P1:87:MET:N	2.30	0.45
2:P3:32:ILE:HD11	2:P3:45:VAL:HG11	1.97	0.45
1:Q1:22:LEU:HG	1:Q1:44:ALA:HB1	1.99	0.45
3:S8:9:ILE:HD12	3:S8:150:TYR:HA	1.98	0.45
3:S8:31:PRO:HD3	3:S8:64:ALA:HB2	1.97	0.45
3:T8:152:VAL:HA	3:T8:155:ALA:HB3	1.99	0.45
2:U5:13:PHE:N	2:U6:9:GLU:OE2	2.39	0.45
3:U8:111:HIS:CG	3:U8:111:HIS:O	2.68	0.45
1:V1:2:VAL:CG2	1:V1:57:TYR:CZ	2.99	0.45
2:W2:4:ALA:HB2	2:W2:50:VAL:HA	1.98	0.45
1:X1:32:PRO:HG3	1:X1:87:MET:CE	2.46	0.45
3:Y8:53:ASP:O	3:Y8:56:LEU:N	2.49	0.45
2:15:41:TYR:N	2:15:41:TYR:CD1	2.85	0.45
2:24:53:VAL:O	2:24:57:THR:OG1	2.30	0.45
3:38:48:ILE:O	3:38:52:THR:OG1	2.31	0.45
2:46:32:ILE:HD11	2:46:47:ARG:HD2	1.97	0.45
2:47:53:VAL:HA	2:47:56:ALA:HB3	1.98	0.45
3:48:194:ALA:O	3:48:198:ILE:HG12	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A8:33:PRO:HA	3:A8:34:GLY:HA2	1.50	0.45
2:D3:52:ALA:HB2	2:P7:49:ALA:CB	2.47	0.45
3:D8:45:GLY:HA3	3:D8:72:TYR:HB2	1.97	0.45
2:E4:78:ARG:HD3	3:E8:163:ASN:CG	2.41	0.45
3:E8:167:VAL:HB	3:E8:179:TYR:HB2	1.98	0.45
2:G3:10:VAL:O	2:G3:12:GLY:N	2.49	0.45
3:G8:22:ILE:O	3:G8:25:THR:OG1	2.30	0.45
2:H3:13:PHE:HB2	2:H4:37:THR:HG21	1.99	0.45
2:H6:21:ASP:OD1	2:H6:25:LYS:HE3	2.15	0.45
3:H8:8:TYR:HA	3:H8:40:VAL:HG22	1.99	0.45
3:H8:24:LYS:NZ	3:H9:134:ILE:O	2.50	0.45
2:J3:21:ASP:OD2	2:J4:76:ILE:HG21	2.16	0.45
2:J4:20:ALA:O	2:J4:24:VAL:HG22	2.17	0.45
2:K2:90:GLY:C	2:K2:92:THR:H	2.16	0.45
2:L3:12:GLY:HA2	2:L4:9:GLU:OE2	2.15	0.45
2:M2:8:ILE:HG12	2:M2:73:VAL:HG22	1.97	0.45
2:M5:89:LEU:C	2:M5:91:ARG:H	2.25	0.45
2:N5:60:GLY:O	2:N5:64:ALA:N	2.43	0.45
3:N8:186:GLU:OE1	3:N8:186:GLU:N	2.33	0.45
3:O8:20:THR:OG1	3:O8:21:PHE:N	2.49	0.45
2:P4:23:MET:HE3	2:P4:46:VAL:CG2	2.46	0.45
2:P5:16:MET:HG2	2:P5:44:ALA:HB2	1.98	0.45
3:Q8:141:PHE:CZ	3:Q8:143:LEU:HB2	2.50	0.45
3:R8:121:GLN:HE22	3:S8:53:ASP:CG	2.16	0.45
3:R8:171:PRO:HD2	3:R8:172:TYR:CD2	2.52	0.45
2:S6:29:VAL:HG11	2:S6:46:VAL:HB	1.98	0.45
3:S8:61:VAL:O	3:S8:62:GLN:HG3	2.16	0.45
2:T7:57:THR:HG21	2:T7:75:VAL:HG22	1.98	0.45
2:U2:45:VAL:HG11	2:U2:89:LEU:HD12	1.98	0.45
3:U8:119:ALA:O	3:U8:122:THR:OG1	2.34	0.45
2:V4:47:ARG:NH2	2:V4:84:ASP:OD1	2.46	0.45
2:W4:20:ALA:HA	2:W4:23:MET:HE3	1.99	0.45
3:W8:61:VAL:CG1	3:W8:77:VAL:HB	2.47	0.45
3:X8:65:VAL:HG12	3:X8:76:GLU:HB3	1.99	0.45
1:Z1:62:SER:OG	1:11:75:ASP:HB3	2.17	0.45
2:Z3:26:ALA:O	3:Z8:12:ASP:HB3	2.16	0.45
2:Z6:10:VAL:HG11	2:Z6:15:GLY:HA3	1.98	0.45
3:Z8:11:LEU:HD23	3:Z8:11:LEU:HA	1.75	0.45
3:18:106:PRO:HG3	3:18:150:TYR:HE2	1.81	0.45
2:25:41:TYR:CD1	2:25:41:TYR:N	2.84	0.45
3:38:35:GLN:HE22	3:38:78:HIS:CE1	2.35	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:42:5:LEU:HB3	2:42:76:ILE:HB	1.99	0.45
3:48:93:LEU:O	3:48:97:GLU:N	2.49	0.45
2:A5:54:LYS:NZ	2:A5:58:GLU:CD	2.74	0.45
1:B1:86:GLU:HG2	1:B1:87:MET:N	2.30	0.45
2:C2:35:GLU:HG2	2:C4:13:PHE:CE2	2.52	0.45
2:C6:4:ALA:HA	2:C6:77:PRO:O	2.16	0.45
3:C8:150:TYR:HE2	3:C8:201:VAL:HG11	1.81	0.45
3:C9:45:GLY:N	3:C9:71:ALA:O	2.50	0.45
3:D8:9:ILE:HD11	3:D8:150:TYR:CD2	2.52	0.45
3:D8:15:GLN:HG3	3:D8:160:LYS:HB2	1.99	0.45
2:E3:45:VAL:HG11	2:E3:89:LEU:HD12	1.98	0.45
2:E6:51:ALA:HB2	3:E8:185:ALA:HB2	1.99	0.45
2:G6:4:ALA:O	2:G6:47:ARG:HG2	2.16	0.45
3:G8:98:VAL:HG12	3:G8:99:ARG:O	2.17	0.45
1:H1:75:ASP:OD1	1:I1:1:MET:N	2.29	0.45
2:I7:47:ARG:HH22	2:I7:84:ASP:CG	2.25	0.45
2:J4:53:VAL:O	2:J4:57:THR:OG1	2.31	0.45
1:K1:73:PRO:O	1:L1:79:MET:HE1	2.17	0.45
2:K7:10:VAL:HG11	2:K7:15:GLY:HA3	1.97	0.45
3:K8:110:THR:OG1	3:18:44:PRO:HG3	2.16	0.45
3:K8:147:PRO:HD2	3:K8:150:TYR:CD1	2.52	0.45
2:N7:27:ALA:O	2:P3:78:ARG:NH1	2.50	0.45
1:O1:62:SER:HB2	1:31:64:ARG:HD3	1.98	0.45
3:P8:24:LYS:HE2	3:P9:122:THR:O	2.17	0.45
3:P9:44:PRO:HA	3:P9:71:ALA:O	2.16	0.45
2:Q7:49:ASP:N	2:Q7:49:ASP:OD1	2.49	0.45
3:R8:121:GLN:O	3:R8:125:ILE:HG13	2.16	0.45
1:S1:45:ASP:OD1	1:S1:46:ALA:N	2.49	0.45
2:W3:23:MET:HG2	2:W3:56:ALA:O	2.16	0.45
2:W6:32:ILE:HG21	2:W6:90:GLY:CA	2.45	0.45
3:W8:117:VAL:HG13	3:W8:121:GLN:HE21	1.82	0.45
1:X1:45:ASP:OD1	1:X1:46:ALA:N	2.49	0.45
3:X8:46:ILE:HG21	3:48:142:ILE:HB	1.98	0.45
2:14:78:ARG:NH2	3:18:159:GLU:OE1	2.49	0.45
3:28:186:GLU:O	3:28:190:ALA:N	2.45	0.45
2:34:82:ASN:HD22	2:34:82:ASN:C	2.20	0.45
3:38:148:ALA:O	3:38:171:PRO:HA	2.16	0.45
3:48:63:PRO:HA	3:48:77:VAL:HA	1.97	0.45
3:B8:7:THR:HG22	3:B8:150:TYR:CD1	2.51	0.45
3:B8:39:TRP:CZ2	3:B8:76:GLU:HG3	2.51	0.45
2:C6:47:ARG:NH2	2:C6:84:ASP:OD1	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C7:78:ARG:HD3	3:28:60:LYS:CG	2.44	0.45
2:D2:13:PHE:HE1	2:E5:7:MET:HE1	1.82	0.45
3:E8:19:ALA:HB3	3:E8:33:PRO:HG3	1.98	0.45
3:E8:100:GLU:O	3:E8:103:ARG:HD3	2.17	0.45
3:E8:123:GLN:HG3	3:E9:23:GLY:HA3	1.97	0.45
1:F1:47:VAL:HG12	1:R1:14:ARG:HG3	1.98	0.45
2:G6:17:VAL:CG2	2:G7:7:MET:HE1	2.44	0.45
3:G8:139:SER:O	3:G8:181:ALA:HA	2.17	0.45
3:I8:59:THR:HB	3:I8:61:VAL:HG23	1.98	0.45
2:J6:4:ALA:HA	2:J6:77:PRO:O	2.17	0.45
2:K2:4:ALA:N	2:K2:48:GLY:O	2.47	0.45
2:L7:19:ALA:HB2	2:L7:64:ALA:HB2	1.98	0.45
2:N7:60:GLY:O	2:N7:64:ALA:N	2.43	0.45
1:O1:70:ASN:O	1:O1:72:ARG:N	2.49	0.45
2:O3:47:ARG:HH22	2:O3:84:ASP:CG	2.23	0.45
2:O5:90:GLY:O	2:O5:91:ARG:HG2	2.16	0.45
3:Q8:122:THR:HG21	3:Q8:136:PRO:CA	2.39	0.45
2:R5:32:ILE:HD11	2:R5:45:VAL:HG12	1.99	0.45
2:R5:90:GLY:O	2:R5:91:ARG:HG2	2.16	0.45
2:S4:16:MET:HG3	2:S4:42:VAL:HG12	1.98	0.45
3:S8:150:TYR:HE2	3:S8:201:VAL:HG11	1.82	0.45
3:S9:88:ALA:O	3:S9:92:ILE:N	2.44	0.45
1:T1:64:ARG:C	1:T1:66:THR:H	2.24	0.45
2:T5:12:GLY:HA2	2:T6:9:GLU:OE2	2.16	0.45
3:T9:10:PHE:HA	3:T9:38:LEU:HA	1.99	0.45
2:U3:47:ARG:HH11	2:U3:91:ARG:CB	2.21	0.45
3:U9:10:PHE:HA	3:U9:38:LEU:HA	1.97	0.45
2:W5:31:LEU:HD12	2:W5:45:VAL:O	2.16	0.45
2:13:84:ASP:O	2:13:92:THR:OG1	2.24	0.45
2:32:29:VAL:CG1	2:32:46:VAL:HB	2.47	0.45
2:34:62:ARG:HD2	2:35:66:ARG:HD2	1.98	0.45
3:A8:122:THR:HG21	3:A8:136:PRO:HA	1.98	0.45
2:B3:47:ARG:NH2	2:B3:79:PRO:HG2	2.28	0.45
2:B7:20:ALA:HB1	2:B7:31:LEU:HD22	1.98	0.45
1:C1:45:ASP:OD1	1:C1:48:GLY:N	2.42	0.45
2:E3:9:GLU:HG3	2:E3:71:VAL:HB	1.98	0.45
2:E4:62:ARG:CZ	2:E5:66:ARG:NH1	2.80	0.45
2:F2:3:ASP:OD2	2:F2:91:ARG:NE	2.47	0.45
2:F6:16:MET:HG3	2:F6:42:VAL:HG12	1.99	0.45
3:F8:45:GLY:HA2	3:F8:48:ILE:HD13	1.98	0.45
3:F8:63:PRO:HB3	3:F8:77:VAL:HG12	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G6:16:MET:HG3	2:G6:42:VAL:HG12	1.99	0.45
2:G6:32:ILE:HD11	2:G6:47:ARG:HD2	1.99	0.45
1:H1:26:LEU:HD12	1:H1:26:LEU:HA	1.83	0.45
2:H5:52:ALA:O	2:H5:56:ALA:N	2.48	0.45
2:H6:55:ALA:HB1	3:H8:115:ARG:HD2	1.98	0.45
3:I8:143:LEU:O	3:I8:177:ARG:HA	2.17	0.45
1:J1:7:VAL:HG12	1:11:87:MET:HG2	1.99	0.45
3:J8:65:VAL:N	3:J8:76:GLU:OE1	2.44	0.45
3:K8:110:THR:O	3:K8:143:LEU:HA	2.17	0.45
3:P9:141:PHE:O	3:P9:179:TYR:HA	2.17	0.45
3:Q8:60:LYS:HB2	3:Q8:84:GLU:HG2	1.99	0.45
1:R1:62:SER:HB2	1:V1:64:ARG:HD3	1.99	0.45
2:R3:4:ALA:HB3	2:R3:48:GLY:O	2.17	0.45
1:S1:64:ARG:C	1:S1:66:THR:H	2.25	0.45
2:S4:47:ARG:NH1	2:S4:89:LEU:HB3	2.32	0.45
2:S4:47:ARG:HH22	2:S4:84:ASP:CG	2.25	0.45
1:T1:2:VAL:CG2	1:T1:57:TYR:CE1	3.00	0.45
1:T1:87:MET:HG3	1:T1:92:ARG:HG3	1.99	0.45
2:T6:10:VAL:HG11	2:T6:15:GLY:HA3	1.98	0.45
2:T6:31:LEU:HD12	2:T6:45:VAL:O	2.16	0.45
3:T8:123:GLN:HG3	3:T9:23:GLY:HA3	1.98	0.45
3:T8:135:LEU:HD22	3:T9:17:GLN:HA	1.99	0.45
3:T8:138:GLU:HB3	3:T8:182:GLY:O	2.17	0.45
2:V4:13:PHE:HD1	2:V4:13:PHE:O	2.00	0.45
2:V6:9:GLU:HB3	2:V6:72:ALA:HB3	1.99	0.45
3:W8:142:ILE:HA	3:W8:178:LEU:O	2.16	0.45
2:X2:47:ARG:NH2	2:X2:79:PRO:HG2	2.32	0.45
3:X8:20:THR:OG1	3:X8:21:PHE:N	2.48	0.45
2:Y7:50:VAL:HG21	2:Y7:77:PRO:HB3	1.99	0.45
3:Z8:39:TRP:CZ2	3:Z8:76:GLU:HG3	2.51	0.45
3:18:138:GLU:HB3	3:18:182:GLY:O	2.17	0.45
2:26:57:THR:HG21	2:26:75:VAL:HG22	1.99	0.45
2:34:70:VAL:O	2:34:70:VAL:HG23	2.16	0.45
1:A1:4:GLY:N	1:A1:55:VAL:O	2.50	0.45
3:C8:60:LYS:CG	2:M7:78:ARG:HD3	2.46	0.45
1:E1:28:ARG:HH11	1:E1:36:PRO:HB2	1.81	0.45
2:G5:12:GLY:HA2	2:G6:9:GLU:OE2	2.17	0.45
3:G8:79:HIS:CE1	3:G8:81:ASP:H	2.34	0.45
1:H1:10:VAL:HG13	1:I1:82:VAL:HG13	1.99	0.45
2:H6:36:LYS:NZ	2:H7:35:GLU:OE1	2.44	0.45
3:H8:133:MET:HE1	3:H9:132:MET:N	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I2:21:ASP:OD2	2:I2:25:LYS:HD2	2.17	0.45
3:I8:147:PRO:HD2	3:I8:150:TYR:CE1	2.52	0.45
2:J2:30:GLU:OE1	2:J2:91:ARG:NH1	2.43	0.45
3:J8:46:ILE:O	3:J8:49:ASN:N	2.50	0.45
2:K3:13:PHE:HB2	2:K4:37:THR:CG2	2.46	0.45
3:K8:104:LEU:HA	3:K8:204:VAL:O	2.17	0.45
3:M8:79:HIS:CG	3:M8:80:PHE:N	2.85	0.45
2:P2:16:MET:HE2	2:P2:42:VAL:HG11	1.99	0.45
1:R1:45:ASP:OD1	1:R1:46:ALA:N	2.49	0.45
2:R2:32:ILE:HD13	2:R2:90:GLY:HA3	1.97	0.45
3:R8:111:HIS:HB3	3:R8:143:LEU:HD13	1.98	0.45
1:T1:22:LEU:HD12	1:T1:22:LEU:HA	1.71	0.45
2:U2:35:GLU:HG2	2:U4:13:PHE:CE1	2.52	0.45
2:U7:23:MET:HG2	2:U7:56:ALA:O	2.17	0.45
3:U8:48:ILE:HG22	3:U8:66:GLN:HE22	1.82	0.45
2:V6:61:GLN:O	2:V6:65:GLU:HG3	2.17	0.45
3:V8:64:ALA:HB3	3:V8:76:GLU:OE2	2.16	0.45
3:V8:79:HIS:CG	3:V8:80:PHE:N	2.84	0.45
3:V9:39:TRP:HA	3:V9:76:GLU:HA	1.98	0.45
3:W8:177:ARG:HG2	3:Y8:46:ILE:HD11	1.99	0.45
3:W9:44:PRO:HA	3:W9:71:ALA:O	2.17	0.45
2:X5:35:GLU:OE2	2:Y2:36:LYS:NZ	2.33	0.45
1:Y1:31:ASP:O	1:Y1:33:ASP:N	2.48	0.45
2:Z3:16:MET:HB2	2:Z3:42:VAL:HG23	1.97	0.45
2:12:45:VAL:HG11	2:12:89:LEU:HD12	1.99	0.45
2:16:4:ALA:O	2:16:47:ARG:NH2	2.50	0.45
2:17:49:ASP:N	2:17:49:ASP:OD1	2.48	0.45
3:18:64:ALA:N	3:18:76:GLU:OE2	2.39	0.45
1:21:68:VAL:C	1:21:72:ARG:NH1	2.73	0.45
3:28:7:THR:HG23	3:28:41:GLU:HB3	1.98	0.45
2:34:62:ARG:CZ	2:35:66:ARG:NH1	2.80	0.45
3:38:79:HIS:HD1	3:38:81:ASP:H	1.65	0.45
3:38:132:MET:SD	3:39:133:MET:N	2.83	0.45
2:45:20:ALA:HB1	2:45:31:LEU:HD21	1.99	0.45
3:48:123:GLN:HE22	3:49:30:LEU:CB	2.29	0.45
2:A2:13:PHE:HB2	2:B5:37:THR:HG21	1.98	0.45
2:A5:9:GLU:OE1	2:E2:13:PHE:N	2.50	0.45
3:A8:93:LEU:HD12	3:A8:94:ASP:N	2.32	0.45
3:B8:130:GLN:OE1	3:B8:168:ASN:HB3	2.17	0.45
1:C1:22:LEU:HD12	1:C1:22:LEU:HA	1.82	0.45
3:D8:11:LEU:HD12	3:D8:39:TRP:NE1	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D8:112:GLN:CD	3:N8:50:ARG:HH21	2.25	0.45
2:E3:5:LEU:O	2:E3:53:VAL:HG11	2.16	0.45
3:E8:35:GLN:HE22	3:E8:78:HIS:CE1	2.35	0.45
2:G7:49:ASP:OD1	2:G7:49:ASP:N	2.45	0.45
2:H5:28:LYS:H	2:H5:28:LYS:HG2	1.48	0.45
3:H8:123:GLN:HE21	3:H8:123:GLN:HB3	1.57	0.45
3:I8:55:ALA:O	3:I8:59:THR:OG1	2.35	0.45
3:I8:186:GLU:OE1	3:I8:186:GLU:N	2.37	0.45
2:J5:21:ASP:OD1	2:J5:25:LYS:HD2	2.17	0.45
3:J8:20:THR:OG1	3:J8:21:PHE:N	2.49	0.45
3:J8:93:LEU:HD12	3:J8:94:ASP:N	2.31	0.45
1:K1:7:VAL:HG12	1:L1:87:MET:HG2	1.99	0.45
1:K1:28:ARG:HH12	1:K1:36:PRO:HB2	1.78	0.45
1:M1:7:VAL:HG12	1:N1:87:MET:HG2	1.99	0.45
2:M2:7:MET:HE1	2:M4:17:VAL:HB	1.98	0.45
3:M8:186:GLU:OE1	3:M8:186:GLU:N	2.33	0.45
2:P4:78:ARG:HD3	3:P8:163:ASN:OD1	2.16	0.45
3:Q8:23:GLY:CA	3:Q8:30:LEU:HG	2.46	0.45
1:R1:31:ASP:O	1:R1:33:ASP:N	2.46	0.45
3:S8:107:GLN:O	3:S8:145:THR:HA	2.17	0.45
1:T1:25:LEU:HD23	1:T1:25:LEU:HA	1.77	0.45
3:T8:93:LEU:HD12	3:T8:94:ASP:N	2.32	0.45
2:U3:84:ASP:HB3	2:U3:91:ARG:O	2.16	0.45
2:V3:4:ALA:HB3	2:V3:48:GLY:O	2.17	0.45
2:V3:10:VAL:O	2:V3:12:GLY:N	2.49	0.45
3:V8:60:LYS:CG	2:X7:78:ARG:HD3	2.44	0.45
3:V8:61:VAL:HG11	3:V8:77:VAL:HB	1.99	0.45
2:W7:78:ARG:HD3	3:Y8:60:LYS:CG	2.36	0.45
2:X7:21:ASP:OD1	2:X7:25:LYS:HE3	2.17	0.45
3:X8:148:ALA:O	3:X8:171:PRO:HA	2.17	0.45
3:Y8:126:ASN:O	3:Y8:129:SER:HB3	2.16	0.45
1:Z1:26:LEU:HD12	1:Z1:26:LEU:HA	1.79	0.45
3:Z8:47:ALA:HB1	3:Z8:50:ARG:HH12	1.82	0.45
3:38:8:TYR:O	3:38:103:ARG:NH1	2.50	0.45
1:41:32:PRO:HG3	1:41:87:MET:CE	2.47	0.45
2:46:56:ALA:O	2:46:60:GLY:N	2.48	0.45
2:B7:19:ALA:HB2	2:B7:64:ALA:HB2	1.99	0.45
3:B8:50:ARG:NH2	3:L8:112:GLN:OE1	2.50	0.45
3:C8:123:GLN:NE2	3:C9:31:PRO:O	2.49	0.45
2:D2:20:ALA:O	2:D2:24:VAL:HG23	2.17	0.45
2:D6:84:ASP:O	2:D6:92:THR:HG23	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E7:21:ASP:OD1	2:E7:25:LYS:HE3	2.17	0.45
2:F7:17:VAL:CG1	2:G3:7:MET:HE1	2.47	0.45
2:G7:87:LEU:HB3	2:G7:89:LEU:CD1	2.47	0.45
2:I4:78:ARG:HD3	3:I8:163:ASN:CG	2.42	0.45
3:I9:144:GLU:HA	3:I9:176:GLY:O	2.17	0.45
3:J8:7:THR:OG1	3:J8:41:GLU:N	2.50	0.45
3:K8:120:TYR:CD1	3:18:29:PHE:CZ	3.05	0.45
1:L1:45:ASP:OD1	1:L1:47:VAL:N	2.37	0.45
2:L5:13:PHE:HB2	2:L6:37:THR:HG21	1.98	0.45
2:L7:78:ARG:NH1	2:L7:78:ARG:HG3	2.32	0.45
2:N3:13:PHE:HB2	2:N4:37:THR:CG2	2.46	0.45
3:N8:93:LEU:O	3:N8:97:GLU:N	2.50	0.45
3:O8:95:LYS:HE3	3:O8:95:LYS:HB2	1.81	0.45
3:U8:52:THR:O	3:U8:56:LEU:HB2	2.17	0.45
1:V1:66:THR:O	1:V1:69:THR:OG1	2.19	0.45
3:V8:21:PHE:HE2	3:V8:169:VAL:HB	1.81	0.45
2:X6:12:GLY:HA2	2:X7:9:GLU:OE2	2.17	0.45
3:X8:118:GLU:HG3	3:X8:119:ALA:N	2.32	0.45
3:X8:122:THR:HG22	3:X8:134:ILE:HG22	1.99	0.45
2:12:29:VAL:HG11	2:12:46:VAL:HB	1.99	0.45
3:18:141:PHE:CZ	3:18:143:LEU:HB2	2.51	0.45
3:28:122:THR:O	3:28:126:ASN:ND2	2.49	0.45
3:28:125:ILE:HD12	3:28:134:ILE:HD12	1.98	0.45
2:32:90:GLY:O	2:32:92:THR:N	2.50	0.45
3:48:11:LEU:HD23	3:48:11:LEU:HA	1.72	0.45
1:A1:54:VAL:O	1:A1:82:VAL:HG23	2.17	0.44
2:B3:8:ILE:HD12	2:B3:19:ALA:HB1	1.99	0.44
1:E1:31:ASP:C	1:E1:33:ASP:H	2.24	0.44
1:E1:64:ARG:C	1:E1:66:THR:H	2.24	0.44
1:E1:68:VAL:C	1:E1:72:ARG:NH1	2.76	0.44
3:G8:3:ILE:HG23	3:G8:44:PRO:HD2	1.99	0.44
3:H8:79:HIS:CE1	3:H8:81:ASP:H	2.35	0.44
3:H8:118:GLU:HG3	3:H8:119:ALA:N	2.32	0.44
2:I4:4:ALA:O	2:I4:47:ARG:NE	2.47	0.44
3:K8:118:GLU:HG3	3:K8:119:ALA:N	2.32	0.44
2:M6:55:ALA:HB1	3:M8:115:ARG:HD2	1.98	0.44
3:M8:67:VAL:HB	3:M8:69:GLU:HG2	1.99	0.44
2:N2:4:ALA:O	2:N2:47:ARG:HG2	2.17	0.44
2:N5:18:GLU:CD	2:N6:74:HIS:HE2	2.24	0.44
1:O1:16:GLU:OE1	1:O1:17:PRO:N	2.49	0.44
2:Q3:5:LEU:HD21	2:Q3:7:MET:HE2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R1:32:PRO:HG3	1:R1:87:MET:CE	2.47	0.44
3:R8:45:GLY:CA	3:R8:73:GLY:H	2.21	0.44
3:R8:119:ALA:O	3:R8:122:THR:OG1	2.35	0.44
2:S5:13:PHE:CD2	2:S6:43:THR:HG21	2.49	0.44
3:S8:103:ARG:HH21	3:S8:201:VAL:HG13	1.82	0.44
2:T5:37:THR:HG21	2:U2:13:PHE:HB2	1.98	0.44
2:U4:50:VAL:HG11	3:U8:186:GLU:HG3	1.98	0.44
2:X3:8:ILE:HD12	2:X3:19:ALA:HB1	1.98	0.44
2:X3:17:VAL:CG2	2:X4:7:MET:HE1	2.43	0.44
3:X8:21:PHE:CE2	3:X8:169:VAL:HB	2.52	0.44
2:Z7:12:GLY:N	2:Z7:40:GLY:O	2.51	0.44
3:Z8:154:ALA:HB2	3:Z8:198:ILE:HD11	1.99	0.44
3:18:51:VAL:HG13	3:18:92:ILE:HG12	1.99	0.44
3:18:170:THR:OG1	3:18:177:ARG:N	2.28	0.44
2:36:14:VAL:HG23	2:37:9:GLU:HB2	1.99	0.44
3:A8:183:SER:HG	3:A8:186:GLU:CD	2.25	0.44
1:B1:27:VAL:O	1:B1:41:VAL:HG12	2.17	0.44
2:B6:61:GLN:CD	2:B6:73:VAL:HG21	2.43	0.44
3:B8:167:VAL:HB	3:B8:179:TYR:HB2	1.98	0.44
2:C3:7:MET:CE	2:D7:17:VAL:HG11	2.47	0.44
2:C6:54:LYS:O	2:C6:58:GLU:HG3	2.17	0.44
1:D1:19:ILE:O	1:D1:22:LEU:HB2	2.17	0.44
1:F1:54:VAL:HG12	1:F1:82:VAL:HG21	1.99	0.44
2:F2:10:VAL:HG22	2:F2:70:VAL:HA	1.99	0.44
2:F6:14:VAL:HG23	2:F7:9:GLU:HB2	1.99	0.44
2:F6:61:GLN:OE1	2:F6:73:VAL:HG11	2.17	0.44
2:G2:35:GLU:OE2	2:G4:36:LYS:NZ	2.41	0.44
3:G8:95:LYS:HE3	3:G8:95:LYS:HB2	1.82	0.44
3:H9:45:GLY:HA2	3:H9:73:GLY:N	2.32	0.44
3:I8:19:ALA:HB3	3:I8:33:PRO:HG3	1.99	0.44
1:J1:10:VAL:HG13	1:11:82:VAL:HG13	1.99	0.44
2:J5:47:ARG:HH12	2:J5:84:ASP:CG	2.10	0.44
1:O1:68:VAL:C	1:O1:72:ARG:NH1	2.75	0.44
1:O1:70:ASN:C	1:O1:72:ARG:N	2.75	0.44
2:O7:23:MET:HG2	2:O7:56:ALA:O	2.17	0.44
3:O8:70:ARG:HE	3:O8:173:GLY:HA2	1.82	0.44
2:P5:31:LEU:HD12	2:P6:86:ALA:HB3	2.00	0.44
3:P8:105:LYS:HG3	3:P8:203:GLY:C	2.42	0.44
2:R3:84:ASP:HB3	2:R3:91:ARG:O	2.17	0.44
2:R5:2:ALA:O	2:R5:78:ARG:NH1	2.51	0.44
3:R8:23:GLY:CA	3:R8:30:LEU:HG	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S1:61:SER:HB2	1:31:61:SER:HB3	1.99	0.44
2:T6:61:GLN:O	2:T6:65:GLU:HG3	2.18	0.44
3:T8:21:PHE:HE2	3:T8:169:VAL:HB	1.79	0.44
3:U8:59:THR:HB	3:U8:61:VAL:HG23	1.99	0.44
1:V1:54:VAL:O	1:V1:82:VAL:HG23	2.17	0.44
1:V1:79:MET:HE1	1:W1:73:PRO:O	2.17	0.44
2:W3:32:ILE:HD12	2:W3:47:ARG:HG3	2.00	0.44
2:W6:45:VAL:HG11	2:W6:89:LEU:HD22	1.99	0.44
1:X1:64:ARG:HD3	1:Y1:62:SER:HB2	1.99	0.44
3:X8:123:GLN:CG	3:X9:23:GLY:HA3	2.47	0.44
3:X8:133:MET:HE1	3:X9:132:MET:N	2.32	0.44
2:Y6:23:MET:HG2	2:Y6:56:ALA:O	2.17	0.44
3:Y8:50:ARG:HD2	3:Y8:95:LYS:HD3	1.99	0.44
3:Z8:45:GLY:HA3	3:Z8:73:GLY:H	1.83	0.44
3:Z8:150:TYR:HE2	3:Z8:201:VAL:HG11	1.81	0.44
3:18:29:PHE:HB2	3:18:63:PRO:O	2.16	0.44
2:22:16:MET:HE2	2:22:42:VAL:HG11	1.98	0.44
2:33:5:LEU:HD12	2:33:6:GLY:H	1.82	0.44
2:33:47:ARG:HH11	2:33:91:ARG:HG2	1.81	0.44
2:36:47:ARG:NH2	2:36:84:ASP:OD1	2.51	0.44
2:43:47:ARG:HE	2:43:91:ARG:HG2	1.81	0.44
1:A1:45:ASP:OD1	1:A1:48:GLY:N	2.40	0.44
1:A1:64:ARG:C	1:A1:66:THR:H	2.25	0.44
3:A8:7:THR:HG21	3:A8:149:GLY:HA3	1.99	0.44
3:B8:110:THR:O	3:B8:143:LEU:HA	2.17	0.44
1:C1:16:GLU:O	1:C1:19:ILE:HG22	2.17	0.44
1:F1:7:VAL:HG12	1:G1:87:MET:HG2	1.99	0.44
3:F8:21:PHE:HE2	3:F8:169:VAL:HB	1.81	0.44
2:J2:16:MET:O	2:J2:20:ALA:N	2.39	0.44
2:J6:16:MET:HG3	2:J6:42:VAL:HG12	1.98	0.44
1:L1:31:ASP:O	1:L1:33:ASP:N	2.47	0.44
1:M1:41:VAL:HG11	1:M1:57:TYR:CZ	2.52	0.44
2:M4:16:MET:HE3	2:M4:16:MET:HB3	1.86	0.44
2:M5:61:GLN:O	2:M5:65:GLU:HG3	2.16	0.44
1:N1:2:VAL:HG23	1:N1:57:TYR:CE1	2.51	0.44
2:N3:5:LEU:HD12	2:N3:6:GLY:H	1.82	0.44
2:N5:41:TYR:N	2:N5:41:TYR:CD1	2.84	0.44
3:N8:118:GLU:HG3	3:N8:119:ALA:N	2.33	0.44
2:O3:4:ALA:O	2:O3:47:ARG:HD2	2.17	0.44
3:P8:23:GLY:CA	3:P8:30:LEU:HG	2.47	0.44
3:P8:61:VAL:CG1	3:P8:77:VAL:HB	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R9:45:GLY:HA2	3:R9:73:GLY:HA3	1.98	0.44
3:U8:17:GLN:O	3:U8:20:THR:OG1	2.25	0.44
3:V8:63:PRO:HA	3:V8:77:VAL:HA	1.98	0.44
3:V8:183:SER:OG	3:V8:186:GLU:OE2	2.34	0.44
2:W3:32:ILE:CD1	2:W3:47:ARG:HG3	2.47	0.44
3:W8:50:ARG:HD3	3:W8:95:LYS:HD3	2.00	0.44
2:X4:66:ARG:HD2	2:X5:62:ARG:HD2	1.98	0.44
3:Z8:8:TYR:O	3:Z8:103:ARG:NH2	2.50	0.44
3:Z8:62:GLN:HA	3:Z8:63:PRO:HD3	1.84	0.44
1:11:22:LEU:HD12	1:11:22:LEU:HA	1.72	0.44
2:23:32:ILE:CD1	2:23:47:ARG:HG3	2.45	0.44
2:33:4:ALA:O	2:33:47:ARG:HD2	2.16	0.44
2:A3:47:ARG:HH11	2:A3:91:ARG:HB2	1.82	0.44
3:C8:21:PHE:HE1	3:C8:130:GLN:HB2	1.80	0.44
3:D8:21:PHE:HE2	3:D8:169:VAL:HB	1.81	0.44
2:E7:29:VAL:CG1	2:E7:46:VAL:HB	2.48	0.44
3:E8:46:ILE:HG21	3:F8:142:ILE:HB	1.99	0.44
3:E8:111:HIS:CG	3:E8:111:HIS:O	2.69	0.44
2:F3:17:VAL:CG2	2:F4:7:MET:HE1	2.42	0.44
3:G8:144:GLU:HA	3:G8:176:GLY:O	2.18	0.44
2:H6:18:GLU:HB2	2:H7:74:HIS:CD2	2.53	0.44
3:I8:35:GLN:HE22	3:I8:78:HIS:CE1	2.35	0.44
3:I9:139:SER:N	3:I9:182:GLY:O	2.35	0.44
1:J1:68:VAL:C	1:J1:72:ARG:NH1	2.76	0.44
2:J2:16:MET:CG	2:J2:44:ALA:HB2	2.47	0.44
2:K6:34:TYR:HD2	2:K6:42:VAL:HG13	1.82	0.44
1:L1:45:ASP:OD1	1:L1:48:GLY:N	2.38	0.44
2:L3:32:ILE:HD11	2:L3:47:ARG:HG3	2.00	0.44
2:L5:10:VAL:HG13	2:L5:69:GLU:O	2.18	0.44
2:M5:13:PHE:HD2	2:M6:43:THR:HG21	1.83	0.44
3:N8:70:ARG:HG2	3:N8:173:GLY:N	2.32	0.44
3:N8:79:HIS:CE1	3:N8:81:ASP:H	2.36	0.44
2:O2:7:MET:HE1	2:O4:17:VAL:HG11	2.00	0.44
3:P8:7:THR:HG21	3:P8:149:GLY:HA3	1.99	0.44
3:P8:118:GLU:HG3	3:P8:119:ALA:N	2.32	0.44
2:R7:57:THR:O	2:R7:60:GLY:N	2.50	0.44
1:S1:26:LEU:HD13	1:S1:42:VAL:HG22	1.99	0.44
1:S1:45:ASP:OD1	1:S1:47:VAL:N	2.36	0.44
2:S5:17:VAL:HB	2:S6:7:MET:HE1	1.99	0.44
3:T8:127:ARG:HD2	3:T8:127:ARG:O	2.18	0.44
1:U1:45:ASP:OD1	1:U1:48:GLY:N	2.43	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W1:64:ARG:C	1:W1:66:THR:H	2.25	0.44
2:W2:78:ARG:NH2	2:W5:28:LYS:HD3	2.33	0.44
3:W8:123:GLN:HE22	3:W9:30:LEU:CB	2.30	0.44
1:Y1:70:ASN:O	1:Y1:72:ARG:N	2.50	0.44
3:Z8:42:ILE:HD11	3:Z8:96:LEU:HD11	1.99	0.44
2:16:29:VAL:HG11	2:16:46:VAL:HB	1.98	0.44
3:19:4:THR:O	3:19:42:ILE:HA	2.18	0.44
2:25:92:THR:O	2:25:94:GLY:N	2.50	0.44
3:28:115:ARG:HA	3:28:139:SER:OG	2.17	0.44
3:48:29:PHE:HB2	3:48:63:PRO:O	2.17	0.44
2:A6:47:ARG:NH2	2:A6:84:ASP:OD1	2.51	0.44
3:A8:141:PHE:O	3:A8:179:TYR:HA	2.17	0.44
3:D8:121:GLN:O	3:D8:125:ILE:HG13	2.17	0.44
1:F1:75:ASP:OD1	1:G1:1:MET:N	2.39	0.44
1:G1:28:ARG:NH2	1:G1:38:GLY:O	2.50	0.44
2:G2:47:ARG:NH2	2:G2:79:PRO:HG2	2.33	0.44
3:H8:59:THR:HB	3:H8:61:VAL:HG23	2.00	0.44
3:H8:127:ARG:HH21	3:W8:67:VAL:HG11	1.83	0.44
2:I5:41:TYR:HE2	2:J2:11:ARG:HG3	1.82	0.44
3:I9:9:ILE:N	3:I9:39:TRP:O	2.44	0.44
2:J3:10:VAL:HG11	2:J3:15:GLY:HA3	1.99	0.44
2:J4:78:ARG:NH2	3:J8:159:GLU:OE2	2.50	0.44
2:J6:4:ALA:O	2:J6:47:ARG:HG2	2.18	0.44
2:L2:32:ILE:HD11	2:L2:90:GLY:HA3	2.00	0.44
3:L8:118:GLU:HG3	3:L8:119:ALA:N	2.32	0.44
1:M1:2:VAL:HG23	1:M1:57:TYR:CE1	2.53	0.44
2:M2:54:LYS:HE3	2:M5:55:ALA:HB2	2.00	0.44
2:M5:41:TYR:CD1	2:M5:41:TYR:N	2.86	0.44
3:M8:53:ASP:O	3:M8:56:LEU:N	2.51	0.44
1:N1:31:ASP:C	1:N1:33:ASP:H	2.25	0.44
2:N6:47:ARG:HH22	2:N6:79:PRO:CG	2.30	0.44
3:P8:93:LEU:HD12	3:P8:94:ASP:N	2.32	0.44
3:R8:143:LEU:O	3:R8:177:ARG:HA	2.17	0.44
2:S3:5:LEU:N	2:S3:76:ILE:O	2.48	0.44
2:T6:52:ALA:O	2:T6:56:ALA:N	2.41	0.44
2:U7:61:GLN:O	2:U7:65:GLU:HB2	2.18	0.44
3:V8:8:TYR:HE2	3:V8:93:LEU:HB3	1.83	0.44
2:W2:2:ALA:N	2:W2:78:ARG:NH1	2.66	0.44
3:W8:39:TRP:CZ2	3:W8:152:VAL:HG11	2.52	0.44
2:Y3:31:LEU:HD12	2:Y3:45:VAL:O	2.17	0.44
2:Z5:9:GLU:HG3	2:Z5:43:THR:OG1	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:13:49:ASP:OD1	2:13:49:ASP:N	2.50	0.44
3:19:104:LEU:HA	3:19:204:VAL:H	1.83	0.44
1:31:66:THR:O	1:31:69:THR:OG1	2.21	0.44
2:37:84:ASP:O	2:37:92:THR:HG22	2.18	0.44
2:45:2:ALA:O	2:45:78:ARG:HD2	2.18	0.44
3:48:19:ALA:HB3	3:48:33:PRO:HG3	2.00	0.44
3:48:144:GLU:HA	3:48:176:GLY:O	2.18	0.44
2:A5:12:GLY:HA2	2:A6:9:GLU:OE2	2.18	0.44
3:B8:23:GLY:HA3	3:B8:30:LEU:HG	2.00	0.44
3:C8:127:ARG:HH12	3:28:67:VAL:CG1	2.25	0.44
2:D3:85:ASP:HB3	2:D3:92:ARG:O	2.18	0.44
2:D5:41:TYR:N	2:D5:41:TYR:CD1	2.85	0.44
3:D8:11:LEU:HD21	3:D8:153:LEU:HA	1.98	0.44
3:D8:107:GLN:HB3	3:D8:109:MET:SD	2.57	0.44
3:E8:127:ARG:HE	3:Q8:27:ARG:HB2	1.82	0.44
2:F7:50:VAL:HG21	2:F7:77:PRO:HB3	1.99	0.44
1:G1:32:PRO:HG3	1:G1:87:MET:CE	2.47	0.44
2:H2:72:ALA:HB1	2:H4:67:VAL:HG12	2.00	0.44
2:H7:47:ARG:NH1	2:H7:89:LEU:HB3	2.32	0.44
1:I1:61:SER:HB2	1:J1:61:SER:CB	2.47	0.44
2:J2:68:GLY:O	2:J2:70:VAL:HG23	2.18	0.44
2:J3:5:LEU:HD21	2:J3:7:MET:HE2	2.00	0.44
2:J5:18:GLU:CD	2:J6:74:HIS:HE2	2.24	0.44
2:K4:57:THR:HG22	2:K4:73:VAL:HG13	1.99	0.44
2:K6:14:VAL:HG23	2:K7:9:GLU:HB2	1.99	0.44
2:L2:47:ARG:HD2	2:L2:89:LEU:O	2.17	0.44
2:M5:3:ASP:HB3	2:M5:48:GLY:C	2.42	0.44
3:M8:142:ILE:HA	3:M8:178:LEU:O	2.17	0.44
2:N5:9:GLU:HA	2:N5:42:VAL:O	2.18	0.44
3:N8:51:VAL:HG13	3:N8:92:ILE:HG12	2.00	0.44
2:P7:7:GLU:HA	2:P7:40:VAL:O	2.17	0.44
2:R4:32:ILE:HD13	2:R4:90:GLY:N	2.33	0.44
2:S2:29:VAL:CG1	2:S2:46:VAL:HB	2.48	0.44
2:S3:5:LEU:HB3	2:S3:76:ILE:HB	2.00	0.44
1:T1:1:MET:HE3	1:T1:79:MET:SD	2.58	0.44
2:U6:32:ILE:HG13	2:U6:33:GLY:N	2.32	0.44
3:U9:144:GLU:HA	3:U9:176:GLY:O	2.16	0.44
2:W2:3:ASP:OD2	2:W2:91:ARG:NE	2.46	0.44
2:X3:5:LEU:HD21	2:X3:7:MET:HE2	2.00	0.44
2:X5:54:LYS:O	2:X5:58:GLU:HG2	2.17	0.44
2:Y2:47:ARG:NH2	2:Y2:84:ASP:OD1	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:Y8:16:PRO:HA	3:Y8:33:PRO:CB	2.42	0.44
2:Z5:41:TYR:N	2:Z5:41:TYR:CD1	2.85	0.44
2:46:20:ALA:O	2:46:24:VAL:HG22	2.18	0.44
3:A8:134:ILE:HD11	3:A8:140:LEU:HD13	2.00	0.44
2:C2:4:ALA:O	2:C2:47:ARG:HG2	2.17	0.44
2:E6:55:ALA:HB1	3:E8:115:ARG:HD2	1.99	0.44
3:E8:31:PRO:HB3	3:E8:78:HIS:CG	2.52	0.44
2:F7:17:VAL:HG11	2:G3:7:MET:HE1	1.99	0.44
3:F8:126:ASN:HD21	3:F8:133:MET:HB2	1.83	0.44
3:F9:151:ALA:HB2	3:F9:176:GLY:HA3	2.00	0.44
2:H6:31:LEU:HD12	2:H6:45:VAL:O	2.18	0.44
3:J8:17:GLN:O	3:J8:20:THR:OG1	2.33	0.44
1:K1:80:ALA:C	1:K1:81:ILE:HD12	2.43	0.44
3:K8:64:ALA:HB3	3:K8:76:GLU:OE2	2.18	0.44
1:M1:14:ARG:HG3	1:N1:47:VAL:CG1	2.48	0.44
3:M8:147:PRO:HD2	3:M8:150:TYR:CD1	2.53	0.44
2:N4:20:ALA:HB1	2:N4:31:LEU:HD22	2.00	0.44
3:N8:20:THR:O	3:N8:23:GLY:N	2.51	0.44
2:O7:47:ARG:NH2	2:O7:84:ASP:OD2	2.45	0.44
2:P2:47:ARG:CD	2:P2:91:ARG:HG2	2.47	0.44
2:P6:31:LEU:HD12	2:P6:45:VAL:O	2.18	0.44
3:P8:148:ALA:O	3:P8:171:PRO:HA	2.17	0.44
2:Q3:47:ARG:NH2	2:Q3:79:PRO:HG2	2.32	0.44
3:S8:11:LEU:HD23	3:S8:11:LEU:HA	1.74	0.44
1:T1:53:GLU:HG3	1:T1:95:LYS:NZ	2.33	0.44
2:T2:54:LYS:HZ1	2:T5:55:ALA:CA	2.31	0.44
2:T4:57:THR:CG2	2:T4:73:VAL:HG13	2.47	0.44
2:T6:27:ALA:HB1	2:T6:52:ALA:HB1	1.99	0.44
3:T8:19:ALA:HB3	3:T8:33:PRO:HG3	1.99	0.44
3:T8:28:GLY:HA3	3:T8:64:ALA:O	2.17	0.44
2:U6:56:ALA:O	2:U6:60:GLY:N	2.51	0.44
2:U7:53:VAL:HA	2:U7:56:ALA:HB3	1.99	0.44
1:V1:55:VAL:HG21	1:V1:78:ILE:HD13	1.99	0.44
2:W5:3:ASP:HB3	2:W5:48:GLY:O	2.17	0.44
3:X8:148:ALA:HA	3:X8:176:GLY:CA	2.47	0.44
2:Y5:60:GLN:O	2:Y5:64:GLU:HG3	2.18	0.44
2:Z7:4:ALA:O	2:Z7:47:ARG:NE	2.48	0.44
1:21:7:VAL:HG21	1:21:28:ARG:CD	2.48	0.44
2:25:61:GLN:HB2	2:25:73:VAL:HG21	1.98	0.44
3:28:20:THR:OG1	3:28:21:PHE:N	2.50	0.44
3:28:111:HIS:ND1	3:28:195:GLU:OE2	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:34:54:LYS:HD2	2:34:75:VAL:HG11	2.00	0.44
2:47:49:ASP:N	2:47:49:ASP:OD1	2.48	0.44
3:A8:145:THR:HG21	3:A8:198:ILE:HG21	2.00	0.44
2:B3:26:ALA:O	3:B8:12:ASP:HB3	2.18	0.44
2:B5:50:VAL:HG13	2:B5:51:ALA:N	2.33	0.44
3:B8:123:GLN:HG3	3:B9:23:GLY:HA3	1.99	0.44
3:B8:143:LEU:O	3:B8:177:ARG:HA	2.18	0.44
1:C1:69:THR:O	1:C1:72:ARG:HB2	2.18	0.44
2:C5:21:ASP:OD1	2:C5:25:LYS:HD2	2.18	0.44
2:C6:27:ALA:HA	3:C8:116:ALA:HB2	2.00	0.44
3:E8:11:LEU:HB3	3:E8:14:LEU:HD21	2.00	0.44
3:E8:16:PRO:HA	3:E8:33:PRO:CB	2.39	0.44
3:E8:134:ILE:CD1	3:E8:140:LEU:HB2	2.47	0.44
3:E8:144:GLU:HA	3:E8:176:GLY:O	2.18	0.44
3:E8:186:GLU:OE1	3:E8:186:GLU:N	2.31	0.44
2:F3:51:ALA:HB2	2:Q7:51:ALA:HB2	1.99	0.44
2:H4:20:ALA:O	2:H4:24:VAL:HG22	2.17	0.44
2:I6:18:GLU:OE1	2:I7:74:HIS:NE2	2.50	0.44
3:I8:29:PHE:HB2	3:I8:63:PRO:O	2.17	0.44
2:J2:19:ALA:HB2	2:J2:64:ALA:HB2	1.98	0.44
1:K1:75:ASP:OD1	1:L1:1:MET:N	2.34	0.44
2:K2:37:THR:HG21	2:K4:13:PHE:HB2	2.00	0.44
2:K3:5:LEU:HD13	2:K3:47:ARG:HD3	1.99	0.44
3:K8:38:LEU:O	3:K8:76:GLU:HA	2.18	0.44
3:L8:79:HIS:HE1	3:L8:81:ASP:HB2	1.81	0.44
3:L9:170:THR:O	3:L9:177:ARG:N	2.45	0.44
2:N6:4:ALA:HA	2:N6:77:PRO:O	2.17	0.44
3:N9:38:LEU:N	3:N9:77:VAL:O	2.49	0.44
2:O7:53:VAL:HG23	2:O7:54:LYS:N	2.33	0.44
2:Q3:36:LYS:HA	2:Q3:42:VAL:HG12	2.00	0.44
2:Q4:32:ILE:HD13	2:Q4:90:GLY:N	2.33	0.44
3:Q8:7:THR:OG1	3:Q8:41:GLU:N	2.49	0.44
3:Q8:51:VAL:HG13	3:Q8:92:ILE:HG12	2.00	0.44
3:R8:139:SER:O	3:R8:181:ALA:HA	2.17	0.44
1:S1:64:ARG:HH21	1:31:62:SER:HA	1.83	0.44
2:T4:10:VAL:HG11	2:T4:15:GLY:HA3	1.99	0.44
2:T4:23:MET:HG2	2:T4:56:ALA:O	2.18	0.44
3:T8:61:VAL:HA	3:T8:79:HIS:HB2	1.99	0.44
3:T8:111:HIS:HA	3:T8:142:ILE:O	2.18	0.44
1:U1:22:LEU:HG	1:U1:44:ALA:HB1	1.99	0.44
3:V8:49:ASN:O	3:X8:121:GLN:NE2	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W1:2:VAL:HG23	1:W1:57:TYR:CE1	2.53	0.44
1:W1:45:ASP:OD1	1:W1:46:ALA:N	2.50	0.44
3:X8:21:PHE:HE2	3:X8:169:VAL:HB	1.83	0.44
3:X9:47:ALA:O	3:X9:51:VAL:N	2.43	0.44
2:Y2:74:HIS:HE2	2:Y4:18:GLU:CD	2.26	0.44
2:Y4:21:ASP:OD2	2:Y4:25:LYS:NZ	2.37	0.44
3:Y8:48:ILE:HG22	3:Y8:66:GLN:OE1	2.16	0.44
1:Z1:19:ILE:HG22	1:Z1:73:PRO:HD2	1.99	0.44
2:Z5:19:ALA:HB2	2:Z5:64:ALA:HB2	2.00	0.44
2:Z6:13:PHE:O	2:Z6:17:VAL:HG23	2.17	0.44
3:Z8:38:LEU:O	3:Z8:76:GLU:HA	2.18	0.44
3:Z8:135:LEU:HD23	3:Z8:135:LEU:HA	1.80	0.44
2:24:5:LEU:HB3	2:24:76:ILE:HB	2.00	0.44
2:42:47:ARG:NH2	2:42:79:PRO:HG2	2.33	0.44
1:A1:25:LEU:O	1:A1:42:VAL:HA	2.18	0.44
2:B4:20:ALA:HB1	2:B4:31:LEU:HD22	2.00	0.44
1:C1:2:VAL:CG2	1:C1:57:TYR:CE1	3.01	0.44
1:C1:45:ASP:OD1	1:C1:47:VAL:N	2.36	0.44
2:C3:82:ASN:HD22	2:C3:82:ASN:C	2.26	0.44
3:C8:128:ASN:O	3:C8:130:GLN:N	2.49	0.44
1:D1:54:VAL:O	1:D1:82:VAL:HG23	2.17	0.44
3:D8:144:GLU:OE1	3:N8:44:PRO:HG3	2.18	0.44
3:D8:171:PRO:HD2	3:D8:172:TYR:CD2	2.52	0.44
2:E5:90:GLY:O	2:E5:91:ARG:HG2	2.18	0.44
2:F4:78:ARG:HD3	3:F8:163:ASN:OD1	2.18	0.44
2:F5:34:TYR:OH	2:F6:35:GLU:OE2	2.36	0.44
2:G7:29:VAL:CG1	2:G7:46:VAL:HB	2.48	0.44
1:I1:86:GLU:HG2	1:I1:87:MET:N	2.32	0.44
2:K4:16:MET:HG3	2:K4:42:VAL:HG12	1.99	0.44
3:K8:63:PRO:HA	3:K8:77:VAL:HA	1.99	0.44
2:L2:23:MET:SD	2:L2:46:VAL:HG21	2.58	0.44
1:M1:45:ASP:OD1	1:M1:46:ALA:N	2.51	0.44
3:M8:169:VAL:HG12	3:M8:171:PRO:HD3	1.99	0.44
2:N5:2:ALA:HB3	2:N5:78:ARG:CZ	2.48	0.44
1:O1:14:ARG:HG3	1:P1:47:VAL:HG12	2.00	0.44
3:O9:20:THR:O	3:O9:24:LYS:N	2.50	0.44
3:Q8:143:LEU:O	3:Q8:177:ARG:HA	2.17	0.44
3:R8:148:ALA:O	3:R8:171:PRO:HA	2.17	0.44
3:S8:169:VAL:HG22	3:S8:178:LEU:HD13	1.99	0.44
2:T5:10:VAL:HG13	2:T5:69:GLU:O	2.18	0.44
2:T6:16:MET:HG3	2:T6:42:VAL:HG12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:U4:16:MET:HE3	2:U4:16:MET:HB3	1.96	0.44
2:U4:61:GLN:HB2	2:U4:73:VAL:HG21	2.00	0.44
3:U8:38:LEU:O	3:U8:76:GLU:HA	2.18	0.44
3:W8:13:ALA:HA	3:W8:35:GLN:O	2.18	0.44
2:X2:9:GLU:HG3	2:X2:43:THR:OG1	2.17	0.44
2:Y4:16:MET:HG3	2:Y4:42:VAL:HG12	2.00	0.44
2:Z3:16:MET:HG2	2:Z3:44:ALA:HB2	2.00	0.44
1:11:68:VAL:C	1:11:72:ARG:NH1	2.76	0.44
1:21:45:ASP:OD1	1:21:46:ALA:N	2.50	0.44
3:28:141:PHE:CD2	3:28:180:LEU:HD12	2.53	0.44
3:38:144:GLU:HA	3:38:176:GLY:O	2.18	0.44
1:A1:54:VAL:HG21	1:A1:93:PHE:CZ	2.52	0.43
1:A1:83:ASP:OD2	1:B1:13:SER:OG	2.30	0.43
2:A3:12:GLY:HA2	2:A4:9:GLU:OE2	2.17	0.43
3:A8:186:GLU:O	3:A8:190:ALA:N	2.43	0.43
3:B8:21:PHE:HE1	3:B8:130:GLN:CB	2.31	0.43
3:B9:52:THR:O	3:B9:56:LEU:N	2.30	0.43
2:C5:29:VAL:CG1	2:C5:46:VAL:HB	2.48	0.43
3:C8:121:GLN:O	3:C8:125:ILE:HG13	2.18	0.43
3:D8:65:VAL:HG12	3:D8:76:GLU:HB3	1.99	0.43
2:E5:57:THR:O	2:E5:60:GLY:N	2.50	0.43
3:E8:21:PHE:HE1	3:E8:130:GLN:CB	2.31	0.43
3:F8:53:ASP:O	3:F8:56:LEU:N	2.51	0.43
3:F8:79:HIS:CE1	3:F8:81:ASP:H	2.35	0.43
3:F8:150:TYR:CE2	3:F8:201:VAL:HG11	2.53	0.43
2:G5:9:GLU:OE2	2:W2:13:PHE:N	2.51	0.43
2:H7:37:THR:OG1	2:H7:41:TYR:HB2	2.18	0.43
3:H8:3:ILE:HD13	3:H8:47:ALA:HB1	1.99	0.43
3:H8:141:PHE:HD2	3:H8:180:LEU:HD12	1.82	0.43
2:K2:4:ALA:HB2	2:K2:50:VAL:HG22	1.99	0.43
2:K3:19:ALA:HB2	2:K3:64:ALA:HB2	1.99	0.43
3:K8:29:PHE:CD2	3:K8:63:PRO:HD2	2.53	0.43
3:K8:117:VAL:HG13	3:K8:121:GLN:HE21	1.83	0.43
2:L4:66:ARG:NH1	2:L5:62:ARG:NE	2.65	0.43
2:M4:8:ILE:HD11	2:M4:57:THR:HG23	1.99	0.43
2:M7:8:ILE:O	2:M7:43:THR:HA	2.18	0.43
1:O1:26:LEU:HD23	1:P1:87:MET:HE1	2.00	0.43
2:O7:17:VAL:HG11	2:P3:7:MET:CE	2.47	0.43
3:O8:23:GLY:CA	3:O8:30:LEU:HG	2.47	0.43
2:R3:5:LEU:O	2:R3:53:VAL:HG11	2.17	0.43
2:S6:29:VAL:CG1	2:S6:46:VAL:HB	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S8:138:GLU:HB3	3:S8:182:GLY:O	2.18	0.43
3:T8:18:LEU:HD23	3:T8:18:LEU:HA	1.66	0.43
1:U1:19:ILE:O	1:U1:22:LEU:HB2	2.17	0.43
3:U8:142:ILE:HA	3:U8:178:LEU:O	2.18	0.43
2:W3:57:THR:HG22	2:W3:73:VAL:HG13	1.99	0.43
1:X1:31:ASP:C	1:X1:33:ASP:H	2.26	0.43
2:X5:61:GLN:O	2:X5:65:GLU:HG3	2.18	0.43
2:Y6:16:MET:HG3	2:Y6:42:VAL:HG12	1.99	0.43
2:15:19:ALA:HB2	2:15:64:ALA:HB2	2.00	0.43
2:15:89:LEU:C	2:15:91:ARG:H	2.24	0.43
2:26:27:ALA:HA	3:28:116:ALA:HB2	2.00	0.43
2:32:29:VAL:HG11	2:32:46:VAL:HB	1.99	0.43
2:34:16:MET:HE3	2:34:16:MET:HB3	1.96	0.43
2:36:8:ILE:O	2:36:43:THR:HA	2.18	0.43
2:36:32:ILE:HD11	2:36:47:ARG:HG3	1.99	0.43
2:45:60:GLY:O	2:45:64:ALA:N	2.48	0.43
1:A1:86:GLU:O	1:B1:8:GLY:HA3	2.18	0.43
2:A5:32:ILE:HD13	2:A5:90:GLY:HA3	2.00	0.43
1:B1:6:VAL:HG23	1:B1:52:GLY:H	1.82	0.43
2:B3:74:HIS:CG	2:B3:75:VAL:H	2.36	0.43
3:B8:144:GLU:HB2	3:J8:46:ILE:CD1	2.48	0.43
3:C8:22:ILE:O	3:C8:25:THR:OG1	2.32	0.43
3:C9:88:ALA:O	3:C9:92:ILE:N	2.42	0.43
3:D8:39:TRP:CZ2	3:D8:76:GLU:HG3	2.52	0.43
3:D8:130:GLN:OE1	3:D8:168:ASN:HB3	2.18	0.43
2:F3:35:GLU:OE2	2:R7:36:LYS:NZ	2.34	0.43
2:G3:5:LEU:HD12	2:G3:6:GLY:H	1.82	0.43
2:G5:13:PHE:HB2	2:G6:37:THR:HG21	2.01	0.43
2:H2:13:PHE:CD1	2:H2:13:PHE:C	2.97	0.43
2:H5:90:GLY:C	2:H5:92:THR:H	2.26	0.43
3:H8:60:LYS:CG	2:Y7:78:ARG:HD3	2.35	0.43
2:I4:78:ARG:HD3	3:I8:163:ASN:OD1	2.18	0.43
1:K1:22:LEU:HD12	1:K1:22:LEU:HA	1.69	0.43
3:K8:125:ILE:HD11	3:18:49:ASN:HD21	1.83	0.43
1:L1:19:ILE:O	1:L1:22:LEU:HB2	2.19	0.43
1:O1:9:THR:HG23	1:P1:86:GLU:OE2	2.17	0.43
2:O5:21:ASP:OD1	2:O5:25:LYS:HD2	2.18	0.43
3:O8:61:VAL:HG11	3:O8:77:VAL:HB	2.00	0.43
2:P2:13:PHE:C	2:P2:13:PHE:CD1	2.96	0.43
2:Q5:13:PHE:HB2	2:Q6:37:THR:HG21	2.00	0.43
1:R1:33:ASP:HB3	1:R1:35:THR:HG23	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R3:9:GLU:HG3	2:R3:71:VAL:HB	1.99	0.43
3:R9:66:GLN:HA	3:R9:74:LEU:O	2.18	0.43
1:S1:22:LEU:HA	1:S1:22:LEU:HD12	1.68	0.43
2:S7:53:VAL:HG23	2:S7:54:LYS:N	2.33	0.43
3:T8:8:TYR:CE2	3:T8:93:LEU:HD23	2.53	0.43
2:U6:19:ALA:HB2	2:U6:64:ALA:HB2	2.00	0.43
2:V7:51:ALA:HB2	2:43:51:ALA:HB2	2.00	0.43
2:X4:3:ASP:OD2	2:X4:91:ARG:NH2	2.42	0.43
1:Y1:41:VAL:HG11	1:Y1:57:TYR:CZ	2.52	0.43
3:Z8:115:ARG:HA	3:Z8:139:SER:OG	2.18	0.43
2:16:32:ILE:HD11	2:16:47:ARG:HD2	1.99	0.43
3:18:122:THR:HG22	3:18:134:ILE:HG22	1.99	0.43
1:21:32:PRO:HG3	1:21:87:MET:HE1	2.00	0.43
2:24:20:ALA:O	2:24:24:VAL:HG22	2.18	0.43
2:27:53:VAL:HG23	2:27:54:LYS:N	2.32	0.43
2:27:92:THR:O	2:27:94:GLY:N	2.50	0.43
2:35:50:VAL:HG13	2:35:51:ALA:N	2.33	0.43
3:38:142:ILE:HA	3:38:178:LEU:O	2.17	0.43
2:45:20:ALA:O	2:45:24:VAL:HG23	2.17	0.43
3:B8:152:VAL:HG23	3:B8:171:PRO:HB3	2.01	0.43
2:C2:90:GLY:C	2:C2:92:THR:H	2.19	0.43
2:C3:5:LEU:HD21	2:C3:7:MET:HE2	1.99	0.43
2:C5:54:LYS:O	2:C5:58:GLU:HG2	2.18	0.43
3:C8:8:TYR:HA	3:C8:40:VAL:HG22	1.99	0.43
3:C8:61:VAL:HG11	3:C8:77:VAL:HB	2.00	0.43
2:D3:55:LYS:O	2:D3:59:GLU:HG3	2.18	0.43
3:D8:106:PRO:HG3	3:D8:150:TYR:CE2	2.53	0.43
3:E8:123:GLN:HE21	3:E8:123:GLN:HB3	1.61	0.43
1:H1:14:ARG:HG3	1:I1:47:VAL:CG1	2.49	0.43
2:H4:53:VAL:O	2:H4:57:THR:OG1	2.29	0.43
3:H8:62:GLN:OE1	3:H8:78:HIS:NE2	2.51	0.43
3:H8:115:ARG:HA	3:H8:139:SER:OG	2.19	0.43
1:I1:2:VAL:HG23	1:I1:57:TYR:CE1	2.53	0.43
1:I1:73:PRO:O	1:J1:79:MET:HE1	2.17	0.43
2:I2:10:VAL:HG22	2:I2:70:VAL:HA	2.00	0.43
2:I2:85:ALA:HA	2:I2:92:THR:HG23	1.99	0.43
3:L8:74:LEU:HD21	3:L8:171:PRO:HB2	1.98	0.43
2:M5:50:VAL:HG13	2:M5:51:ALA:N	2.33	0.43
2:P6:4:ALA:O	2:P6:47:ARG:NH1	2.52	0.43
3:Q8:93:LEU:HD12	3:Q8:94:ASP:N	2.33	0.43
2:T6:47:ARG:NH2	2:T6:84:ASP:OD1	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:U8:79:HIS:CE1	3:U8:81:ASP:HB2	2.54	0.43
2:V4:70:VAL:O	2:V4:70:VAL:HG23	2.17	0.43
2:V5:90:GLY:O	2:V5:91:ARG:HG2	2.18	0.43
3:X8:7:THR:HG21	3:X8:149:GLY:HA3	1.99	0.43
3:X8:42:ILE:CD1	3:X8:96:LEU:HD11	2.48	0.43
2:Z4:16:MET:HE3	2:Z4:16:MET:HB3	1.96	0.43
1:21:19:ILE:O	1:21:22:LEU:HB2	2.18	0.43
2:33:32:ILE:HD11	2:33:47:ARG:HG3	2.00	0.43
2:A2:16:MET:O	2:A2:20:ALA:N	2.28	0.43
2:A3:21:ASP:OD1	2:A4:83:VAL:HG21	2.18	0.43
3:A8:64:ALA:HB3	3:A8:76:GLU:OE2	2.19	0.43
2:B7:54:LYS:O	2:B7:58:GLU:HG2	2.18	0.43
3:B8:38:LEU:HB2	3:B8:85:VAL:HG13	1.99	0.43
2:C6:19:ALA:HB2	2:C6:64:ALA:HB2	2.00	0.43
3:C8:122:THR:HG22	3:C8:134:ILE:HG22	2.00	0.43
1:D1:45:ASP:OD1	1:D1:48:GLY:N	2.42	0.43
2:D2:16:MET:HG2	2:D2:44:ALA:HB2	2.00	0.43
2:D4:77:PRO:O	2:D4:79:PRO:HD3	2.18	0.43
3:D8:29:PHE:HB2	3:D8:63:PRO:O	2.17	0.43
3:F8:7:THR:HG23	3:F8:41:GLU:HB3	2.00	0.43
1:G1:26:LEU:HD13	1:G1:42:VAL:HG22	1.99	0.43
3:G8:11:LEU:HD23	3:G8:11:LEU:HA	1.70	0.43
2:H3:84:ASP:HB3	2:H3:91:ARG:O	2.19	0.43
1:I1:70:ASN:C	1:I1:72:ARG:N	2.76	0.43
2:I5:18:GLU:HA	2:I6:76:ILE:HD11	2.01	0.43
2:I5:50:VAL:HG13	2:I5:51:ALA:N	2.33	0.43
2:I5:84:ASP:O	2:I5:92:THR:OG1	2.27	0.43
2:I6:16:MET:HG2	2:I6:44:ALA:HB2	2.00	0.43
2:I7:90:GLY:O	2:I7:91:ARG:HD3	2.18	0.43
3:I8:140:LEU:HA	3:I8:180:LEU:O	2.18	0.43
2:K6:3:ASP:O	2:K6:47:ARG:NH1	2.50	0.43
2:L2:9:GLU:HG3	2:L2:43:THR:OG1	2.17	0.43
2:L4:31:LEU:HD12	2:L4:45:VAL:O	2.18	0.43
3:M8:46:ILE:O	3:M8:49:ASN:N	2.51	0.43
2:N4:84:ASP:O	2:N4:92:THR:HG22	2.19	0.43
3:O8:140:LEU:HA	3:O8:180:LEU:O	2.18	0.43
1:P1:22:LEU:HA	1:P1:22:LEU:HD12	1.74	0.43
2:P4:8:ILE:O	2:P4:43:THR:HA	2.18	0.43
2:P6:32:ILE:HG21	2:P6:90:GLY:CA	2.46	0.43
3:P8:53:ASP:O	3:P8:56:LEU:N	2.51	0.43
2:Q2:54:LYS:HZ2	2:Q5:55:ALA:HB2	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Q3:47:ARG:HH12	2:Q3:84:ASP:CG	2.26	0.43
2:R4:19:ALA:HB2	2:R4:64:ALA:HB2	2.00	0.43
2:S2:47:ARG:NH2	2:S2:79:PRO:HG2	2.33	0.43
3:S8:62:GLN:HA	3:S8:63:PRO:HD3	1.84	0.43
3:S8:134:ILE:HD13	3:S8:140:LEU:HB2	2.00	0.43
1:T1:64:ARG:HB3	1:T1:70:ASN:O	2.19	0.43
1:T1:66:THR:HG22	1:T1:67:GLU:O	2.17	0.43
2:T5:13:PHE:HB2	2:T6:37:THR:HG21	2.00	0.43
2:U2:47:ARG:HD3	2:U2:91:ARG:HG2	2.00	0.43
3:U8:53:ASP:O	3:U8:57:LYS:N	2.24	0.43
2:V3:32:ILE:HD11	2:V3:47:ARG:HG3	1.99	0.43
3:V8:15:GLN:HG3	3:V8:160:LYS:HB2	2.00	0.43
2:W2:47:ARG:HD3	2:W2:91:ARG:HG2	1.99	0.43
3:W8:93:LEU:HB2	3:W8:98:VAL:O	2.18	0.43
3:X8:59:THR:HG21	3:X8:88:ALA:HB2	2.00	0.43
2:Y3:25:LYS:HB3	3:Y8:160:LYS:HE3	1.99	0.43
1:Z1:70:ASN:C	1:Z1:72:ARG:N	2.76	0.43
2:13:18:GLU:OE1	2:14:74:HIS:NE2	2.51	0.43
2:14:13:PHE:O	2:14:13:PHE:HD1	2.00	0.43
2:16:20:ALA:HA	2:16:23:MET:HE3	2.01	0.43
3:18:61:VAL:HG11	3:18:77:VAL:HB	1.99	0.43
3:28:67:VAL:HB	3:28:69:GLU:HG2	2.00	0.43
2:32:5:LEU:HB3	2:32:76:ILE:HB	2.00	0.43
2:32:9:GLU:HA	2:32:42:VAL:O	2.18	0.43
2:35:90:GLY:O	2:35:91:ARG:HG2	2.19	0.43
3:38:9:ILE:HD11	3:38:150:TYR:CD2	2.53	0.43
3:38:11:LEU:HD23	3:38:11:LEU:HA	1.83	0.43
3:38:107:GLN:O	3:38:145:THR:HA	2.19	0.43
1:41:31:ASP:O	1:41:33:ASP:N	2.45	0.43
3:48:111:HIS:CG	3:48:111:HIS:O	2.71	0.43
3:A8:123:GLN:CG	3:A9:23:GLY:HA3	2.48	0.43
1:C1:22:LEU:HG	1:C1:44:ALA:HB1	2.00	0.43
1:C1:79:MET:HE1	1:D1:73:PRO:O	2.19	0.43
2:C3:4:ALA:O	2:C3:47:ARG:HD2	2.18	0.43
3:C8:62:GLN:HA	3:C8:63:PRO:HD3	1.85	0.43
2:D4:20:ALA:O	2:D4:24:VAL:HG22	2.18	0.43
2:D4:32:ILE:HD13	2:D4:90:GLY:N	2.33	0.43
1:E1:70:ASN:C	1:E1:72:ARG:H	2.27	0.43
2:E5:13:PHE:HD2	2:E6:43:THR:HG21	1.83	0.43
2:F2:89:LEU:N	2:F2:89:LEU:HD22	2.33	0.43
1:G1:2:VAL:CG2	1:G1:57:TYR:CE1	3.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G5:57:THR:O	2:G5:60:GLY:N	2.45	0.43
2:H6:13:PHE:N	2:H7:9:GLU:OE1	2.51	0.43
3:H8:51:VAL:HG13	3:H8:92:ILE:HG12	1.99	0.43
2:I5:35:GLU:HG2	2:J2:13:PHE:CE2	2.53	0.43
3:I8:111:HIS:O	3:I8:111:HIS:CG	2.71	0.43
3:K8:76:GLU:OE1	3:K8:78:HIS:HB3	2.18	0.43
1:L1:45:ASP:OD1	1:L1:46:ALA:N	2.51	0.43
3:L8:53:ASP:O	3:L8:56:LEU:N	2.51	0.43
1:M1:80:ALA:C	1:M1:81:ILE:HD12	2.44	0.43
2:M2:47:ARG:HD2	2:M2:89:LEU:O	2.18	0.43
2:M7:53:VAL:HG23	2:M7:54:LYS:N	2.34	0.43
2:N6:16:MET:HG3	2:N6:42:VAL:HG12	2.01	0.43
2:N7:53:VAL:HA	2:N7:56:ALA:HB3	2.00	0.43
3:O8:169:VAL:HG12	3:O8:171:PRO:HD3	1.99	0.43
1:P1:20:GLU:O	2:Q2:62:ARG:NH1	2.48	0.43
2:P5:13:PHE:HD2	2:P6:43:THR:HG21	1.83	0.43
2:Q3:32:ILE:CD1	2:Q3:47:ARG:HG3	2.46	0.43
2:Q4:61:GLN:O	2:Q4:65:GLU:HG3	2.18	0.43
2:Q7:53:VAL:HG23	2:Q7:54:LYS:N	2.34	0.43
3:Q8:121:GLN:O	3:Q8:124:ILE:HG22	2.19	0.43
3:R8:59:THR:HB	3:R8:61:VAL:HG23	2.00	0.43
3:S8:8:TYR:OH	3:S8:93:LEU:HD23	2.18	0.43
2:T3:8:ILE:HG23	2:T3:73:VAL:HG22	2.00	0.43
2:T3:27:ALA:HB3	2:T3:56:ALA:HB2	1.98	0.43
3:T9:59:THR:CB	3:T9:88:ALA:HB2	2.48	0.43
3:U8:35:GLN:HA	3:U8:80:PHE:HA	2.01	0.43
3:U8:62:GLN:O	3:U8:78:HIS:N	2.42	0.43
3:U8:170:THR:HG1	3:U8:177:ARG:H	1.59	0.43
1:V1:68:VAL:HA	1:V1:72:ARG:NH1	2.32	0.43
1:X1:41:VAL:HG11	1:X1:57:TYR:CZ	2.54	0.43
2:Y5:33:TYR:CE2	2:Y5:35:LYS:HD2	2.54	0.43
3:Y8:123:GLN:CG	3:Y9:23:GLY:HA3	2.48	0.43
1:Z1:22:LEU:HD12	1:Z1:22:LEU:HA	1.74	0.43
3:Z8:16:PRO:HA	3:Z8:33:PRO:CB	2.39	0.43
2:16:16:MET:HG3	2:16:42:VAL:HG12	1.99	0.43
3:28:11:LEU:HB3	3:28:14:LEU:HD21	2.00	0.43
2:46:4:ALA:O	2:46:47:ARG:HG2	2.18	0.43
3:49:148:ALA:HA	3:49:176:GLY:H	1.83	0.43
2:A6:34:TYR:CZ	2:A6:36:LYS:NZ	2.86	0.43
1:B1:22:LEU:HD12	1:B1:22:LEU:HA	1.78	0.43
1:B1:45:ASP:OD1	1:B1:46:ALA:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C2:47:ARG:NH1	2:C2:84:ASP:OD1	2.35	0.43
3:C8:57:LYS:C	2:M7:78:ARG:HH21	2.26	0.43
3:C8:63:PRO:HB3	3:C8:77:VAL:HG12	2.00	0.43
3:C8:187:ILE:O	3:C8:191:ALA:N	2.34	0.43
2:D6:64:ALA:O	2:D6:68:GLY:N	2.51	0.43
1:F1:18:ARG:O	1:F1:72:ARG:NE	2.51	0.43
2:F5:90:GLY:O	2:F5:91:ARG:HG2	2.18	0.43
1:G1:80:ALA:C	1:G1:81:ILE:HD12	2.43	0.43
2:G2:4:ALA:HB2	2:G2:50:VAL:HG22	2.01	0.43
2:G2:47:ARG:HD2	2:G2:89:LEU:O	2.19	0.43
2:G3:13:PHE:HB2	2:G4:37:THR:CG2	2.41	0.43
2:G4:47:ARG:NH1	2:G4:89:LEU:O	2.52	0.43
3:G8:123:GLN:HG3	3:G9:23:GLY:HA3	2.00	0.43
2:H2:50:VAL:HG11	2:H5:28:LYS:HZ1	1.83	0.43
2:H3:23:MET:HG2	2:H3:56:ALA:O	2.19	0.43
3:H8:144:GLU:HA	3:H8:176:GLY:O	2.19	0.43
3:I8:95:LYS:HE3	3:I8:95:LYS:HB2	1.88	0.43
3:I9:107:GLN:N	3:I9:146:GLN:O	2.48	0.43
1:J1:14:ARG:HG3	1:I1:47:VAL:CG1	2.48	0.43
2:J3:54:LYS:O	2:J3:58:GLU:HG3	2.19	0.43
2:K5:19:ALA:HB2	2:K5:64:ALA:HB2	2.01	0.43
2:K5:47:ARG:HH12	2:K5:84:ASP:CG	2.27	0.43
2:L4:62:ARG:HD2	2:L5:66:ARG:HD2	2.01	0.43
2:L5:57:THR:O	2:L5:60:GLY:N	2.51	0.43
3:M8:35:GLN:HE22	3:M8:78:HIS:CE1	2.36	0.43
2:N3:90:GLY:O	2:N3:92:THR:N	2.52	0.43
3:N8:133:MET:HE1	3:N9:132:MET:N	2.33	0.43
2:O2:68:GLY:O	2:O2:70:VAL:HG23	2.19	0.43
3:O8:8:TYR:CE2	3:O8:93:LEU:HD23	2.54	0.43
1:P1:50:GLY:N	1:P1:53:GLU:OE1	2.33	0.43
2:Q2:20:ALA:HA	2:Q2:23:MET:HE3	2.01	0.43
2:Q7:19:ALA:HB2	2:Q7:64:ALA:HB2	2.00	0.43
3:Q8:11:LEU:HB3	3:Q8:14:LEU:HD21	2.01	0.43
2:R2:47:ARG:NH2	2:R2:84:ASP:OD1	2.51	0.43
3:R9:44:PRO:HA	3:R9:71:ALA:O	2.19	0.43
1:S1:41:VAL:HG11	1:S1:57:TYR:CZ	2.54	0.43
3:S8:3:ILE:HD11	3:S8:50:ARG:NH2	2.33	0.43
3:S8:104:LEU:HA	3:S8:204:VAL:O	2.19	0.43
3:T8:122:THR:HB	3:T8:134:ILE:O	2.18	0.43
2:U4:57:THR:HG22	2:U4:73:VAL:HG13	2.01	0.43
2:U6:7:MET:HG2	2:U6:45:VAL:HG13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:V2:18:GLU:OE1	2:W5:74:HIS:NE2	2.50	0.43
3:V8:49:ASN:OD1	3:X8:121:GLN:NE2	2.51	0.43
3:V8:167:VAL:HB	3:V8:179:TYR:HB2	1.99	0.43
3:W8:8:TYR:O	3:W8:103:ARG:NH2	2.51	0.43
2:X5:47:ARG:HH12	2:X5:84:ASP:CG	2.25	0.43
2:X5:60:GLY:O	2:X5:64:ALA:N	2.51	0.43
3:X8:88:ALA:O	3:X8:91:THR:OG1	2.34	0.43
3:X8:117:VAL:HG12	3:X8:121:GLN:HB3	2.01	0.43
1:11:41:VAL:HG11	1:11:57:TYR:OH	2.19	0.43
1:11:70:ASN:C	1:11:72:ARG:H	2.26	0.43
2:14:53:VAL:O	2:14:57:THR:OG1	2.34	0.43
3:18:44:PRO:C	3:18:46:ILE:N	2.68	0.43
3:18:152:VAL:HG22	3:18:169:VAL:HG11	1.99	0.43
2:22:9:GLU:HB2	2:24:14:VAL:HG23	2.01	0.43
2:25:21:ASP:OD1	2:25:25:LYS:HD2	2.18	0.43
1:41:33:ASP:HB3	1:41:35:THR:HG23	2.01	0.43
2:45:50:VAL:HG13	2:45:51:ALA:N	2.32	0.43
3:48:162:ALA:HB3	3:48:190:ALA:HB2	1.99	0.43
2:A3:78:ARG:NH1	2:I7:27:ALA:O	2.50	0.43
2:B3:10:VAL:O	2:B3:12:GLY:N	2.52	0.43
2:D5:10:VAL:HG12	2:D5:12:GLY:H	1.84	0.43
3:E8:9:ILE:CD1	3:E8:150:TYR:HA	2.32	0.43
3:G8:18:LEU:HD11	3:G8:156:ASN:HA	2.01	0.43
2:H4:31:LEU:HA	2:H4:46:VAL:HG12	2.01	0.43
3:H8:50:ARG:HB2	3:Y8:114:ILE:HD11	2.01	0.43
3:H8:167:VAL:HB	3:H8:179:TYR:HB2	2.01	0.43
3:L9:65:VAL:O	3:L9:75:LEU:HA	2.19	0.43
2:M2:16:MET:O	2:M2:20:ALA:N	2.35	0.43
2:O2:47:ARG:HD3	2:O2:91:ARG:HG2	2.00	0.43
2:O2:92:THR:O	2:O2:94:GLY:N	2.52	0.43
3:O8:35:GLN:HG2	3:O8:80:PHE:CD1	2.53	0.43
3:O8:39:TRP:CZ2	3:O8:76:GLU:HG3	2.53	0.43
3:O8:64:ALA:HB3	3:O8:76:GLU:OE2	2.18	0.43
2:P7:56:GLU:O	2:P7:60:ARG:HG3	2.19	0.43
3:P8:183:SER:OG	3:P8:186:GLU:OE2	2.37	0.43
2:Q6:32:ILE:CD1	2:Q6:47:ARG:HD2	2.48	0.43
3:Q9:96:LEU:C	3:Q9:98:VAL:H	2.27	0.43
1:R1:2:VAL:HG23	1:R1:57:TYR:CE1	2.54	0.43
3:R8:134:ILE:HG12	3:R8:181:ALA:HB2	2.01	0.43
3:R8:141:PHE:O	3:R8:179:TYR:HA	2.19	0.43
2:T4:16:MET:HE3	2:T4:16:MET:HB3	1.90	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:T8:132:MET:HE2	3:T8:165:HIS:ND1	2.34	0.43
2:U4:8:ILE:HD12	2:U4:73:VAL:HG22	2.00	0.43
3:U8:7:THR:HG22	3:U8:150:TYR:CE1	2.53	0.43
3:U8:18:LEU:HD11	3:U8:156:ASN:HA	2.00	0.43
3:U8:61:VAL:CG1	3:U8:77:VAL:HB	2.49	0.43
3:U8:183:SER:O	3:U8:187:ILE:HG12	2.19	0.43
2:V3:18:GLU:CD	2:V4:74:HIS:HE2	2.23	0.43
2:V3:47:ARG:NH1	2:V3:84:ASP:OD1	2.52	0.43
2:V5:11:ARG:HG3	2:V5:41:TYR:HE1	1.83	0.43
2:V5:41:TYR:N	2:V5:41:TYR:CD1	2.87	0.43
2:V7:50:VAL:HG21	2:V7:77:PRO:HB3	2.00	0.43
1:X1:18:ARG:NH1	1:Y1:65:GLN:C	2.74	0.43
2:Y6:54:LYS:O	2:Y6:58:GLU:HG3	2.19	0.43
3:Y8:62:GLN:O	3:Y8:78:HIS:N	2.37	0.43
3:Y9:139:SER:N	3:Y9:182:GLY:O	2.43	0.43
1:31:32:PRO:HG3	1:31:87:MET:CE	2.48	0.43
2:34:31:LEU:HD12	2:34:45:VAL:O	2.18	0.43
2:35:14:VAL:HG13	2:36:7:MET:HE3	2.01	0.43
2:35:61:GLN:HB2	2:35:73:VAL:HG21	2.00	0.43
3:39:126:ASN:CB	3:39:134:ILE:H	2.32	0.43
2:44:4:ALA:O	2:44:47:ARG:NE	2.51	0.43
3:48:20:THR:OG1	3:48:21:PHE:N	2.50	0.43
3:48:40:VAL:O	3:48:74:LEU:HD12	2.19	0.43
2:A3:5:LEU:HD12	2:A3:76:ILE:HD13	2.01	0.43
2:A7:16:MET:SD	2:A7:44:ALA:HB2	2.59	0.43
3:A8:20:THR:OG1	3:A8:21:PHE:N	2.52	0.43
2:C7:89:LEU:HD23	2:C7:89:LEU:HA	1.82	0.43
2:E6:47:ARG:HH22	2:E6:79:PRO:CG	2.31	0.43
3:E8:126:ASN:HD21	3:E8:133:MET:HB2	1.83	0.43
2:F4:20:ALA:O	2:F4:24:VAL:HG22	2.19	0.43
2:F7:53:VAL:HA	2:F7:56:ALA:HB3	2.00	0.43
2:G6:45:VAL:HG11	2:G6:89:LEU:HD22	2.01	0.43
2:G6:61:GLN:CD	2:G6:73:VAL:HG21	2.44	0.43
1:H1:32:PRO:HG3	1:H1:87:MET:CE	2.49	0.43
2:H5:61:GLN:O	2:H5:65:GLU:HG3	2.19	0.43
2:H6:52:ALA:HA	3:H8:184:GLU:OE1	2.19	0.43
2:I5:18:GLU:OE1	2:I6:74:HIS:NE2	2.49	0.43
3:I8:38:LEU:O	3:I8:76:GLU:HA	2.18	0.43
3:I8:148:ALA:O	3:I8:171:PRO:HA	2.19	0.43
2:J7:21:ASP:OD1	2:J7:25:LYS:HE3	2.18	0.43
3:J8:45:GLY:HA3	3:J8:72:TYR:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L1:22:LEU:HD12	1:L1:22:LEU:HA	1.69	0.43
2:L5:39:GLY:HA2	2:L6:39:GLY:HA3	2.01	0.43
3:L9:105:LYS:N	3:L9:204:VAL:O	2.23	0.43
2:O2:3:ASP:CG	2:O2:91:ARG:HH21	2.25	0.43
1:P1:64:ARG:HH11	1:Q1:62:SER:HB3	1.84	0.43
2:P6:18:GLU:CD	2:P7:72:HIS:HE2	2.27	0.43
3:P8:52:THR:O	3:P8:56:LEU:HB2	2.19	0.43
1:Q1:54:VAL:O	1:Q1:82:VAL:HG23	2.19	0.43
2:R3:5:LEU:HD12	2:R3:6:GLY:H	1.83	0.43
3:R9:45:GLY:N	3:R9:71:ALA:O	2.51	0.43
3:S8:16:PRO:HA	3:S8:33:PRO:CB	2.41	0.43
1:T1:10:VAL:HG22	1:U1:85:VAL:HG22	2.00	0.43
2:T5:34:TYR:CE2	2:T5:36:LYS:HD2	2.54	0.43
2:T6:30:GLU:OE1	2:T6:91:ARG:NH2	2.43	0.43
3:U8:117:VAL:HG12	3:U8:121:GLN:HB3	2.01	0.43
1:V1:31:ASP:C	1:V1:33:ASP:H	2.26	0.43
3:V8:4:THR:O	3:V8:42:ILE:HG23	2.18	0.43
3:V8:38:LEU:O	3:V8:76:GLU:HA	2.18	0.43
2:W5:5:LEU:HB3	2:W5:76:ILE:HB	2.01	0.43
2:X2:21:ASP:OD1	2:X2:25:LYS:HE3	2.18	0.43
2:X4:66:ARG:NH1	2:X5:62:ARG:NE	2.66	0.43
2:Y2:5:LEU:HD11	2:Y2:45:VAL:HG13	2.01	0.43
2:Y5:31:ILE:HD11	2:Y5:44:VAL:CG1	2.49	0.43
1:Z1:61:SER:HB3	1:11:61:SER:HB2	2.01	0.43
1:Z1:62:SER:HA	1:11:64:ARG:HH21	1.83	0.43
2:Z2:74:HIS:NE2	2:Z4:18:GLU:OE1	2.49	0.43
3:Z8:135:LEU:HD12	3:Z8:138:GLU:OE1	2.19	0.43
2:13:20:ALA:HB1	2:13:31:LEU:HD22	2.01	0.43
3:18:65:VAL:HG13	3:18:74:LEU:O	2.19	0.43
2:B4:10:VAL:HG11	2:B4:15:GLY:HA3	2.00	0.43
3:B9:52:THR:HA	3:B9:55:ALA:HB3	2.01	0.43
2:C5:47:ARG:NH1	2:C5:84:ASP:OD1	2.52	0.43
3:C8:134:ILE:HG12	3:C8:181:ALA:CB	2.47	0.43
1:D1:45:ASP:OD1	1:D1:46:ALA:N	2.51	0.43
3:D8:56:LEU:HD23	3:D8:56:LEU:HA	1.82	0.43
2:E5:32:ILE:HD13	2:E5:47:ARG:HG3	2.01	0.43
3:E8:24:LYS:NZ	3:E9:134:ILE:O	2.50	0.43
3:E8:105:LYS:HG3	3:E8:203:GLY:C	2.44	0.43
2:F4:16:MET:HG2	2:F4:44:ALA:HB2	2.00	0.43
3:F8:31:PRO:HD3	3:F8:64:ALA:HB2	2.01	0.43
3:F8:42:ILE:CD1	3:F8:96:LEU:HD11	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G1:58:ALA:N	1:G1:77:THR:O	2.52	0.43
1:G1:75:ASP:OD1	1:W1:1:MET:N	2.34	0.43
2:G5:21:ASP:OD1	2:G5:25:LYS:HD2	2.19	0.43
1:J1:66:THR:HG22	1:J1:67:GLU:O	2.19	0.43
2:L2:68:GLY:O	2:L2:70:VAL:HG23	2.18	0.43
3:L8:35:GLN:HE22	3:L8:78:HIS:CE1	2.37	0.43
3:L8:103:ARG:HH21	3:L8:201:VAL:CG1	2.31	0.43
3:L8:119:ALA:O	3:L8:122:THR:OG1	2.36	0.43
2:M3:9:GLU:HG3	2:M3:71:VAL:HB	2.00	0.43
2:N2:68:GLY:O	2:N2:70:VAL:HG23	2.19	0.43
3:N8:103:ARG:HH21	3:N8:201:VAL:HG13	1.83	0.43
2:O5:47:ARG:HH12	2:O5:84:ASP:CG	2.27	0.43
3:O8:70:ARG:HG2	3:O8:173:GLY:N	2.34	0.43
1:P1:27:VAL:O	1:P1:41:VAL:HG12	2.19	0.43
3:P8:7:THR:HG23	3:P8:41:GLU:HB3	2.01	0.43
2:R2:16:MET:HE2	2:R2:42:VAL:HG11	1.99	0.43
2:R3:47:ARG:HH11	2:R3:91:ARG:HB2	1.83	0.43
3:R8:21:PHE:CE2	3:R8:169:VAL:HB	2.54	0.43
3:R8:120:TYR:HD1	3:S8:29:PHE:CZ	2.36	0.43
2:S4:62:ARG:NE	2:S5:66:ARG:NH1	2.67	0.43
3:S8:35:GLN:HE22	3:S8:78:HIS:CE1	2.36	0.43
3:S8:64:ALA:HB3	3:S8:76:GLU:OE1	2.18	0.43
1:T1:33:ASP:HB3	1:T1:35:THR:HG23	2.00	0.43
3:T8:111:HIS:O	3:T8:111:HIS:CG	2.72	0.43
2:V5:50:VAL:HG13	2:V5:51:ALA:N	2.34	0.43
2:V6:16:MET:HG2	2:V6:44:ALA:HB2	2.00	0.43
2:V7:53:VAL:HG23	2:V7:54:LYS:N	2.34	0.43
3:V8:29:PHE:CZ	3:X8:120:TYR:HD1	2.36	0.43
2:W5:57:THR:O	2:W5:60:GLY:N	2.48	0.43
2:W7:21:ASP:OD1	2:W7:25:LYS:HE3	2.18	0.43
3:X8:11:LEU:HA	3:X8:11:LEU:HD23	1.75	0.43
2:Y3:84:ASP:O	2:Y3:92:THR:OG1	2.29	0.43
3:Z8:13:ALA:HA	3:Z8:35:GLN:O	2.18	0.43
3:Z8:29:PHE:HB2	3:Z8:63:PRO:O	2.19	0.43
3:Z8:79:HIS:CE1	3:Z8:81:ASP:HB2	2.54	0.43
2:14:5:LEU:HD11	2:14:7:MET:SD	2.59	0.43
3:28:17:GLN:O	3:28:20:THR:OG1	2.32	0.43
2:33:39:GLY:HA2	2:34:39:GLY:HA3	2.00	0.43
3:38:140:LEU:HA	3:38:180:LEU:O	2.17	0.43
2:A2:36:LYS:NZ	2:B5:35:GLU:OE2	2.47	0.43
3:A8:11:LEU:HD12	3:A8:39:TRP:NE1	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A8:140:LEU:HA	3:A8:180:LEU:O	2.17	0.43
3:C8:115:ARG:HA	3:C8:139:SER:OG	2.19	0.43
3:C8:170:THR:OG1	3:C8:177:ARG:N	2.23	0.43
2:D4:78:ARG:HD3	3:D8:163:ASN:OD1	2.18	0.43
2:D5:21:ASP:OD1	2:D5:25:LYS:HD2	2.19	0.43
2:E2:32:ILE:HD11	2:E2:90:GLY:HA3	2.01	0.43
2:E7:29:VAL:H	2:Q3:78:ARG:HH12	1.67	0.43
3:E8:53:ASP:O	3:E8:57:LYS:N	2.27	0.43
3:E8:130:GLN:NE2	3:E8:172:TYR:OH	2.44	0.43
2:H5:47:ARG:NH2	2:H5:84:ASP:OD1	2.51	0.43
1:I1:45:ASP:OD1	1:I1:46:ALA:N	2.52	0.43
2:I2:16:MET:O	2:I2:20:ALA:N	2.39	0.43
2:J2:34:TYR:CE2	2:J2:36:LYS:NZ	2.87	0.43
3:J8:142:ILE:HB	3:L8:46:ILE:HG21	2.01	0.43
2:K4:31:LEU:HD12	2:K4:45:VAL:O	2.19	0.43
2:L2:78:ARG:CZ	2:L5:28:LYS:HB2	2.49	0.43
3:L8:6:ARG:NH2	3:L8:72:TYR:OH	2.52	0.43
2:O2:13:PHE:CD1	2:O2:13:PHE:C	2.97	0.43
2:O5:92:THR:O	2:O5:94:GLY:N	2.51	0.43
2:O6:16:MET:HG2	2:O6:44:ALA:HB2	2.01	0.43
3:P8:38:LEU:O	3:P8:76:GLU:HA	2.18	0.43
3:P8:121:GLN:O	3:P8:125:ILE:HG13	2.19	0.43
3:Q8:8:TYR:CE2	3:Q8:93:LEU:HD23	2.54	0.43
3:Q8:35:GLN:HE22	3:Q8:78:HIS:CE1	2.36	0.43
1:R1:19:ILE:O	1:R1:22:LEU:HB2	2.19	0.43
2:R2:47:ARG:HD3	2:R2:91:ARG:HG2	2.00	0.43
2:R5:50:VAL:HG13	2:R5:51:ALA:N	2.34	0.43
3:R8:11:LEU:HD23	3:R8:11:LEU:HA	1.76	0.43
3:S8:20:THR:OG1	3:S8:21:PHE:N	2.52	0.43
3:S8:92:ILE:O	3:S8:95:LYS:HB3	2.19	0.43
3:S8:141:PHE:HB3	3:S8:180:LEU:HB2	2.00	0.43
3:S9:113:ILE:HA	3:S9:141:PHE:HA	2.00	0.43
2:T4:51:ALA:HB2	3:T8:185:ALA:HB2	2.00	0.43
2:V7:10:VAL:HG11	2:V7:15:GLY:HA3	2.00	0.43
2:W3:5:LEU:O	2:W3:53:VAL:HG11	2.19	0.43
2:Y4:31:LEU:HD12	2:Y4:45:VAL:O	2.19	0.43
2:Y4:61:GLN:O	2:Y4:65:GLU:HG3	2.19	0.43
3:Y8:110:THR:O	3:Y8:143:LEU:HA	2.19	0.43
3:Y9:62:GLN:O	3:Y9:77:VAL:HA	2.19	0.43
1:Z1:47:VAL:CG1	1:11:14:ARG:HG3	2.49	0.43
2:Z2:54:LYS:NZ	2:Z5:55:ALA:HB2	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:13:54:LYS:O	2:13:58:GLU:HG3	2.19	0.43
2:14:31:LEU:HD12	2:14:45:VAL:O	2.19	0.43
2:15:5:LEU:HB3	2:15:76:ILE:HB	2.00	0.43
3:28:79:HIS:CG	3:28:80:PHE:N	2.87	0.43
1:41:83:ASP:O	1:41:84:LEU:HD23	2.19	0.43
2:43:10:VAL:O	2:43:12:GLY:N	2.52	0.43
2:43:47:ARG:NH1	2:43:84:ASP:CG	2.66	0.43
3:A9:5:LEU:HA	3:A9:42:ILE:HA	2.00	0.42
2:B7:50:VAL:CG2	2:B7:77:PRO:HB3	2.50	0.42
3:B8:64:ALA:H	3:B8:76:GLU:CD	2.27	0.42
3:B8:123:GLN:NE2	3:B9:31:PRO:O	2.51	0.42
2:C6:53:VAL:O	2:C6:57:THR:HG23	2.18	0.42
2:D6:47:ARG:HD3	2:D6:91:ARG:HG2	2.01	0.42
2:D7:92:THR:O	2:D7:94:GLY:N	2.50	0.42
1:E1:25:LEU:HD12	1:E1:78:ILE:HD12	2.01	0.42
3:F8:11:LEU:HA	3:F8:11:LEU:HD23	1.70	0.42
2:H2:47:ARG:NH1	2:H2:84:ASP:OD2	2.52	0.42
3:H8:98:VAL:HG12	3:H8:99:ARG:O	2.19	0.42
1:I1:41:VAL:HG11	1:I1:57:TYR:CZ	2.54	0.42
1:J1:22:LEU:HD12	1:J1:22:LEU:HA	1.85	0.42
3:K8:7:THR:HG22	3:K8:150:TYR:CD1	2.54	0.42
1:L1:31:ASP:C	1:L1:33:ASP:H	2.25	0.42
3:M8:119:ALA:O	3:M8:122:THR:OG1	2.35	0.42
3:N8:61:VAL:HG11	3:N8:77:VAL:HB	2.01	0.42
2:O6:18:GLU:OE1	2:O7:74:HIS:NE2	2.51	0.42
3:O8:29:PHE:HB2	3:O8:63:PRO:O	2.18	0.42
3:O8:140:LEU:HD11	3:O8:179:TYR:CD2	2.54	0.42
1:P1:64:ARG:HD3	1:Q1:62:SER:CB	2.49	0.42
2:P5:18:GLU:OE1	2:P6:74:HIS:NE2	2.51	0.42
2:S6:47:ARG:NH2	2:S6:84:ASP:OD1	2.51	0.42
3:U8:134:ILE:HD11	3:U8:140:LEU:HD13	2.01	0.42
2:V2:45:VAL:HG11	2:V2:89:LEU:HD12	2.00	0.42
3:V8:67:VAL:HB	3:V8:69:GLU:HG2	1.99	0.42
3:W9:62:GLN:N	3:W9:78:HIS:O	2.46	0.42
1:X1:22:LEU:HD12	1:X1:22:LEU:HA	1.72	0.42
1:X1:63:ALA:HB1	1:X1:77:THR:HG22	2.01	0.42
2:X7:36:LYS:NZ	2:Y3:35:GLU:OE2	2.25	0.42
3:19:154:ALA:O	3:19:158:ALA:N	2.52	0.42
1:21:54:VAL:O	1:21:82:VAL:HG23	2.19	0.42
3:28:23:GLY:CA	3:28:30:LEU:HG	2.49	0.42
2:34:5:LEU:HD12	2:34:76:ILE:HD12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:36:27:ALA:HB1	2:36:52:ALA:HB1	2.00	0.42
3:48:54:ALA:HB2	3:48:95:LYS:NZ	2.34	0.42
1:A1:31:ASP:OD1	1:A1:35:THR:OG1	2.26	0.42
2:A3:8:ILE:HD12	2:A3:19:ALA:HB1	2.00	0.42
3:A9:47:ALA:O	3:A9:51:VAL:N	2.47	0.42
2:B2:13:PHE:N	2:C5:9:GLU:OE2	2.52	0.42
2:B2:16:MET:HE1	2:B2:34:TYR:HB2	2.01	0.42
2:B5:13:PHE:N	2:B6:9:GLU:OE1	2.52	0.42
1:C1:80:ALA:C	1:C1:81:ILE:HD12	2.44	0.42
2:C4:31:LEU:HA	2:C4:46:VAL:HG12	2.01	0.42
3:C8:144:GLU:HA	3:C8:176:GLY:O	2.19	0.42
2:D2:11:ARG:NH1	2:D2:41:TYR:CE1	2.87	0.42
3:D9:7:THR:O	3:D9:41:GLU:N	2.31	0.42
3:E8:7:THR:OG1	3:E8:41:GLU:N	2.52	0.42
3:E9:3:ILE:HA	3:E9:43:ALA:O	2.18	0.42
2:G6:76:ILE:HG21	2:G6:79:PRO:HB3	2.01	0.42
2:H2:90:GLY:C	2:H2:92:THR:H	2.20	0.42
3:H8:79:HIS:CE1	3:H8:81:ASP:HB2	2.54	0.42
2:I6:19:ALA:HB2	2:I6:64:ALA:HB2	2.01	0.42
3:I8:48:ILE:HG23	3:I8:75:LEU:HB2	2.02	0.42
2:J7:53:VAL:HA	2:J7:56:ALA:HB3	2.01	0.42
3:J8:11:LEU:HA	3:J8:11:LEU:HD23	1.72	0.42
1:K1:63:ALA:HB1	1:K1:77:THR:HG22	2.01	0.42
3:K8:7:THR:HG22	3:K8:150:TYR:CE1	2.54	0.42
2:L2:35:GLU:HG2	2:L4:13:PHE:CE2	2.53	0.42
3:M8:143:LEU:O	3:M8:177:ARG:HA	2.19	0.42
2:N5:50:VAL:HG13	2:N5:51:ALA:N	2.34	0.42
3:N8:7:THR:HG21	3:N8:149:GLY:HA3	2.01	0.42
3:N8:50:ARG:O	3:N8:53:ASP:HB2	2.18	0.42
3:N8:121:GLN:O	3:N8:125:ILE:HG13	2.19	0.42
2:O4:27:ALA:HB1	2:O4:52:ALA:HB1	2.00	0.42
2:P4:16:MET:HE3	2:P4:16:MET:HB3	1.90	0.42
2:P4:78:ARG:HD3	3:P8:163:ASN:CG	2.44	0.42
2:P7:82:ASP:O	2:P7:90:THR:HG22	2.19	0.42
3:P8:70:ARG:HG2	3:P8:172:TYR:HB2	2.01	0.42
3:P8:135:LEU:HB2	3:P8:138:GLU:HG3	2.01	0.42
3:P8:147:PRO:HD2	3:P8:150:TYR:CD1	2.54	0.42
3:P8:186:GLU:OE1	3:P8:186:GLU:N	2.39	0.42
2:Q2:40:GLY:O	2:Q2:42:VAL:HG23	2.19	0.42
2:R7:27:ALA:O	2:S3:78:ARG:NH1	2.49	0.42
3:R8:14:LEU:HD11	3:R8:37:SER:OG	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R8:39:TRP:CE2	3:R8:76:GLU:HG3	2.54	0.42
2:S3:19:ALA:HB2	2:S3:64:ALA:HB2	2.00	0.42
2:S7:78:ARG:NH2	3:U8:57:LYS:O	2.52	0.42
1:V1:23:SER:O	1:V1:44:ALA:HA	2.19	0.42
2:V2:35:GLU:HG2	2:V4:13:PHE:CE2	2.54	0.42
2:V2:90:GLY:C	2:V2:92:THR:N	2.77	0.42
2:V4:8:ILE:HD11	2:V4:57:THR:HG23	2.02	0.42
2:V4:16:MET:O	2:V4:20:ALA:N	2.43	0.42
2:V5:31:LEU:H	2:V6:82:ASN:ND2	2.17	0.42
3:V8:95:LYS:HE3	3:V8:95:LYS:HB2	1.85	0.42
3:W8:18:LEU:HB3	3:W8:22:ILE:CD1	2.49	0.42
3:W8:62:GLN:HA	3:W8:63:PRO:HD3	1.88	0.42
3:W8:95:LYS:HE3	3:W8:95:LYS:HB2	1.82	0.42
3:W8:142:ILE:HB	3:Y8:46:ILE:HG21	2.00	0.42
2:X5:34:TYR:OH	2:X6:35:GLU:OE2	2.33	0.42
3:Z8:41:GLU:OE1	3:Z8:149:GLY:N	2.52	0.42
1:11:31:ASP:O	1:11:33:ASP:N	2.47	0.42
2:32:68:GLY:O	2:32:70:VAL:HG23	2.19	0.42
3:38:93:LEU:HD12	3:38:94:ASP:N	2.34	0.42
3:38:122:THR:HG22	3:38:134:ILE:HG22	2.01	0.42
1:A1:18:ARG:NH1	1:E1:65:GLN:O	2.53	0.42
2:A5:57:THR:O	2:A5:60:GLY:N	2.48	0.42
2:B3:4:ALA:HB3	2:B3:48:GLY:O	2.19	0.42
3:B8:32:VAL:HG22	3:B8:35:GLN:NE2	2.34	0.42
2:C5:60:GLY:O	2:C5:63:ALA:N	2.50	0.42
2:D3:6:LEU:O	2:D3:54:VAL:HG11	2.18	0.42
2:D3:8:MET:CE	2:E7:17:VAL:HG11	2.47	0.42
2:D6:31:LEU:HD12	2:D6:45:VAL:O	2.18	0.42
2:D7:49:ASP:O	2:D7:53:VAL:HG23	2.18	0.42
3:D8:167:VAL:HB	3:D8:179:TYR:HB2	2.01	0.42
2:E3:47:ARG:HH11	2:E3:91:ARG:CB	2.16	0.42
3:E8:27:ARG:O	3:F8:127:ARG:HG3	2.19	0.42
1:F1:18:ARG:NH1	1:G1:65:GLN:C	2.77	0.42
2:F2:31:LEU:HB3	2:R5:82:ASN:OD1	2.18	0.42
3:F8:42:ILE:HD11	3:F8:96:LEU:HD11	2.01	0.42
3:F8:127:ARG:O	3:F8:127:ARG:HD2	2.18	0.42
2:G5:50:VAL:HG13	2:G5:51:ALA:N	2.33	0.42
3:H8:93:LEU:HB2	3:H8:98:VAL:O	2.19	0.42
1:J1:74:VAL:HG23	1:11:1:MET:SD	2.59	0.42
3:J8:123:GLN:HA	3:J8:126:ASN:HD22	1.84	0.42
3:J8:170:THR:OG1	3:J8:177:ARG:N	2.32	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K1:32:PRO:HG3	1:K1:87:MET:HE3	2.00	0.42
3:K8:60:LYS:HB2	3:K8:84:GLU:HG2	2.02	0.42
2:L3:4:ALA:O	2:L3:47:ARG:HD2	2.18	0.42
2:L4:16:MET:HG3	2:L4:42:VAL:HG12	1.99	0.42
3:L8:44:PRO:C	3:L8:46:ILE:H	2.26	0.42
3:N8:93:LEU:HB2	3:N8:98:VAL:O	2.18	0.42
1:O1:64:ARG:C	1:O1:66:THR:H	2.27	0.42
3:Q8:4:THR:O	3:Q8:42:ILE:HG23	2.19	0.42
3:Q8:95:LYS:HE3	3:Q8:95:LYS:HB2	1.90	0.42
2:R2:18:GLU:OE1	2:V5:74:HIS:NE2	2.53	0.42
3:S8:20:THR:O	3:S8:23:GLY:N	2.53	0.42
3:T8:8:TYR:HE2	3:T8:93:LEU:HD23	1.84	0.42
2:U2:29:VAL:HG11	2:U2:46:VAL:HB	2.01	0.42
3:U8:54:ALA:HB2	3:U8:95:LYS:HZ1	1.84	0.42
3:U8:63:PRO:HA	3:U8:77:VAL:HA	2.01	0.42
3:V8:29:PHE:HB2	3:V8:63:PRO:O	2.19	0.42
1:Y1:54:VAL:HG12	1:Y1:82:VAL:HG21	2.01	0.42
2:24:3:ASP:OD2	2:24:91:ARG:NE	2.40	0.42
3:38:183:SER:O	3:38:187:ILE:HG12	2.18	0.42
2:B2:47:ARG:NH2	2:B2:79:PRO:HG2	2.35	0.42
2:B2:47:ARG:HH22	2:B2:79:PRO:HG2	1.85	0.42
2:B4:57:THR:HG21	2:B4:75:VAL:HG22	2.00	0.42
3:C8:63:PRO:HA	3:C8:77:VAL:HA	2.00	0.42
3:C8:147:PRO:HD2	3:C8:150:TYR:CD1	2.53	0.42
2:D2:47:ARG:HD3	2:D2:91:ARG:HG2	2.01	0.42
2:D3:48:ARG:NH1	2:D3:85:ASP:CG	2.72	0.42
3:D8:95:LYS:HB2	3:D8:95:LYS:HE3	1.85	0.42
1:E1:60:GLY:N	1:E1:75:ASP:O	2.40	0.42
3:E8:29:PHE:CE2	3:F8:120:TYR:HD1	2.37	0.42
1:H1:89:GLY:O	2:H2:28:LYS:HE3	2.20	0.42
2:H4:66:ARG:HH12	2:H5:62:ARG:CZ	2.30	0.42
2:I5:39:GLY:HA3	2:J2:39:GLY:HA2	2.01	0.42
1:J1:10:VAL:HG22	1:J1:85:VAL:HG22	2.02	0.42
1:J1:70:ASN:C	1:J1:72:ARG:N	2.77	0.42
1:L1:70:ASN:C	1:L1:72:ARG:N	2.75	0.42
2:L4:78:ARG:HD3	3:L8:163:ASN:OD1	2.20	0.42
2:L5:50:VAL:HG13	2:L5:51:ALA:N	2.34	0.42
3:P8:122:THR:HG21	3:P8:136:PRO:HA	2.00	0.42
3:P8:130:GLN:NE2	3:P8:172:TYR:OH	2.45	0.42
2:Q2:68:GLY:O	2:Q2:70:VAL:HG23	2.19	0.42
1:R1:45:ASP:OD1	1:R1:48:GLY:N	2.47	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U1:32:PRO:HG3	1:U1:87:MET:HE1	2.01	0.42
2:U6:20:ALA:O	2:U6:24:VAL:HG22	2.19	0.42
2:V3:54:LYS:O	2:V3:58:GLU:HG3	2.19	0.42
3:V8:70:ARG:CB	3:V8:172:TYR:HB2	2.49	0.42
3:W8:194:ALA:O	3:W8:198:ILE:HG12	2.20	0.42
2:Y3:9:GLU:HG3	2:Y3:71:VAL:HB	2.02	0.42
2:Z4:53:VAL:O	2:Z4:57:THR:OG1	2.28	0.42
3:Z8:38:LEU:HB2	3:Z8:85:VAL:HG13	2.02	0.42
3:Z8:64:ALA:HB3	3:Z8:76:GLU:OE2	2.19	0.42
2:12:9:GLU:HB2	2:14:14:VAL:HG23	2.01	0.42
2:17:92:THR:C	2:17:94:GLY:H	2.27	0.42
3:28:118:GLU:HG3	3:28:119:ALA:N	2.35	0.42
2:47:19:ALA:HB2	2:47:64:ALA:HB2	2.02	0.42
1:B1:2:VAL:HG23	1:B1:57:TYR:CE1	2.55	0.42
1:B1:62:SER:HB3	1:C1:64:ARG:HH11	1.85	0.42
3:B8:121:GLN:O	3:B8:125:ILE:HG13	2.19	0.42
3:B8:140:LEU:HA	3:B8:180:LEU:O	2.20	0.42
2:C3:47:ARG:HH11	2:C3:91:ARG:HB2	1.85	0.42
2:C5:41:TYR:N	2:C5:41:TYR:CD1	2.86	0.42
2:C6:16:MET:HG3	2:C6:42:VAL:HG12	2.01	0.42
3:C8:144:GLU:HB2	3:28:46:ILE:CD1	2.48	0.42
3:C9:121:GLN:O	3:C9:125:ILE:N	2.44	0.42
2:D6:54:LYS:O	2:D6:58:GLU:HG3	2.19	0.42
2:E6:40:GLY:N	2:E7:38:GLY:O	2.52	0.42
1:F1:45:ASP:OD1	1:F1:48:GLY:N	2.46	0.42
2:I3:26:ALA:O	3:I8:12:ASP:HB3	2.19	0.42
2:I6:10:VAL:HG11	2:I6:15:GLY:HA3	2.00	0.42
3:I8:22:ILE:O	3:I8:25:THR:OG1	2.36	0.42
2:J3:30:GLU:OE1	2:J3:91:ARG:NH1	2.51	0.42
3:J8:8:TYR:CD1	3:J8:8:TYR:C	2.98	0.42
2:L2:32:ILE:HD13	2:L2:89:LEU:O	2.20	0.42
2:L6:31:LEU:HD12	2:L6:45:VAL:O	2.19	0.42
2:M5:11:ARG:HG2	2:M5:11:ARG:O	2.19	0.42
2:M5:21:ASP:OD1	2:M5:25:LYS:HD2	2.19	0.42
3:M8:134:ILE:HG12	3:M8:181:ALA:HB2	2.00	0.42
1:N1:31:ASP:HB2	1:N1:32:PRO:HD2	2.01	0.42
3:N8:95:LYS:HE3	3:N8:95:LYS:HB2	1.77	0.42
3:N8:122:THR:HG21	3:N8:136:PRO:HA	2.00	0.42
1:O1:42:VAL:HG11	1:P1:56:LEU:HD21	1.99	0.42
2:O3:45:VAL:HG11	2:O3:89:LEU:HD12	2.01	0.42
1:P1:63:ALA:HB1	1:P1:77:THR:HG22	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P3:10:VAL:O	2:P3:12:GLY:N	2.53	0.42
3:P8:95:LYS:HB2	3:P8:95:LYS:HE3	1.75	0.42
2:Q5:41:TYR:N	2:Q5:41:TYR:CD1	2.88	0.42
3:Q8:127:ARG:O	3:Q8:127:ARG:HD2	2.19	0.42
2:R2:2:ALA:N	2:R2:78:ARG:NH1	2.68	0.42
3:S8:93:LEU:HD12	3:S8:94:ASP:N	2.34	0.42
1:T1:70:ASN:C	1:T1:72:ARG:H	2.28	0.42
3:T8:7:THR:HA	3:T8:150:TYR:HE1	1.83	0.42
1:V1:28:ARG:HH12	1:V1:36:PRO:C	2.28	0.42
1:V1:45:ASP:OD1	1:V1:48:GLY:N	2.43	0.42
1:V1:59:SER:N	1:W1:75:ASP:OD2	2.37	0.42
2:V7:16:MET:HG3	2:V7:42:VAL:HG23	2.00	0.42
2:V7:20:ALA:O	2:V7:24:VAL:HG22	2.20	0.42
1:W1:41:VAL:HG11	1:W1:57:TYR:CZ	2.54	0.42
2:X2:16:MET:HG2	2:X2:44:ALA:HB2	2.01	0.42
1:Z1:70:ASN:O	1:Z1:72:ARG:N	2.52	0.42
3:Z8:79:HIS:CE1	3:Z8:81:ASP:H	2.36	0.42
2:15:47:ARG:NH2	2:15:79:PRO:HG2	2.34	0.42
2:25:10:VAL:HG13	2:25:69:GLU:O	2.19	0.42
3:38:18:LEU:CD1	3:38:156:ASN:HA	2.50	0.42
2:46:30:GLU:OE1	2:46:91:ARG:NH1	2.51	0.42
1:A1:45:ASP:OD1	1:A1:46:ALA:N	2.52	0.42
1:A1:86:GLU:HG2	1:A1:87:MET:N	2.33	0.42
2:A2:4:ALA:O	2:A2:47:ARG:HG2	2.20	0.42
2:A7:8:ILE:HD13	2:A7:19:ALA:CB	2.46	0.42
1:B1:70:ASN:C	1:B1:72:ARG:H	2.27	0.42
3:B8:42:ILE:HD13	3:B8:96:LEU:HD11	2.01	0.42
2:C7:10:VAL:HG11	2:C7:15:GLY:HA3	2.02	0.42
2:C7:51:ALA:HB2	2:23:51:ALA:HB2	2.02	0.42
3:C8:47:ALA:HB1	3:C8:50:ARG:HH12	1.84	0.42
2:E6:61:GLN:O	2:E6:65:GLU:HG3	2.20	0.42
3:F8:39:TRP:CH2	3:F8:152:VAL:HG21	2.54	0.42
2:G3:12:GLY:HA2	2:G4:9:GLU:OE2	2.19	0.42
2:I4:78:ARG:NH1	3:I8:159:GLU:CD	2.77	0.42
2:I5:19:ALA:HB2	2:I5:64:ALA:HB2	2.00	0.42
2:J5:50:VAL:HG13	2:J5:51:ALA:N	2.33	0.42
2:J7:8:ILE:O	2:J7:43:THR:HA	2.19	0.42
3:J8:70:ARG:HE	3:J8:173:GLY:HA2	1.83	0.42
3:J8:122:THR:HG22	3:J8:134:ILE:HG22	2.02	0.42
2:K3:47:ARG:HE	2:K3:91:ARG:HG2	1.85	0.42
2:K5:35:GLU:HG2	2:L2:13:PHE:CE2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:K8:19:ALA:HB3	3:K8:33:PRO:HG3	2.02	0.42
2:L2:95:MET:HE3	2:L2:95:MET:HB3	1.86	0.42
3:L8:62:GLN:HA	3:L8:63:PRO:HD3	1.86	0.42
3:L8:140:LEU:HA	3:L8:180:LEU:O	2.20	0.42
2:M2:37:THR:HG21	2:M4:13:PHE:HB2	2.01	0.42
2:N3:16:MET:SD	2:N3:44:ALA:HB2	2.60	0.42
3:N8:56:LEU:HA	3:N8:56:LEU:HD23	1.76	0.42
1:O1:79:MET:HE1	1:31:73:PRO:CB	2.47	0.42
1:O1:80:ALA:HA	1:31:15:LYS:HA	2.01	0.42
3:P8:139:SER:O	3:P8:181:ALA:HA	2.20	0.42
1:Q1:22:LEU:HD12	1:Q1:22:LEU:HA	1.85	0.42
1:Q1:32:PRO:HG3	1:Q1:87:MET:HE3	2.01	0.42
3:Q8:79:HIS:CE1	3:Q8:81:ASP:H	2.37	0.42
3:Q9:106:PRO:HA	3:Q9:146:GLN:O	2.19	0.42
1:R1:54:VAL:O	1:R1:82:VAL:HG23	2.20	0.42
2:T5:57:THR:O	2:T5:60:GLY:N	2.52	0.42
3:T8:76:GLU:OE2	3:T8:78:HIS:HB3	2.20	0.42
3:T8:95:LYS:HE3	3:T8:95:LYS:HB2	1.91	0.42
3:T8:140:LEU:HA	3:T8:180:LEU:O	2.19	0.42
3:U8:95:LYS:HE3	3:U8:95:LYS:HB2	1.84	0.42
3:U8:118:GLU:HG3	3:U8:119:ALA:N	2.34	0.42
3:V8:45:GLY:HA3	3:V8:72:TYR:HB2	2.01	0.42
2:W2:9:GLU:HB2	2:W4:14:VAL:HG23	2.00	0.42
2:W5:41:TYR:CD1	2:W5:41:TYR:N	2.88	0.42
2:X3:4:ALA:HB3	2:X3:48:GLY:O	2.19	0.42
2:X6:4:ALA:HA	2:X6:77:PRO:O	2.20	0.42
2:Y5:56:THR:O	2:Y5:59:GLY:N	2.53	0.42
2:Y6:32:ILE:HD11	2:Y6:47:ARG:HD2	2.02	0.42
2:Z3:18:GLU:OE1	2:Z4:74:HIS:NE2	2.52	0.42
2:15:89:LEU:O	2:15:91:ARG:N	2.46	0.42
3:18:140:LEU:HA	3:18:180:LEU:O	2.20	0.42
2:22:47:ARG:NH2	2:22:84:ASP:OD2	2.53	0.42
2:36:23:MET:HG2	2:36:56:ALA:O	2.20	0.42
3:38:9:ILE:HG21	3:38:153:LEU:HB2	2.02	0.42
3:38:123:GLN:HE22	3:39:30:LEU:CB	2.33	0.42
1:41:54:VAL:O	1:41:82:VAL:HG23	2.19	0.42
2:47:21:ASP:OD1	2:47:25:LYS:HE3	2.19	0.42
2:A5:13:PHE:HB2	2:A6:37:THR:HG21	2.02	0.42
2:B5:45:VAL:HG11	2:B5:89:LEU:HD22	2.02	0.42
2:B7:78:ARG:NH2	3:J8:56:LEU:O	2.53	0.42
2:D4:52:ALA:O	2:D4:56:ALA:N	2.36	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D6:27:ALA:HB1	2:D6:52:ALA:HB1	2.02	0.42
3:D8:27:ARG:HD3	3:P8:127:ARG:HD3	2.00	0.42
3:D8:152:VAL:CG2	3:D8:171:PRO:HG3	2.49	0.42
2:E2:41:TYR:CE2	2:E2:71:VAL:HG21	2.54	0.42
2:E2:47:ARG:NH2	2:E2:84:ASP:OD2	2.52	0.42
2:H4:10:VAL:HG11	2:H4:15:GLY:HA3	2.01	0.42
3:H8:142:ILE:HA	3:H8:178:LEU:O	2.18	0.42
3:H9:148:ALA:HA	3:H9:176:GLY:N	2.34	0.42
3:I8:42:ILE:CD1	3:I8:96:LEU:HD11	2.50	0.42
1:J1:21:GLY:HA2	2:12:58:GLU:HB3	2.01	0.42
2:J4:32:ILE:HD13	2:J4:90:GLY:N	2.35	0.42
3:J8:20:THR:O	3:J8:23:GLY:N	2.52	0.42
3:J8:62:GLN:HA	3:J8:63:PRO:HD3	1.88	0.42
3:K8:70:ARG:HG2	3:K8:173:GLY:N	2.34	0.42
2:M3:24:VAL:HG11	2:M4:82:ASN:HB3	2.01	0.42
2:M6:32:ILE:HG21	2:M6:90:GLY:CA	2.50	0.42
2:N5:31:LEU:HA	2:N5:46:VAL:HG12	2.02	0.42
3:N8:7:THR:HA	3:N8:150:TYR:HE1	1.84	0.42
1:O1:83:ASP:OD2	1:31:13:SER:CB	2.68	0.42
2:O2:90:GLY:C	2:O2:92:THR:N	2.76	0.42
2:O3:64:ALA:O	2:O3:68:GLY:N	2.52	0.42
3:O8:8:TYR:HE2	3:O8:93:LEU:HB3	1.83	0.42
3:O8:17:GLN:CD	3:O8:159:GLU:HG3	2.44	0.42
3:O8:61:VAL:HG12	3:O8:62:GLN:N	2.29	0.42
2:P3:53:VAL:O	2:P3:57:THR:OG1	2.37	0.42
2:Q6:30:GLU:OE1	2:Q6:91:ARG:NH2	2.44	0.42
2:U5:47:ARG:NH1	2:U5:84:ASP:OD1	2.52	0.42
2:U5:82:ASN:OD1	2:42:31:LEU:HB3	2.18	0.42
2:W4:66:ARG:NH1	2:W5:62:ARG:NH2	2.68	0.42
3:W8:130:GLN:HB2	3:W8:168:ASN:OD1	2.19	0.42
2:Y2:47:ARG:CD	2:Y2:91:ARG:HG2	2.49	0.42
3:Z8:183:SER:OG	3:Z8:186:GLU:OE2	2.37	0.42
2:22:7:MET:HE3	2:22:7:MET:HB2	1.94	0.42
3:38:13:ALA:HA	3:38:35:GLN:O	2.20	0.42
3:38:123:GLN:HG3	3:39:23:GLY:HA3	2.02	0.42
3:48:44:PRO:C	3:48:46:ILE:H	2.28	0.42
2:A2:3:ASP:OD2	2:A2:91:ARG:NH2	2.51	0.42
2:A4:57:THR:CG2	2:A4:73:VAL:HG13	2.50	0.42
2:A6:16:MET:HG2	2:A6:44:ALA:HB2	2.02	0.42
3:A8:63:PRO:HB3	3:A8:77:VAL:HG12	2.01	0.42
3:A9:4:THR:N	3:A9:43:ALA:O	2.42	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B3:32:ILE:HG13	2:B3:33:GLY:N	2.33	0.42
3:C8:8:TYR:CZ	3:C8:93:LEU:HD23	2.53	0.42
3:C9:140:LEU:HA	3:C9:181:ALA:HA	2.02	0.42
1:D1:47:VAL:CG1	1:E1:14:ARG:HG3	2.49	0.42
3:D8:66:GLN:HB3	3:P8:124:ILE:HG21	2.01	0.42
3:E8:8:TYR:HB3	3:E8:103:ARG:HD2	2.01	0.42
3:G8:118:GLU:HG3	3:G8:119:ALA:N	2.35	0.42
3:H8:186:GLU:OE1	3:H8:186:GLU:N	2.38	0.42
2:I7:5:LEU:HD23	2:I7:47:ARG:HD3	2.01	0.42
1:K1:86:GLU:OE1	1:K1:89:GLY:N	2.52	0.42
2:K3:4:ALA:HB2	2:K3:50:VAL:HG22	2.01	0.42
1:L1:2:VAL:HG23	1:L1:57:TYR:CE1	2.54	0.42
2:L2:32:ILE:HD13	2:L2:90:GLY:HA3	2.02	0.42
2:L5:32:ILE:HD13	2:L5:90:GLY:HA3	2.02	0.42
2:L5:41:TYR:N	2:L5:41:TYR:CD1	2.88	0.42
2:L6:4:ALA:O	2:L6:47:ARG:HG2	2.19	0.42
2:L7:32:ILE:HD13	2:L7:90:GLY:CA	2.49	0.42
3:M8:42:ILE:HD11	3:M8:96:LEU:HD11	2.01	0.42
3:O8:111:HIS:CG	3:O8:111:HIS:O	2.71	0.42
2:P5:9:GLU:HG3	2:P5:43:THR:OG1	2.20	0.42
2:P5:50:VAL:HG13	2:P5:51:ALA:N	2.35	0.42
2:Q5:57:THR:O	2:Q5:60:GLY:N	2.49	0.42
3:R8:39:TRP:CZ2	3:R8:76:GLU:HG3	2.55	0.42
2:T5:34:TYR:HA	2:T5:43:THR:O	2.19	0.42
2:U2:32:ILE:HG22	2:U2:45:VAL:HB	2.02	0.42
3:U8:7:THR:HG22	3:U8:147:PRO:HG2	2.01	0.42
2:W2:78:ARG:NE	2:W5:28:LYS:HB2	2.34	0.42
2:W5:18:GLU:CD	2:W6:74:HIS:HE2	2.28	0.42
2:X3:47:ARG:NH1	2:X3:84:ASP:CG	2.76	0.42
3:X8:53:ASP:OD2	3:48:117:VAL:HG13	2.19	0.42
2:Y3:13:PHE:HB2	2:Y4:37:THR:HG21	2.01	0.42
2:Y6:4:ALA:HB2	2:Y6:50:VAL:HA	2.01	0.42
3:Y8:186:GLU:O	3:Y8:190:ALA:N	2.46	0.42
2:Z7:10:VAL:HG11	2:Z7:15:GLY:HA3	2.02	0.42
3:Z8:111:HIS:O	3:Z8:111:HIS:CG	2.72	0.42
3:Z9:94:ASP:C	3:Z9:97:GLU:H	2.27	0.42
2:13:5:LEU:O	2:13:75:VAL:HG13	2.19	0.42
2:15:57:THR:O	2:15:60:GLY:N	2.53	0.42
2:17:21:ASP:OD1	2:17:25:LYS:HE3	2.20	0.42
2:23:84:ASP:HB3	2:23:91:ARG:O	2.19	0.42
2:34:66:ARG:HE	2:34:66:ARG:HB3	1.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:42:19:ALA:HB2	2:42:64:ALA:HB2	2.02	0.42
3:48:51:VAL:HG13	3:48:92:ILE:HG12	2.00	0.42
2:A2:47:ARG:HD3	2:A2:91:ARG:HG2	2.02	0.42
3:A8:123:GLN:HG3	3:A9:23:GLY:HA3	2.02	0.42
3:A8:144:GLU:HA	3:A8:176:GLY:O	2.20	0.42
3:B8:32:VAL:H	3:B8:35:GLN:CD	2.25	0.42
3:B8:74:LEU:HD22	3:B8:171:PRO:O	2.20	0.42
1:C1:26:LEU:HD12	1:C1:26:LEU:HA	1.87	0.42
3:C8:40:VAL:O	3:C8:74:LEU:HD12	2.20	0.42
3:C8:50:ARG:HB2	3:M8:114:ILE:HD11	2.02	0.42
2:D2:2:ALA:N	2:D2:78:ARG:NH1	2.67	0.42
2:D4:82:ASN:O	2:D4:82:ASN:ND2	2.41	0.42
2:D6:20:ALA:O	2:D6:24:VAL:HG22	2.20	0.42
3:D8:106:PRO:HG2	3:D8:201:VAL:HB	2.01	0.42
3:D9:11:LEU:N	3:D9:37:SER:O	2.44	0.42
3:F8:23:GLY:HA2	3:F8:30:LEU:HG	2.02	0.42
3:F9:109:MET:N	3:F9:144:GLU:O	2.50	0.42
1:G1:25:LEU:O	1:G1:42:VAL:HA	2.19	0.42
2:H4:70:VAL:HG23	2:H4:70:VAL:O	2.19	0.42
2:H7:17:VAL:CG1	2:I3:7:MET:HE1	2.47	0.42
3:H8:35:GLN:HG2	3:H8:80:PHE:CG	2.54	0.42
1:I1:45:ASP:OD1	1:I1:47:VAL:N	2.35	0.42
2:I5:90:GLY:C	2:I5:92:THR:H	2.28	0.42
3:I8:23:GLY:CA	3:I8:30:LEU:HG	2.49	0.42
3:I9:139:SER:O	3:I9:181:ALA:HA	2.20	0.42
3:I9:148:ALA:HA	3:I9:176:GLY:N	2.35	0.42
1:J1:41:VAL:HG11	1:J1:57:TYR:OH	2.19	0.42
2:J7:58:GLU:O	2:J7:62:ARG:HG3	2.19	0.42
2:K6:21:ASP:OD1	2:K6:25:LYS:HE3	2.20	0.42
2:K6:32:ILE:HD11	2:K6:47:ARG:HD2	2.02	0.42
3:K8:11:LEU:HD23	3:K8:11:LEU:HA	1.81	0.42
3:K8:62:GLN:HA	3:K8:63:PRO:HD3	1.88	0.42
3:K9:38:LEU:N	3:K9:77:VAL:O	2.49	0.42
1:N1:2:VAL:CG2	1:N1:57:TYR:CE1	3.03	0.42
2:N7:28:LYS:HA	2:P3:78:ARG:HH12	1.82	0.42
2:O5:14:VAL:HG13	2:O6:7:MET:HE3	2.01	0.42
2:O6:13:PHE:HB2	2:O7:37:THR:HG21	2.02	0.42
2:O7:21:ASP:OD1	2:O7:25:LYS:HE3	2.20	0.42
3:O8:186:GLU:O	3:O8:190:ALA:N	2.48	0.42
3:P8:20:THR:OG1	3:P8:21:PHE:N	2.51	0.42
1:R1:16:GLU:O	1:R1:19:ILE:HG12	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:R8:35:GLN:HG2	3:R8:80:PHE:CG	2.55	0.42
1:U1:70:ASN:C	1:U1:72:ARG:H	2.26	0.42
2:V5:10:VAL:HG13	2:V5:69:GLU:O	2.20	0.42
2:W5:13:PHE:CD2	2:W6:43:THR:HG21	2.53	0.42
2:W6:47:ARG:HH22	2:W6:79:PRO:HG3	1.84	0.42
3:W8:21:PHE:O	3:W8:25:THR:OG1	2.38	0.42
3:W8:93:LEU:HD12	3:W8:94:ASP:N	2.35	0.42
1:X1:33:ASP:HB3	1:X1:35:THR:HG23	2.01	0.42
2:X3:78:ARG:HH11	2:47:28:LYS:HA	1.80	0.42
2:X6:30:GLU:OE1	2:X6:91:ARG:NH2	2.44	0.42
3:X8:35:GLN:HB3	3:X8:36:ALA:H	1.66	0.42
3:X8:63:PRO:HB3	3:X8:77:VAL:HG12	2.02	0.42
3:Z9:148:ALA:HA	3:Z9:176:GLY:H	1.84	0.42
1:11:28:ARG:NH2	1:11:38:GLY:O	2.53	0.42
2:23:13:PHE:HB2	2:24:37:THR:HG21	2.02	0.42
2:23:30:GLU:OE1	2:23:91:ARG:NH2	2.50	0.42
2:A2:29:VAL:HG11	2:A2:46:VAL:CG2	2.48	0.42
2:A2:30:GLU:OE1	2:A2:91:ARG:NH1	2.37	0.42
3:A8:37:SER:HA	3:A8:78:HIS:HA	2.02	0.42
1:B1:69:THR:H	1:B1:72:ARG:HH21	1.66	0.42
2:B2:20:ALA:HA	2:B2:23:MET:HE3	2.01	0.42
2:C4:8:ILE:HD12	2:C4:73:VAL:HG22	2.01	0.42
2:D4:82:ASN:HD22	2:D4:82:ASN:C	2.24	0.42
3:D8:59:THR:HB	3:D8:84:GLU:HG3	2.02	0.42
2:E4:57:THR:HG22	2:E4:73:VAL:HG13	2.02	0.42
2:F4:20:ALA:HB1	2:F4:31:LEU:HD22	2.02	0.42
3:F8:110:THR:O	3:F8:143:LEU:HA	2.20	0.42
2:G2:84:ASP:O	2:G2:92:THR:HG22	2.19	0.42
2:G4:31:LEU:HD12	2:G4:45:VAL:O	2.19	0.42
3:H8:183:SER:O	3:H8:187:ILE:HG12	2.19	0.42
3:K8:111:HIS:HA	3:K8:142:ILE:O	2.20	0.42
3:K8:186:GLU:O	3:K8:190:ALA:N	2.44	0.42
1:M1:22:LEU:HG	1:M1:44:ALA:HB1	2.02	0.42
2:M5:13:PHE:N	2:M6:9:GLU:OE1	2.53	0.42
2:M5:23:MET:HG2	2:M5:56:ALA:O	2.20	0.42
2:N3:53:VAL:O	2:N3:57:THR:OG1	2.35	0.42
2:N5:7:MET:HA	2:N5:44:ALA:O	2.19	0.42
3:N8:9:ILE:O	3:N8:39:TRP:N	2.53	0.42
3:N8:31:PRO:HB3	3:N8:78:HIS:CG	2.55	0.42
2:O6:23:MET:HB3	2:O6:56:ALA:HB1	2.02	0.42
1:P1:2:VAL:HG23	1:P1:57:TYR:CE1	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P1:28:ARG:NH2	1:P1:38:GLY:O	2.52	0.42
2:P5:46:VAL:O	2:P5:47:ARG:HG2	2.20	0.42
2:Q2:47:ARG:HD2	2:Q2:89:LEU:O	2.19	0.42
3:Q8:70:ARG:HG2	3:Q8:173:GLY:N	2.35	0.42
2:R6:14:VAL:HG23	2:R7:9:GLU:HB2	2.02	0.42
2:T3:17:VAL:CG2	2:T4:7:MET:HE1	2.49	0.42
3:T9:39:TRP:HA	3:T9:76:GLU:HA	2.00	0.42
3:U8:42:ILE:CD1	3:U8:96:LEU:HD11	2.49	0.42
3:U8:45:GLY:HA3	3:U8:72:TYR:HB2	2.02	0.42
2:W2:37:THR:OG1	2:W4:40:GLY:HA2	2.20	0.42
3:X8:70:ARG:CB	3:X8:172:TYR:HB2	2.50	0.42
3:Y8:127:ARG:O	3:Y8:127:ARG:HD2	2.20	0.42
1:Z1:28:ARG:HH11	1:Z1:36:PRO:HB2	1.85	0.42
1:Z1:32:PRO:HG3	1:Z1:87:MET:HE1	2.02	0.42
3:Z8:6:ARG:NH1	3:Z8:72:TYR:OH	2.53	0.42
2:16:47:ARG:NH1	2:16:84:ASP:OD2	2.53	0.42
1:21:7:VAL:HG21	1:21:28:ARG:HD3	2.02	0.42
2:22:47:ARG:CD	2:22:91:ARG:HG2	2.43	0.42
2:23:49:ASP:N	2:23:49:ASP:OD1	2.46	0.42
2:A7:20:ALA:HB1	2:A7:31:LEU:HD22	2.02	0.41
2:B2:16:MET:O	2:B2:20:ALA:N	2.30	0.41
3:C8:120:TYR:HD1	3:28:29:PHE:CZ	2.37	0.41
3:C8:162:ALA:HB1	3:C8:186:GLU:HB3	2.02	0.41
2:D6:57:THR:HG21	2:D6:75:VAL:HG22	2.02	0.41
3:D8:148:ALA:O	3:D8:171:PRO:HA	2.20	0.41
2:E2:68:GLY:O	2:E2:70:VAL:HG23	2.19	0.41
3:F8:29:PHE:CZ	3:Q8:120:TYR:HD1	2.38	0.41
3:F8:111:HIS:HB3	3:F8:143:LEU:HD13	2.02	0.41
3:F8:142:ILE:HA	3:F8:178:LEU:O	2.20	0.41
1:G1:28:ARG:NH2	1:G1:38:GLY:H	2.17	0.41
1:H1:7:VAL:HG12	1:I1:87:MET:HG2	2.01	0.41
1:H1:47:VAL:CG1	1:Z1:14:ARG:HG3	2.50	0.41
2:H2:76:ILE:HA	2:H2:77:PRO:HD3	1.93	0.41
2:H5:9:GLU:HG3	2:H5:43:THR:OG1	2.19	0.41
3:H8:29:PHE:CD2	3:H8:63:PRO:HD2	2.55	0.41
3:H8:127:ARG:HH21	3:W8:67:VAL:CG1	2.32	0.41
2:J7:53:VAL:HG23	2:J7:54:LYS:N	2.35	0.41
2:K7:53:VAL:HA	2:K7:56:ALA:HB3	2.00	0.41
2:L3:49:ASP:OD1	2:L3:49:ASP:N	2.53	0.41
3:L8:111:HIS:CG	3:L8:111:HIS:O	2.72	0.41
1:N1:33:ASP:HB3	1:N1:35:THR:HG23	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N1:66:THR:O	1:N1:69:THR:OG1	2.30	0.41
3:N8:50:ARG:CD	3:N8:95:LYS:HD3	2.47	0.41
3:N8:62:GLN:HA	3:N8:63:PRO:HD3	1.87	0.41
3:N8:127:ARG:O	3:N8:127:ARG:HD2	2.19	0.41
3:O8:11:LEU:HD23	3:O8:11:LEU:HA	1.53	0.41
3:O8:93:LEU:HD12	3:O8:94:ASP:N	2.35	0.41
1:P1:70:ASN:C	1:P1:72:ARG:H	2.28	0.41
3:P8:50:ARG:CD	3:P8:95:LYS:HD3	2.50	0.41
3:R8:70:ARG:HE	3:R8:173:GLY:HA2	1.85	0.41
3:R8:95:LYS:HE3	3:R8:95:LYS:HB2	1.81	0.41
2:S4:20:ALA:HB1	2:S4:31:LEU:HD22	2.02	0.41
1:T1:31:ASP:HB2	1:T1:32:PRO:HD2	2.02	0.41
2:T2:9:GLU:HG3	2:T2:43:THR:OG1	2.20	0.41
2:T2:68:GLY:O	2:T2:70:VAL:HG23	2.20	0.41
3:U8:20:THR:OG1	3:U8:21:PHE:N	2.52	0.41
1:V1:25:LEU:O	1:V1:42:VAL:HA	2.20	0.41
3:W8:127:ARG:HD3	3:Y8:27:ARG:HD2	2.01	0.41
3:X8:27:ARG:HD2	3:48:127:ARG:HD3	2.01	0.41
3:X9:45:GLY:N	3:X9:71:ALA:O	2.53	0.41
2:Y2:11:ARG:HB3	2:Y2:69:GLU:HG2	2.00	0.41
2:Y5:49:VAL:HG13	2:Y5:50:ALA:N	2.35	0.41
2:Y7:19:ALA:HB2	2:Y7:64:ALA:HB2	2.02	0.41
3:Y8:47:ALA:HB1	3:Y8:50:ARG:HH12	1.84	0.41
3:Y8:63:PRO:HB3	3:Y8:77:VAL:HG12	2.02	0.41
3:Y8:148:ALA:O	3:Y8:171:PRO:HA	2.20	0.41
2:Z7:29:VAL:HG13	2:Z7:52:ALA:HB1	2.01	0.41
2:12:13:PHE:CD1	2:12:13:PHE:C	2.98	0.41
2:14:31:LEU:HA	2:14:46:VAL:HG12	2.02	0.41
3:18:60:LYS:HE2	3:18:84:GLU:CD	2.45	0.41
3:18:61:VAL:CG1	3:18:77:VAL:HB	2.49	0.41
3:29:107:GLN:N	3:29:146:GLN:O	2.30	0.41
2:35:24:VAL:HG11	2:36:82:ASN:HB3	2.01	0.41
2:35:41:TYR:N	2:35:41:TYR:CD1	2.88	0.41
3:38:17:GLN:NE2	3:38:159:GLU:HG3	2.34	0.41
3:38:87:ALA:O	3:38:91:THR:HG23	2.20	0.41
1:A1:16:GLU:O	1:A1:19:ILE:HG12	2.20	0.41
2:C4:20:ALA:O	2:C4:24:VAL:HG22	2.20	0.41
3:D8:8:TYR:HE2	3:D8:93:LEU:HD23	1.81	0.41
2:E4:53:VAL:O	2:E4:57:THR:OG1	2.30	0.41
3:E8:8:TYR:OH	3:E8:93:LEU:HD23	2.20	0.41
2:F5:46:VAL:O	2:F5:47:ARG:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H8:152:VAL:CG2	3:H8:171:PRO:HG3	2.50	0.41
3:I8:9:ILE:O	3:I8:38:LEU:HD12	2.19	0.41
2:J3:49:ASP:N	2:J3:49:ASP:OD1	2.53	0.41
3:L8:106:PRO:HG3	3:L8:150:TYR:CD2	2.55	0.41
2:M2:35:GLU:HG2	2:M4:13:PHE:CE2	2.55	0.41
1:N1:81:ILE:HD12	2:N5:77:PRO:HG2	2.02	0.41
2:N2:47:ARG:HH22	2:N2:79:PRO:HG2	1.85	0.41
3:N8:7:THR:HG22	3:N8:150:TYR:CE1	2.54	0.41
2:O7:45:VAL:HG11	2:O7:89:LEU:HD22	2.01	0.41
2:Q2:10:VAL:HG12	2:Q2:12:GLY:H	1.85	0.41
3:Q8:18:LEU:HB3	3:Q8:22:ILE:CD1	2.50	0.41
2:R2:92:THR:HA	2:R2:93:PRO:HD3	1.95	0.41
3:R8:87:ALA:O	3:R8:91:THR:HG23	2.20	0.41
3:R8:144:GLU:OE1	3:S8:44:PRO:HG3	2.21	0.41
2:S7:92:THR:C	2:S7:94:GLY:H	2.28	0.41
2:T2:23:MET:HG2	2:T2:56:ALA:O	2.20	0.41
3:U8:23:GLY:CA	3:U8:30:LEU:HG	2.50	0.41
3:U8:93:LEU:HD12	3:U8:94:ASP:N	2.35	0.41
2:V5:47:ARG:CZ	2:V5:91:ARG:HG3	2.49	0.41
2:W5:2:ALA:HB1	2:W5:78:ARG:NH1	2.35	0.41
2:W5:2:ALA:HB1	2:W5:78:ARG:HH22	1.85	0.41
3:W8:70:ARG:HE	3:W8:173:GLY:HA2	1.85	0.41
3:W8:170:THR:HG1	3:W8:177:ARG:H	1.61	0.41
1:X1:45:ASP:OD1	1:X1:48:GLY:N	2.43	0.41
3:Y8:122:THR:HG22	3:Y8:134:ILE:HG22	2.01	0.41
2:Z3:27:ALA:HB1	2:Z3:52:ALA:HB1	2.01	0.41
2:13:4:ALA:HB3	2:13:48:GLY:O	2.20	0.41
2:16:4:ALA:O	2:16:47:ARG:HG2	2.20	0.41
2:33:19:ALA:HB2	2:33:64:ALA:HB2	2.02	0.41
2:36:5:LEU:HD11	2:36:7:MET:HE2	2.01	0.41
2:45:41:TYR:N	2:45:41:TYR:CD1	2.88	0.41
3:48:95:LYS:HE3	3:48:95:LYS:HB2	1.86	0.41
3:48:118:GLU:HG3	3:48:119:ALA:N	2.36	0.41
3:48:186:GLU:OE1	3:48:186:GLU:N	2.35	0.41
2:A3:3:ASP:OD2	2:A3:91:ARG:NH1	2.53	0.41
2:B6:47:ARG:HH22	2:B6:79:PRO:CG	2.32	0.41
2:C3:51:ALA:HB2	2:M7:51:ALA:HB2	2.03	0.41
3:C8:51:VAL:HG13	3:C8:92:ILE:HG12	2.02	0.41
2:D2:16:MET:HE2	2:D2:42:VAL:HG11	2.03	0.41
2:D3:13:GLY:HA2	2:D4:9:GLU:OE2	2.21	0.41
2:E2:8:ILE:O	2:E2:43:THR:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E8:8:TYR:CE2	3:E8:93:LEU:HD23	2.56	0.41
3:E8:11:LEU:HD23	3:E8:11:LEU:HA	1.69	0.41
3:E8:169:VAL:HG22	3:E8:178:LEU:CD1	2.50	0.41
1:F1:8:GLY:HA3	1:G1:86:GLU:O	2.21	0.41
1:F1:64:ARG:NH1	1:G1:62:SER:HA	2.35	0.41
1:G1:45:ASP:OD1	1:G1:46:ALA:N	2.53	0.41
2:G6:14:VAL:HG23	2:G7:9:GLU:HB2	2.02	0.41
3:G8:4:THR:O	3:G8:42:ILE:HG23	2.20	0.41
3:G8:9:ILE:CD1	3:G8:150:TYR:HA	2.35	0.41
3:G8:62:GLN:HA	3:G8:63:PRO:HD3	1.86	0.41
2:H7:51:ALA:HB2	2:W3:51:ALA:HB2	2.01	0.41
3:H8:74:LEU:HA	3:H8:74:LEU:HD12	1.79	0.41
2:I2:47:ARG:HD2	2:I2:89:LEU:O	2.20	0.41
3:I8:13:ALA:HA	3:I8:35:GLN:O	2.20	0.41
3:J8:142:ILE:HB	3:L8:46:ILE:CG2	2.50	0.41
2:K6:13:PHE:HB2	2:K7:37:THR:CG2	2.49	0.41
3:K8:9:ILE:HD13	3:K8:153:LEU:HB2	2.01	0.41
3:L8:139:SER:O	3:L8:181:ALA:HA	2.21	0.41
2:M3:5:LEU:HD12	2:M3:6:GLY:H	1.85	0.41
2:M4:78:ARG:HD3	3:M8:163:ASN:OD1	2.20	0.41
2:M6:3:ASP:O	2:M6:47:ARG:NH1	2.41	0.41
3:M8:110:THR:O	3:M8:143:LEU:HA	2.20	0.41
3:O8:79:HIS:CE1	3:O8:81:ASP:H	2.38	0.41
1:P1:64:ARG:C	1:P1:66:THR:H	2.27	0.41
3:Q8:123:GLN:CG	3:Q9:23:GLY:HA3	2.49	0.41
1:R1:45:ASP:OD1	1:R1:47:VAL:N	2.38	0.41
2:R4:62:ARG:NE	2:R5:66:ARG:NH1	2.68	0.41
3:R8:104:LEU:HA	3:R8:204:VAL:O	2.20	0.41
3:R9:126:ASN:CB	3:R9:134:ILE:H	2.34	0.41
2:S2:5:LEU:HD11	2:S2:45:VAL:HG13	2.02	0.41
3:S9:44:PRO:HA	3:S9:71:ALA:O	2.19	0.41
2:T5:50:VAL:HG13	2:T5:51:ALA:N	2.35	0.41
2:T7:36:LYS:NZ	2:U3:36:LYS:O	2.34	0.41
2:U4:31:LEU:HA	2:U4:46:VAL:HG12	2.01	0.41
2:U5:18:GLU:OE1	2:U6:74:HIS:NE2	2.50	0.41
3:U8:6:ARG:NH1	3:U8:72:TYR:OH	2.53	0.41
3:W8:26:ALA:HB1	3:W8:64:ALA:HB1	2.01	0.41
3:W8:118:GLU:HG3	3:W8:119:ALA:N	2.34	0.41
2:Y3:74:HIS:CG	2:Y3:75:VAL:H	2.39	0.41
3:Y8:109:MET:HB2	3:Y8:144:GLU:HB3	2.00	0.41
2:Z2:54:LYS:HZ2	2:Z5:55:ALA:HB2	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z3:13:PHE:HB2	2:Z4:37:THR:CG2	2.47	0.41
2:Z7:23:MET:HG2	2:Z7:56:ALA:O	2.20	0.41
3:Z8:35:GLN:OE1	3:Z8:78:HIS:ND1	2.54	0.41
3:18:41:GLU:HB2	3:18:74:LEU:HD13	2.02	0.41
2:27:87:LEU:HB3	2:27:89:LEU:CD1	2.50	0.41
1:31:2:VAL:HG23	1:31:57:TYR:CE1	2.56	0.41
2:33:27:ALA:HB3	2:33:56:ALA:HB2	2.02	0.41
3:38:79:HIS:CE1	3:38:81:ASP:HB2	2.55	0.41
3:38:119:ALA:O	3:38:122:THR:OG1	2.37	0.41
2:44:95:MET:N	2:44:95:MET:SD	2.93	0.41
2:46:40:GLY:N	2:47:38:GLY:O	2.53	0.41
1:A1:66:THR:HG22	1:A1:67:GLU:O	2.21	0.41
2:B5:36:LYS:HZ1	2:B6:35:GLU:CD	2.24	0.41
3:B8:47:ALA:HB1	3:B8:50:ARG:HH12	1.86	0.41
1:C1:68:VAL:C	1:C1:72:ARG:HH12	2.28	0.41
2:E6:16:MET:HG3	2:E6:42:VAL:HG12	2.02	0.41
3:E8:93:LEU:HD12	3:E8:94:ASP:N	2.34	0.41
3:F9:144:GLU:HA	3:F9:176:GLY:O	2.20	0.41
2:G5:49:ASP:O	2:G5:53:VAL:HG23	2.20	0.41
2:H5:61:GLN:HB2	2:H5:73:VAL:HG21	2.02	0.41
3:H8:63:PRO:HA	3:H8:77:VAL:HA	2.02	0.41
2:I2:13:PHE:CD1	2:I2:13:PHE:C	2.97	0.41
2:I6:32:ILE:HG21	2:I6:90:GLY:CA	2.50	0.41
3:I8:61:VAL:O	3:I8:62:GLN:HG3	2.20	0.41
3:I8:169:VAL:HG22	3:I8:178:LEU:HD13	2.01	0.41
2:J2:34:TYR:OH	2:J2:36:LYS:NZ	2.54	0.41
2:J3:17:VAL:CG2	2:J4:7:MET:HE1	2.44	0.41
2:J5:9:GLU:HB2	2:12:14:VAL:CG2	2.50	0.41
3:K8:93:LEU:HD12	3:K8:94:ASP:N	2.35	0.41
3:K8:169:VAL:HG12	3:K8:171:PRO:HD3	2.03	0.41
2:L4:16:MET:HE3	2:L4:16:MET:HB3	1.96	0.41
2:L6:16:MET:O	2:L6:20:ALA:N	2.46	0.41
2:L7:12:GLY:HA3	2:23:9:GLU:OE2	2.20	0.41
3:L8:171:PRO:HD2	3:L8:172:TYR:CD2	2.55	0.41
2:M3:90:GLY:O	2:M3:91:ARG:C	2.62	0.41
2:M7:89:LEU:HD23	2:M7:89:LEU:HA	1.80	0.41
2:P5:13:PHE:HB2	2:P6:37:THR:HG21	2.02	0.41
3:P8:21:PHE:HE2	3:P8:169:VAL:HB	1.84	0.41
3:P8:40:VAL:O	3:P8:74:LEU:HD12	2.20	0.41
3:Q8:76:GLU:OE1	3:Q8:78:HIS:HB3	2.21	0.41
2:R3:5:LEU:HD21	2:R3:7:MET:HE2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R7:74:HIS:CG	2:R7:75:VAL:N	2.88	0.41
3:R8:171:PRO:HD2	3:R8:172:TYR:CE2	2.55	0.41
2:S3:45:VAL:HG11	2:S3:89:LEU:HD12	2.02	0.41
3:S8:39:TRP:CZ3	3:S8:152:VAL:HG21	2.55	0.41
3:S8:79:HIS:CE1	3:S8:81:ASP:H	2.38	0.41
1:T1:59:SER:HA	1:T1:76:ALA:HA	2.02	0.41
2:T3:34:TYR:OH	2:T4:35:GLU:OE2	2.29	0.41
2:T6:13:PHE:O	2:T6:17:VAL:HG23	2.20	0.41
3:T8:117:VAL:HG12	3:T8:121:GLN:HB3	2.01	0.41
1:V1:28:ARG:NH2	1:V1:38:GLY:H	2.19	0.41
3:V8:186:GLU:OE1	3:V8:186:GLU:N	2.39	0.41
2:W4:4:ALA:HA	2:W4:77:PRO:O	2.20	0.41
2:W5:50:VAL:HG13	2:W5:51:ALA:N	2.35	0.41
2:X2:13:PHE:C	2:X2:13:PHE:CD1	2.99	0.41
2:Y6:47:ARG:HD3	2:Y6:91:ARG:HG2	2.02	0.41
3:Y8:11:LEU:HD23	3:Y8:11:LEU:HA	1.73	0.41
1:Z1:54:VAL:O	1:Z1:82:VAL:HG23	2.21	0.41
1:Z1:64:ARG:C	1:Z1:66:THR:H	2.28	0.41
3:Z8:125:ILE:HD12	3:Z8:134:ILE:HD12	2.02	0.41
3:Z8:127:ARG:HD2	3:Z8:127:ARG:O	2.19	0.41
2:25:61:GLN:O	2:25:65:GLU:HG3	2.21	0.41
3:29:144:GLU:HA	3:29:176:GLY:O	2.20	0.41
3:38:8:TYR:HA	3:38:40:VAL:HG22	2.03	0.41
2:43:47:ARG:NH2	2:43:79:PRO:HG2	2.35	0.41
2:A2:3:ASP:O	2:A2:47:ARG:NH1	2.38	0.41
2:A3:8:ILE:CD1	2:A3:19:ALA:HB1	2.51	0.41
3:B8:19:ALA:HB3	3:B8:33:PRO:HG3	2.02	0.41
3:B8:65:VAL:N	3:B8:76:GLU:OE2	2.45	0.41
3:B8:125:ILE:HD13	3:J8:49:ASN:HD21	1.86	0.41
3:C8:140:LEU:HA	3:C8:180:LEU:O	2.20	0.41
1:D1:45:ASP:OD1	1:D1:47:VAL:N	2.35	0.41
2:D4:19:ALA:HB2	2:D4:64:ALA:HB2	2.02	0.41
2:D4:57:THR:HG22	2:D4:73:VAL:HG13	2.03	0.41
3:D8:121:GLN:NE2	3:N8:49:ASN:O	2.50	0.41
2:E4:78:ARG:HD3	3:E8:163:ASN:OD1	2.20	0.41
1:F1:41:VAL:HG11	1:F1:57:TYR:OH	2.20	0.41
2:G4:70:VAL:HG23	2:G4:70:VAL:O	2.20	0.41
3:G8:29:PHE:CD2	3:G8:63:PRO:HD2	2.56	0.41
3:H8:44:PRO:C	3:H8:46:ILE:H	2.27	0.41
3:H8:110:THR:O	3:H8:143:LEU:HA	2.20	0.41
2:I3:52:ALA:O	2:I3:56:ALA:N	2.43	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I8:105:LYS:HG3	3:I8:203:GLY:C	2.45	0.41
1:J1:32:PRO:HG3	1:J1:87:MET:HE1	2.02	0.41
3:J8:9:ILE:HD11	3:J8:150:TYR:CD2	2.56	0.41
3:J8:186:GLU:OE1	3:J8:186:GLU:N	2.35	0.41
2:K4:88:PRO:O	2:K4:89:LEU:HD23	2.20	0.41
2:K5:49:ASP:OD1	2:K5:49:ASP:C	2.63	0.41
3:K8:20:THR:HG21	3:K9:135:LEU:HA	2.03	0.41
2:L6:47:ARG:HH22	2:L6:79:PRO:HG3	1.86	0.41
3:L8:95:LYS:HE3	3:L8:95:LYS:HB2	1.90	0.41
2:M2:9:GLU:HB2	2:M4:14:VAL:HG23	2.02	0.41
3:N9:65:VAL:O	3:N9:75:LEU:HA	2.20	0.41
1:O1:66:THR:O	1:O1:69:THR:OG1	2.24	0.41
1:P1:14:ARG:HG3	1:Q1:47:VAL:HG12	2.03	0.41
1:P1:45:ASP:OD1	1:P1:47:VAL:N	2.43	0.41
2:P5:21:ASP:OD1	2:P5:25:LYS:HD2	2.20	0.41
2:Q5:92:THR:O	2:Q5:94:GLY:N	2.53	0.41
1:R1:45:ASP:CG	1:R1:49:ALA:H	2.16	0.41
1:R1:61:SER:HB3	1:V1:61:SER:HB2	2.03	0.41
2:R6:10:VAL:HA	2:R6:70:VAL:O	2.20	0.41
3:R8:59:THR:HG21	3:R8:88:ALA:HB2	2.03	0.41
2:T2:4:ALA:O	2:T2:47:ARG:HG2	2.20	0.41
2:U6:55:ALA:HB1	3:U8:115:ARG:HD2	2.02	0.41
2:V6:47:ARG:HH22	2:V6:79:PRO:CG	2.32	0.41
2:W4:32:ILE:HD13	2:W4:90:GLY:N	2.35	0.41
2:X5:50:VAL:HG13	2:X5:51:ALA:N	2.36	0.41
3:X8:143:LEU:O	3:X8:177:ARG:HA	2.20	0.41
2:Z3:9:GLU:HG3	2:Z3:71:VAL:HB	2.03	0.41
3:Z8:144:GLU:HA	3:Z8:176:GLY:O	2.19	0.41
3:18:38:LEU:O	3:18:76:GLU:HA	2.19	0.41
3:38:186:GLU:OE1	3:38:186:GLU:N	2.34	0.41
3:48:12:ASP:C	3:48:82:GLN:HE22	2.27	0.41
1:A1:47:VAL:CG1	1:B1:14:ARG:HG3	2.50	0.41
2:A6:47:ARG:NH2	2:A6:79:PRO:HG3	2.31	0.41
3:A8:62:GLN:HA	3:A8:63:PRO:HD3	1.83	0.41
1:B1:2:VAL:CG2	1:B1:57:TYR:CE1	3.04	0.41
3:B8:105:LYS:HE3	3:B8:203:GLY:O	2.20	0.41
2:C4:20:ALA:HB1	2:C4:31:LEU:HD22	2.03	0.41
2:E6:60:GLY:O	2:E6:64:ALA:N	2.43	0.41
3:E8:57:LYS:O	2:F7:78:ARG:NH2	2.54	0.41
1:F1:64:ARG:C	1:F1:66:THR:H	2.28	0.41
2:F6:31:LEU:HD12	2:F6:45:VAL:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G5:82:ASN:OD1	2:W2:31:LEU:HB3	2.21	0.41
2:G7:57:THR:O	2:G7:60:GLY:N	2.53	0.41
2:H2:47:ARG:NH1	2:H2:84:ASP:CG	2.79	0.41
2:H5:9:GLU:OE2	2:I2:13:PHE:N	2.53	0.41
2:I2:9:GLU:HG3	2:I2:43:THR:OG1	2.21	0.41
3:I8:123:GLN:O	3:I8:123:GLN:HG2	2.20	0.41
1:J1:73:PRO:HB2	1:11:79:MET:HE1	2.01	0.41
2:J3:4:ALA:HB3	2:J3:48:GLY:O	2.20	0.41
3:L8:133:MET:HE1	3:L9:132:MET:N	2.36	0.41
1:M1:84:LEU:HA	1:M1:93:PHE:O	2.21	0.41
2:M2:5:LEU:CD1	2:M2:7:MET:HE2	2.48	0.41
2:M5:52:ALA:O	2:M5:56:ALA:N	2.50	0.41
3:M8:11:LEU:HA	3:M8:11:LEU:HD23	1.77	0.41
3:N8:106:PRO:HB2	3:N8:198:ILE:HG22	2.03	0.41
2:O5:37:THR:HG22	2:P2:13:PHE:HD2	1.86	0.41
2:Q4:70:VAL:O	2:Q4:70:VAL:HG23	2.20	0.41
3:Q8:17:GLN:O	3:Q8:20:THR:OG1	2.33	0.41
3:Q9:94:ASP:C	3:Q9:97:GLU:H	2.27	0.41
2:R4:16:MET:HG2	2:R4:44:ALA:HB2	2.02	0.41
2:R6:45:VAL:HG11	2:R6:89:LEU:HD22	2.02	0.41
3:R8:46:ILE:HG22	3:U8:179:TYR:CZ	2.55	0.41
3:R8:170:THR:O	3:R8:176:GLY:HA2	2.20	0.41
2:S6:16:MET:HG2	2:S6:44:ALA:HB2	2.02	0.41
2:T6:4:ALA:O	2:T6:47:ARG:HG2	2.19	0.41
3:T9:62:GLN:O	3:T9:77:VAL:HA	2.21	0.41
3:U8:53:ASP:CG	3:U8:57:LYS:HE3	2.46	0.41
1:V1:45:ASP:OD1	1:V1:46:ALA:N	2.53	0.41
2:V4:5:LEU:HD11	2:V4:7:MET:SD	2.60	0.41
1:X1:64:ARG:C	1:X1:66:THR:H	2.29	0.41
2:X5:11:ARG:O	2:X5:11:ARG:HG2	2.21	0.41
3:X8:61:VAL:HA	3:X8:79:HIS:HB2	2.03	0.41
3:X8:152:VAL:HG22	3:X8:169:VAL:HG11	2.03	0.41
3:Y8:171:PRO:HD2	3:Y8:172:TYR:CD2	2.55	0.41
2:Z7:5:LEU:HD23	2:Z7:76:ILE:HD12	2.03	0.41
3:Z8:140:LEU:HA	3:Z8:180:LEU:O	2.21	0.41
1:11:26:LEU:HD12	1:11:26:LEU:HA	1.91	0.41
1:21:86:GLU:HG2	1:21:87:MET:N	2.36	0.41
3:28:11:LEU:HD23	3:28:11:LEU:HA	1.64	0.41
1:A1:2:VAL:CG2	1:A1:57:TYR:CE1	3.04	0.41
2:A2:7:MET:HE3	2:A2:7:MET:HB2	1.95	0.41
3:C8:152:VAL:HG22	3:C8:169:VAL:HG11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D5:61:GLN:HB2	2:D5:73:VAL:HG21	2.02	0.41
3:D8:123:GLN:HE21	3:D8:123:GLN:HB3	1.68	0.41
2:G7:61:GLN:O	2:G7:65:GLU:HB2	2.21	0.41
3:G8:7:THR:HG23	3:G8:41:GLU:HB3	2.03	0.41
3:H8:48:ILE:HG23	3:H8:75:LEU:HB2	2.02	0.41
1:I1:66:THR:HG22	1:I1:67:GLU:O	2.20	0.41
3:I8:76:GLU:OE1	3:I8:78:HIS:HB3	2.20	0.41
3:I8:119:ALA:O	3:I8:122:THR:OG1	2.38	0.41
1:K1:41:VAL:HG11	1:K1:57:TYR:CZ	2.56	0.41
1:K1:45:ASP:OD1	1:K1:46:ALA:N	2.53	0.41
2:L6:16:MET:HG2	2:L6:44:ALA:HB2	2.03	0.41
3:L8:18:LEU:HD11	3:L8:156:ASN:HA	2.02	0.41
2:O6:21:ASP:OD1	2:O6:25:LYS:HE3	2.20	0.41
3:R8:63:PRO:HB3	3:R8:77:VAL:HG12	2.02	0.41
3:R8:93:LEU:HD12	3:R8:94:ASP:N	2.35	0.41
2:U2:61:GLN:OE1	2:U2:73:VAL:HG11	2.20	0.41
2:U4:88:PRO:C	2:U4:89:LEU:HD12	2.46	0.41
2:V4:30:GLU:OE1	2:V4:91:ARG:NH1	2.48	0.41
2:V7:92:THR:O	2:V7:94:GLY:N	2.46	0.41
2:W2:5:LEU:HB3	2:W2:76:ILE:HB	2.02	0.41
2:W3:10:VAL:HG11	2:W3:15:GLY:HA3	2.02	0.41
3:W8:61:VAL:HG12	3:W8:62:GLN:N	2.32	0.41
3:W8:79:HIS:CE1	3:W8:81:ASP:HB2	2.56	0.41
3:W8:140:LEU:HA	3:W8:180:LEU:O	2.19	0.41
1:Y1:64:ARG:C	1:Y1:66:THR:H	2.28	0.41
2:Y3:74:HIS:CG	2:Y3:75:VAL:N	2.89	0.41
2:Z5:57:THR:O	2:Z5:60:GLY:N	2.52	0.41
2:Z6:20:ALA:O	2:Z6:24:VAL:HG22	2.21	0.41
2:13:47:ARG:HH21	2:13:91:ARG:CB	2.27	0.41
3:28:39:TRP:CZ2	3:28:76:GLU:HG3	2.55	0.41
3:28:61:VAL:HG11	3:28:77:VAL:HB	2.03	0.41
3:48:16:PRO:HA	3:48:33:PRO:CB	2.40	0.41
2:A4:47:ARG:HH22	2:A4:84:ASP:CG	2.28	0.41
3:C8:117:VAL:HG12	3:C8:121:GLN:HB3	2.03	0.41
3:C8:167:VAL:HB	3:C8:179:TYR:HB2	2.03	0.41
1:E1:28:ARG:HH12	1:E1:36:PRO:HB2	1.83	0.41
2:E7:53:VAL:HA	2:E7:56:ALA:HB3	2.03	0.41
2:F4:66:ARG:HH12	2:F5:62:ARG:NH2	2.19	0.41
2:F5:8:ILE:HG12	2:F5:73:VAL:HG22	2.03	0.41
2:F7:17:VAL:HG11	2:G3:7:MET:SD	2.60	0.41
2:G7:54:LYS:HD2	2:G7:54:LYS:HA	1.91	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H8:140:LEU:HD12	3:H8:180:LEU:O	2.20	0.41
3:I8:3:ILE:HD13	3:I8:47:ALA:HB1	2.02	0.41
3:J8:17:GLN:NE2	3:J8:159:GLU:HG3	2.36	0.41
2:K2:13:PHE:CD1	2:K2:13:PHE:C	2.99	0.41
2:K2:47:ARG:HD2	2:K2:89:LEU:O	2.21	0.41
1:L1:41:VAL:HG11	1:L1:57:TYR:CZ	2.55	0.41
2:M4:37:THR:OG1	2:M4:41:TYR:HB2	2.21	0.41
2:M5:46:VAL:O	2:M5:47:ARG:HG2	2.21	0.41
1:N1:68:VAL:C	1:N1:72:ARG:HH12	2.29	0.41
2:O3:5:LEU:HB3	2:O3:76:ILE:HB	2.03	0.41
2:O7:10:VAL:HG22	2:O7:70:VAL:HA	2.03	0.41
3:O8:31:PRO:HD3	3:O8:64:ALA:CB	2.50	0.41
2:P3:17:VAL:CG2	2:P4:7:MET:HE1	2.50	0.41
2:Q5:5:LEU:N	2:Q5:76:ILE:O	2.52	0.41
2:R6:70:VAL:HG12	2:R6:72:ALA:N	2.36	0.41
3:R8:60:LYS:CG	2:U7:78:ARG:HD3	2.31	0.41
3:R8:62:GLN:HA	3:R8:63:PRO:HD3	1.81	0.41
2:T6:76:ILE:HG21	2:T6:79:PRO:HB3	2.02	0.41
3:T8:62:GLN:HA	3:T8:63:PRO:HD3	1.94	0.41
2:U7:16:MET:HG2	2:U7:44:ALA:HB2	2.01	0.41
2:U7:32:ILE:HD13	2:U7:89:LEU:C	2.46	0.41
1:V1:45:ASP:OD1	1:V1:47:VAL:N	2.42	0.41
3:V8:17:GLN:NE2	3:V8:159:GLU:HG3	2.36	0.41
3:V8:111:HIS:HA	3:V8:142:ILE:O	2.21	0.41
3:V8:142:ILE:HB	3:48:46:ILE:HG23	2.01	0.41
2:W7:51:ALA:CB	2:Y3:51:ALA:HB2	2.50	0.41
3:W8:87:ALA:O	3:W8:91:THR:HG23	2.21	0.41
2:X4:62:ARG:CZ	2:X5:66:ARG:NH1	2.84	0.41
3:X8:6:ARG:HD2	3:X8:41:GLU:HG2	2.02	0.41
3:X8:7:THR:HG22	3:X8:150:TYR:CE1	2.56	0.41
1:Y1:54:VAL:O	1:Y1:82:VAL:HG23	2.21	0.41
2:Y3:21:ASP:OD1	2:Y3:25:LYS:HE3	2.21	0.41
3:Y8:143:LEU:O	3:Y8:177:ARG:HA	2.20	0.41
3:18:118:GLU:HG3	3:18:119:ALA:N	2.35	0.41
2:23:23:MET:HG2	2:23:56:ALA:O	2.20	0.41
2:25:60:GLY:O	2:25:64:ALA:N	2.52	0.41
2:26:5:LEU:HB3	2:26:76:ILE:HB	2.02	0.41
2:33:49:ASP:OD1	2:33:49:ASP:N	2.54	0.41
1:A1:22:LEU:HD12	1:A1:22:LEU:HA	1.66	0.41
2:A2:3:ASP:HB2	2:A2:47:ARG:NH1	2.36	0.41
2:A4:32:ILE:HD12	2:A4:89:LEU:C	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A7:4:ALA:O	2:A7:47:ARG:NE	2.50	0.41
2:A7:17:VAL:CG1	2:E3:7:MET:HE1	2.45	0.41
2:A7:27:ALA:O	2:G3:78:ARG:NH2	2.49	0.41
3:A8:11:LEU:HD23	3:A8:11:LEU:HA	1.79	0.41
3:A8:18:LEU:HB3	3:A8:22:ILE:CD1	2.51	0.41
3:A8:124:ILE:HD11	3:G8:28:GLY:HA2	2.02	0.41
1:B1:81:ILE:HD12	2:B5:77:PRO:HG2	2.03	0.41
3:B8:60:LYS:NZ	2:L7:78:ARG:HH21	2.19	0.41
1:C1:33:ASP:HB3	1:C1:35:THR:HG23	2.03	0.41
1:C1:64:ARG:C	1:C1:66:THR:H	2.29	0.41
2:C3:8:ILE:O	2:C3:44:ALA:N	2.46	0.41
2:C3:31:LEU:HD12	2:C3:45:VAL:O	2.21	0.41
2:C6:36:LYS:NZ	2:C7:35:GLU:OE1	2.47	0.41
3:C8:11:LEU:HD21	3:C8:153:LEU:HA	2.03	0.41
3:C8:21:PHE:HE1	3:C8:130:GLN:CB	2.33	0.41
3:C8:123:GLN:HE21	3:C8:123:GLN:HB3	1.64	0.41
2:D3:8:MET:HE1	2:E7:17:VAL:HG21	2.03	0.41
3:D8:51:VAL:HG12	3:D8:75:LEU:HD22	2.03	0.41
3:D8:70:ARG:HE	3:D8:173:GLY:CA	2.34	0.41
2:E4:66:ARG:HE	2:E4:66:ARG:HB3	1.74	0.41
2:E6:18:GLU:OE1	2:E7:74:HIS:NE2	2.51	0.41
1:F1:70:ASN:C	1:F1:72:ARG:N	2.77	0.41
2:F2:20:ALA:O	2:F2:24:VAL:HG23	2.19	0.41
2:F3:78:ARG:NH2	2:Q7:29:VAL:O	2.53	0.41
2:F5:50:VAL:HG13	2:F5:51:ALA:N	2.36	0.41
3:F8:11:LEU:HD21	3:F8:153:LEU:HA	2.02	0.41
1:G1:22:LEU:HA	1:G1:22:LEU:HD12	1.76	0.41
3:G8:8:TYR:CE2	3:G8:93:LEU:HD23	2.51	0.41
3:G9:108:VAL:HA	3:G9:145:THR:HA	2.02	0.41
2:H3:13:PHE:CD2	2:H4:43:THR:HG21	2.52	0.41
2:H3:54:LYS:O	2:H3:58:GLU:HG3	2.21	0.41
2:H4:50:VAL:HG11	3:H8:186:GLU:HG3	2.02	0.41
3:H8:9:ILE:N	3:H8:39:TRP:O	2.29	0.41
3:H8:111:HIS:O	3:H8:111:HIS:CG	2.74	0.41
3:H8:123:GLN:HG3	3:H9:23:GLY:HA3	2.03	0.41
3:H8:169:VAL:HG22	3:H8:178:LEU:HD13	2.03	0.41
1:J1:68:VAL:HA	1:J1:72:ARG:NH1	2.36	0.41
2:J2:5:LEU:HB3	2:J2:76:ILE:HB	2.03	0.41
3:K8:111:HIS:HB3	3:K8:143:LEU:HD13	2.03	0.41
3:K8:128:ASN:O	3:K8:130:GLN:N	2.50	0.41
2:L4:57:THR:HG22	2:L4:73:VAL:HG13	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L7:59:ALA:HA	2:L7:62:ARG:NH1	2.36	0.41
2:L7:78:ARG:HG3	2:L7:78:ARG:HH11	1.85	0.41
3:L8:123:GLN:HE22	3:L9:30:LEU:CB	2.34	0.41
3:L8:170:THR:OG1	3:L8:177:ARG:N	2.23	0.41
2:M2:30:GLU:CD	2:M2:91:ARG:HH12	2.23	0.41
2:M4:62:ARG:NE	2:M5:66:ARG:NH1	2.69	0.41
2:N5:13:PHE:H	2:N6:9:GLU:CD	2.29	0.41
3:N8:111:HIS:HA	3:N8:142:ILE:O	2.21	0.41
3:N9:37:SER:HA	3:N9:78:HIS:HA	2.03	0.41
1:O1:61:SER:HB2	1:P1:61:SER:CB	2.51	0.41
2:O2:20:ALA:HA	2:O2:23:MET:HE3	2.02	0.41
2:O4:16:MET:HG2	2:O4:44:ALA:HB2	2.03	0.41
2:O5:10:VAL:HG12	2:O5:12:GLY:H	1.85	0.41
2:P7:10:GLY:CA	2:Q3:9:GLU:OE2	2.69	0.41
3:P8:61:VAL:O	3:P8:62:GLN:HG3	2.21	0.41
2:Q2:4:ALA:O	2:Q2:47:ARG:HG2	2.21	0.41
2:Q7:41:TYR:CE2	2:Q7:71:VAL:HG21	2.56	0.41
3:Q8:119:ALA:HA	3:Q8:136:PRO:HB3	2.01	0.41
1:R1:22:LEU:HD12	1:R1:22:LEU:HA	1.89	0.41
1:S1:28:ARG:NH1	1:S1:36:PRO:HB2	2.36	0.41
2:S2:68:GLY:O	2:S2:70:VAL:HG23	2.20	0.41
3:S8:42:ILE:CD1	3:S8:96:LEU:HD11	2.51	0.41
3:S8:128:ASN:O	3:S8:168:ASN:ND2	2.53	0.41
3:T8:118:GLU:HG2	3:T8:120:TYR:HD2	1.86	0.41
3:U9:44:PRO:HA	3:U9:71:ALA:O	2.20	0.41
1:V1:86:GLU:O	1:W1:8:GLY:HA3	2.21	0.41
2:V2:47:ARG:NH2	2:V2:79:PRO:HG2	2.35	0.41
2:V6:14:VAL:HG23	2:V7:9:GLU:HB2	2.03	0.41
2:V6:45:VAL:HG11	2:V6:89:LEU:HD22	2.02	0.41
2:V6:54:LYS:O	2:V6:58:GLU:HG3	2.20	0.41
3:V8:114:ILE:HD11	3:48:50:ARG:HB2	2.03	0.41
2:W2:84:ASP:O	2:W2:92:THR:OG1	2.32	0.41
2:W5:46:VAL:O	2:W5:47:ARG:HG2	2.21	0.41
2:X2:47:ARG:NH2	2:X2:84:ASP:OD2	2.54	0.41
3:X8:70:ARG:HG2	3:X8:172:TYR:HB2	2.03	0.41
3:X8:106:PRO:HG3	3:X8:150:TYR:HE2	1.84	0.41
3:X8:146:GLN:HB2	3:X8:175:PHE:HD1	1.86	0.41
2:Y5:89:GLY:O	2:Y5:90:ARG:HG2	2.20	0.41
3:Y8:9:ILE:O	3:Y8:38:LEU:HD12	2.20	0.41
3:Z8:59:THR:HB	3:Z8:61:VAL:HG23	2.03	0.41
2:12:47:ARG:NH1	2:12:84:ASP:CG	2.78	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:15:50:VAL:HG13	2:15:51:ALA:N	2.35	0.41
3:18:43:ALA:HB2	3:18:72:TYR:CG	2.56	0.41
3:18:115:ARG:HA	3:18:139:SER:OG	2.21	0.41
3:18:152:VAL:CG2	3:18:171:PRO:HG3	2.51	0.41
2:23:17:VAL:CG2	2:24:7:MET:HE1	2.48	0.41
3:28:7:THR:HG21	3:28:149:GLY:HA3	2.03	0.41
3:28:65:VAL:CG1	3:28:76:GLU:HB3	2.47	0.41
3:29:87:ALA:O	3:29:91:THR:N	2.40	0.41
1:31:43:CYS:HB2	1:31:77:THR:HA	2.03	0.41
1:31:45:ASP:OD1	1:31:47:VAL:N	2.41	0.41
3:38:79:HIS:CG	3:38:80:PHE:N	2.89	0.41
2:42:16:MET:HG2	2:42:44:ALA:HB2	2.03	0.41
2:43:47:ARG:HH22	2:43:79:PRO:HG2	1.85	0.41
3:48:23:GLY:CA	3:48:30:LEU:HG	2.51	0.41
2:A2:92:THR:HA	2:A2:93:PRO:HD3	1.91	0.41
2:B3:52:ALA:O	2:B3:56:ALA:N	2.31	0.41
2:B4:62:ARG:NE	2:B5:66:ARG:NH1	2.68	0.41
2:B5:52:ALA:O	2:B5:56:ALA:N	2.54	0.41
3:B8:64:ALA:HB3	3:B8:76:GLU:OE2	2.21	0.41
2:C7:27:ALA:HA	2:23:77:PRO:HB2	2.02	0.41
2:C7:29:VAL:HB	2:C7:46:VAL:CG1	2.51	0.41
3:D8:114:ILE:HD11	3:N8:50:ARG:HB2	2.02	0.41
3:E8:23:GLY:CA	3:E8:30:LEU:HG	2.50	0.41
2:F4:83:VAL:HG13	2:F4:87:LEU:HD13	2.03	0.41
2:F5:21:ASP:OD1	2:F5:25:LYS:HD2	2.21	0.41
3:F8:54:ALA:HB2	3:F8:95:LYS:NZ	2.35	0.41
2:G4:13:PHE:O	2:G4:13:PHE:HD1	2.03	0.41
2:G5:10:VAL:HG11	2:G5:15:GLY:HA3	2.03	0.41
1:H1:47:VAL:HG12	1:Z1:14:ARG:HG3	2.03	0.41
2:H6:47:ARG:HD3	2:H6:91:ARG:HG2	2.03	0.41
3:H8:7:THR:HG22	3:H8:150:TYR:CE2	2.56	0.41
2:I4:8:ILE:O	2:I4:43:THR:HA	2.21	0.41
2:I5:46:VAL:O	2:I5:47:ARG:HG2	2.21	0.41
3:J8:64:ALA:HB3	3:J8:76:GLU:OE1	2.21	0.41
2:K2:9:GLU:HG3	2:K2:43:THR:OG1	2.21	0.41
2:K4:66:ARG:HE	2:K4:66:ARG:HB3	1.73	0.41
3:K8:18:LEU:HB3	3:K8:22:ILE:CD1	2.51	0.41
2:L2:78:ARG:CG	2:L5:27:ALA:HA	2.51	0.41
3:L8:41:GLU:HB2	3:L8:74:LEU:HD13	2.02	0.41
3:L9:107:GLN:N	3:L9:146:GLN:O	2.35	0.41
3:M8:31:PRO:HB3	3:M8:78:HIS:CD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:M8:57:LYS:O	2:27:78:ARG:NH2	2.54	0.41
1:N1:70:ASN:C	1:N1:72:ARG:N	2.76	0.41
1:O1:66:THR:HG22	1:O1:67:GLU:O	2.20	0.41
2:O5:41:TYR:N	2:O5:41:TYR:CD1	2.87	0.41
2:O6:5:LEU:HB3	2:O6:76:ILE:HB	2.01	0.41
2:O7:57:THR:O	2:O7:60:GLY:N	2.54	0.41
3:O8:148:ALA:O	3:O8:171:PRO:HA	2.20	0.41
2:P7:15:VAL:HG22	2:Q3:87:LEU:HD13	2.03	0.41
2:Q3:27:ALA:HB1	2:Q3:52:ALA:HB1	2.03	0.41
3:Q8:15:GLN:HG3	3:Q8:160:LYS:HB2	2.02	0.41
3:Q8:144:GLU:HA	3:Q8:176:GLY:O	2.21	0.41
2:R4:31:LEU:HA	2:R4:46:VAL:HG12	2.03	0.41
2:R6:31:LEU:HD12	2:R6:45:VAL:O	2.21	0.41
2:U4:23:MET:HG2	2:U4:56:ALA:O	2.21	0.41
2:U6:12:GLY:HA2	2:U7:9:GLU:OE2	2.21	0.41
3:U8:148:ALA:O	3:U8:171:PRO:HA	2.21	0.41
2:V4:3:ASP:HB3	2:V4:48:GLY:H	1.86	0.41
3:V8:15:GLN:HG2	3:V8:156:ASN:OD1	2.20	0.41
3:V8:111:HIS:O	3:V8:111:HIS:CG	2.74	0.41
2:W2:13:PHE:CD1	2:W2:13:PHE:C	2.99	0.41
2:X5:2:ALA:HB3	2:X5:91:ARG:HE	1.86	0.41
1:Y1:19:ILE:O	1:Y1:22:LEU:HB2	2.21	0.41
2:Y3:4:ALA:HB1	2:Y3:76:ILE:O	2.21	0.41
2:Y4:51:ALA:HB2	3:Y8:185:ALA:HB2	2.03	0.41
2:Y7:20:ALA:O	2:Y7:24:VAL:HG22	2.21	0.41
2:13:32:ILE:CD1	2:13:47:ARG:HG3	2.50	0.41
2:15:45:VAL:HG11	2:15:89:LEU:HD22	2.03	0.41
2:16:3:ASP:O	2:16:47:ARG:NH2	2.42	0.41
3:18:170:THR:O	3:18:176:GLY:HA2	2.20	0.41
1:21:64:ARG:C	1:21:66:THR:H	2.29	0.41
2:24:66:ARG:HE	2:24:66:ARG:HB3	1.70	0.41
1:31:45:ASP:OD1	1:31:46:ALA:N	2.54	0.41
2:35:86:ALA:O	2:35:87:LEU:HD23	2.21	0.41
3:49:65:VAL:O	3:49:75:LEU:HA	2.20	0.41
3:49:66:GLN:HA	3:49:74:LEU:O	2.21	0.41
2:B6:27:ALA:HA	3:B8:116:ALA:CB	2.51	0.40
3:B8:35:GLN:HB3	3:B8:36:ALA:H	1.58	0.40
2:C5:11:ARG:O	2:C5:11:ARG:HG2	2.21	0.40
3:C8:7:THR:HG22	3:C8:150:TYR:CD1	2.56	0.40
3:C8:95:LYS:HE3	3:C8:95:LYS:HB2	1.89	0.40
2:D5:50:VAL:HG13	2:D5:51:ALA:N	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E5:12:GLY:HA2	2:E6:9:GLU:OE2	2.20	0.40
1:F1:55:VAL:HG21	1:F1:78:ILE:HD13	2.01	0.40
2:G2:90:GLY:C	2:G2:92:THR:N	2.78	0.40
2:G3:13:PHE:HA	2:G3:42:VAL:HG21	2.03	0.40
2:G7:17:VAL:HG11	2:W3:7:MET:CE	2.51	0.40
3:G8:107:GLN:O	3:G8:145:THR:HA	2.22	0.40
3:H8:122:THR:HG22	3:H8:134:ILE:HG22	2.02	0.40
3:H8:126:ASN:ND2	3:H8:133:MET:HB2	2.36	0.40
2:I2:47:ARG:NH1	2:I2:84:ASP:OD2	2.54	0.40
2:I6:40:GLY:N	2:I7:38:GLY:O	2.54	0.40
3:I8:18:LEU:HB3	3:I8:22:ILE:CD1	2.51	0.40
3:I9:42:ILE:O	3:I9:73:GLY:N	2.38	0.40
2:J5:37:THR:HG21	2:J2:13:PHE:HB2	2.03	0.40
3:J8:124:ILE:HG21	3:L8:66:GLN:HB3	2.03	0.40
3:K8:13:ALA:HA	3:K8:35:GLN:O	2.21	0.40
2:L2:29:VAL:HB	2:L2:46:VAL:HG13	2.03	0.40
2:L4:32:ILE:HD13	2:L4:90:GLY:N	2.36	0.40
2:L4:53:VAL:O	2:L4:57:THR:OG1	2.25	0.40
2:M3:32:ILE:HG13	2:M3:33:GLY:N	2.35	0.40
2:M4:10:VAL:HG22	2:M4:70:VAL:HG12	2.03	0.40
2:M7:19:ALA:HB2	2:M7:64:ALA:HB2	2.02	0.40
3:M8:7:THR:HG23	3:M8:41:GLU:HB3	2.02	0.40
3:M8:13:ALA:HA	3:M8:35:GLN:O	2.21	0.40
3:M8:50:ARG:NH2	3:28:112:GLN:OE1	2.52	0.40
3:N8:35:GLN:HB3	3:N8:36:ALA:H	1.62	0.40
2:Q6:8:ILE:O	2:Q6:43:THR:HA	2.21	0.40
2:R3:49:ASP:OD1	2:R3:49:ASP:N	2.53	0.40
3:R9:113:ILE:HA	3:R9:141:PHE:HA	2.03	0.40
2:S4:16:MET:HB3	2:S4:16:MET:HE3	1.88	0.40
2:S7:58:GLU:O	2:S7:62:ARG:HG3	2.20	0.40
1:V1:22:LEU:HA	1:V1:22:LEU:HD12	1.73	0.40
2:Y2:68:GLY:O	2:Y2:70:VAL:HG23	2.21	0.40
3:18:63:PRO:HA	3:18:77:VAL:HA	2.03	0.40
3:18:76:GLU:OE1	3:18:78:HIS:HB3	2.21	0.40
3:28:4:THR:O	3:28:42:ILE:HG23	2.21	0.40
3:28:59:THR:HB	3:28:61:VAL:HG23	2.02	0.40
1:31:28:ARG:NH2	1:31:38:GLY:O	2.50	0.40
3:38:38:LEU:HD21	3:38:89:GLY:HA2	2.01	0.40
3:38:110:THR:O	3:38:143:LEU:HA	2.21	0.40
2:A7:21:ASP:OD1	2:A7:25:LYS:HE3	2.22	0.40
1:B1:50:GLY:N	1:B1:53:GLU:OE1	2.29	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B2:47:ARG:HD2	2:B2:89:LEU:O	2.22	0.40
3:B8:63:PRO:HB3	3:B8:77:VAL:HG12	2.04	0.40
3:B8:133:MET:HE1	3:B9:132:MET:N	2.36	0.40
2:C4:8:ILE:O	2:C4:43:THR:HA	2.21	0.40
2:C5:16:MET:HG2	2:C5:44:ALA:HB2	2.03	0.40
3:D8:178:LEU:HD12	3:D8:179:TYR:H	1.86	0.40
2:E3:32:ILE:HG13	2:E3:33:GLY:N	2.36	0.40
2:E7:20:ALA:HB1	2:E7:31:LEU:CD1	2.51	0.40
3:E8:7:THR:HG23	3:E8:41:GLU:HB3	2.03	0.40
1:F1:54:VAL:O	1:F1:82:VAL:HG23	2.21	0.40
2:F4:54:LYS:HD2	2:F4:75:VAL:HG11	2.02	0.40
3:F8:186:GLU:OE1	3:F8:186:GLU:N	2.37	0.40
1:G1:22:LEU:HG	1:G1:44:ALA:HB1	2.03	0.40
2:G6:18:GLU:OE1	2:G7:74:HIS:NE2	2.50	0.40
2:G6:19:ALA:HB2	2:G6:64:ALA:HB2	2.02	0.40
3:G8:7:THR:HG21	3:G8:149:GLY:HA3	2.03	0.40
2:H3:49:ASP:OD1	2:H3:49:ASP:N	2.55	0.40
3:H8:62:GLN:HA	3:H8:63:PRO:HD3	1.94	0.40
3:H9:105:LYS:N	3:H9:204:VAL:O	2.34	0.40
3:I8:20:THR:OG1	3:I8:21:PHE:N	2.54	0.40
3:I8:122:THR:HG21	3:I8:136:PRO:CA	2.46	0.40
2:J7:47:ARG:NH1	2:J7:89:LEU:O	2.53	0.40
2:L3:27:ALA:HB1	2:L3:52:ALA:HB1	2.02	0.40
2:L3:49:ASP:O	2:L3:53:VAL:HG23	2.22	0.40
2:L6:91:ARG:HD3	2:L6:91:ARG:HA	1.89	0.40
2:L7:18:GLU:HB2	2:23:74:HIS:CD2	2.56	0.40
3:L8:8:TYR:C	3:L8:8:TYR:CD1	2.99	0.40
3:M8:9:ILE:HD12	3:M8:150:TYR:HA	2.02	0.40
2:N6:7:MET:HG2	2:N6:45:VAL:HG13	2.03	0.40
3:N8:7:THR:HG22	3:N8:150:TYR:CD1	2.56	0.40
2:O4:32:ILE:HD13	2:O4:90:GLY:N	2.36	0.40
3:O8:123:GLN:HG3	3:O9:23:GLY:HA3	2.03	0.40
2:P3:32:ILE:HD11	2:P3:45:VAL:CG1	2.51	0.40
3:P8:79:HIS:CE1	3:P8:81:ASP:H	2.38	0.40
2:Q6:47:ARG:HH22	2:Q6:79:PRO:HG2	1.86	0.40
2:Q7:84:ASP:O	2:Q7:92:THR:HG22	2.21	0.40
3:Q8:186:GLU:OE1	3:Q8:186:GLU:N	2.41	0.40
2:R7:47:ARG:HH22	2:R7:84:ASP:CG	2.29	0.40
3:S8:79:HIS:CG	3:S8:80:PHE:N	2.89	0.40
3:S9:66:GLN:HA	3:S9:74:LEU:O	2.21	0.40
2:V2:32:ILE:HD13	2:V2:89:LEU:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:V8:144:GLU:HA	3:V8:176:GLY:O	2.21	0.40
2:W5:45:VAL:HG11	2:W5:89:LEU:HD22	2.03	0.40
3:W8:107:GLN:O	3:W8:145:THR:HA	2.21	0.40
2:X2:20:ALA:O	2:X2:24:VAL:HG23	2.21	0.40
1:Y1:22:LEU:HD12	1:Y1:22:LEU:HA	1.77	0.40
3:Y8:39:TRP:CZ2	3:Y8:76:GLU:HG3	2.56	0.40
3:Y8:147:PRO:HD2	3:Y8:150:TYR:HD2	1.86	0.40
3:Z8:92:ILE:O	3:Z8:95:LYS:HB3	2.21	0.40
3:38:123:GLN:O	3:38:123:GLN:HG2	2.21	0.40
1:41:28:ARG:NH2	1:41:38:GLY:O	2.54	0.40
1:B1:16:GLU:O	1:B1:19:ILE:HG22	2.21	0.40
2:B7:37:THR:OG1	2:B7:41:TYR:HB2	2.21	0.40
2:C2:31:LEU:HB3	2:D5:82:ASN:OD1	2.21	0.40
2:D2:30:GLU:CD	2:D2:91:ARG:HH12	2.25	0.40
2:F6:16:MET:HG2	2:F6:44:ALA:HB2	2.03	0.40
3:G8:20:THR:HB	3:G8:24:LYS:NZ	2.36	0.40
2:H5:27:ALA:HB1	2:H5:52:ALA:HB1	2.03	0.40
3:H8:126:ASN:O	3:H8:129:SER:HB3	2.21	0.40
1:I1:25:LEU:HD23	1:I1:25:LEU:HA	1.91	0.40
1:I1:32:PRO:HG3	1:I1:87:MET:CE	2.51	0.40
1:I1:95:LYS:HD2	1:I1:95:LYS:HA	1.91	0.40
2:J2:5:LEU:HD23	2:J2:76:ILE:HD12	2.03	0.40
2:J7:5:LEU:HB3	2:J7:76:ILE:HB	2.03	0.40
3:J8:127:ARG:HD3	3:L8:27:ARG:CD	2.51	0.40
2:K2:49:ASP:OD1	2:K2:49:ASP:N	2.54	0.40
3:N8:20:THR:OG1	3:N8:21:PHE:N	2.53	0.40
3:N8:120:TYR:HD1	3:P8:29:PHE:CZ	2.39	0.40
2:O7:20:ALA:HB1	2:O7:31:LEU:HD22	2.03	0.40
3:O8:44:PRO:C	3:O8:46:ILE:H	2.29	0.40
3:O8:118:GLU:HG3	3:O8:119:ALA:N	2.36	0.40
3:O8:171:PRO:HD2	3:O8:172:TYR:CD2	2.55	0.40
3:O8:183:SER:O	3:O8:187:ILE:HG12	2.22	0.40
2:P3:57:THR:HG22	2:P3:73:VAL:HG13	2.03	0.40
2:P4:37:THR:OG1	2:P4:41:TYR:HB2	2.22	0.40
3:Q8:117:VAL:CG1	3:Q8:121:GLN:HB3	2.52	0.40
3:Q9:19:ALA:O	3:Q9:23:GLY:N	2.51	0.40
3:R8:23:GLY:HA3	3:R8:30:LEU:HG	2.03	0.40
1:S1:70:ASN:C	1:S1:72:ARG:N	2.78	0.40
2:S2:13:PHE:CD1	2:S2:13:PHE:C	2.99	0.40
2:S2:30:GLU:CD	2:S2:91:ARG:HH12	2.25	0.40
2:S5:20:ALA:O	2:S5:24:VAL:HG23	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S8:8:TYR:OH	3:S8:89:GLY:O	2.35	0.40
3:V8:9:ILE:HD13	3:V8:9:ILE:HG21	1.83	0.40
3:W8:62:GLN:OE1	3:W8:78:HIS:NE2	2.54	0.40
1:X1:31:ASP:HB2	1:X1:32:PRO:HD2	2.02	0.40
3:X9:40:VAL:O	3:X9:74:LEU:HA	2.22	0.40
2:Y4:77:PRO:HB2	3:Y8:161:ALA:O	2.22	0.40
3:Y8:45:GLY:HA2	3:Y8:48:ILE:HD13	2.03	0.40
1:Z1:28:ARG:NH2	1:Z1:38:GLY:O	2.54	0.40
1:31:6:VAL:CG2	1:31:51:VAL:HA	2.51	0.40
2:35:3:ASP:O	2:35:47:ARG:NH2	2.45	0.40
2:35:57:THR:O	2:35:60:GLY:N	2.52	0.40
2:45:90:GLY:O	2:45:91:ARG:HG2	2.20	0.40
1:A1:26:LEU:HD22	1:A1:40:ALA:HB1	2.02	0.40
2:A6:31:LEU:HD12	2:A6:45:VAL:O	2.21	0.40
3:A9:110:THR:O	3:A9:144:GLU:N	2.53	0.40
2:B5:30:GLU:CD	2:B5:91:ARG:HH22	2.19	0.40
3:B8:9:ILE:O	3:B8:38:LEU:HD12	2.22	0.40
3:B8:39:TRP:HA	3:B8:75:LEU:O	2.21	0.40
2:D6:21:ASP:OD1	2:D6:25:LYS:HE3	2.22	0.40
3:D8:45:GLY:HA3	3:D8:73:GLY:H	1.87	0.40
1:E1:54:VAL:HG12	1:E1:82:VAL:HG21	2.04	0.40
3:F8:45:GLY:HA3	3:F8:73:GLY:H	1.86	0.40
3:F8:150:TYR:O	3:F8:153:LEU:HB3	2.21	0.40
1:G1:70:ASN:C	1:G1:72:ARG:H	2.29	0.40
2:G5:11:ARG:O	2:G5:11:ARG:HG2	2.21	0.40
3:G8:144:GLU:OE1	3:I8:44:PRO:HG3	2.21	0.40
1:H1:22:LEU:HG	1:H1:44:ALA:HB1	2.03	0.40
2:H6:47:ARG:HH22	2:H6:79:PRO:HG3	1.86	0.40
2:I3:64:ALA:O	2:I3:68:GLY:N	2.55	0.40
3:I8:6:ARG:NH1	3:I8:72:TYR:OH	2.54	0.40
3:I8:169:VAL:HG22	3:I8:178:LEU:CD1	2.51	0.40
3:I9:148:ALA:HA	3:I9:176:GLY:H	1.86	0.40
3:J8:48:ILE:O	3:J8:52:THR:OG1	2.36	0.40
3:K8:92:ILE:O	3:K8:95:LYS:HB3	2.21	0.40
2:L7:29:VAL:HB	2:L7:46:VAL:HG12	2.03	0.40
3:M8:8:TYR:HA	3:M8:40:VAL:HG22	2.03	0.40
2:N4:16:MET:HE3	2:N4:16:MET:HB3	2.02	0.40
3:N8:41:GLU:HB2	3:N8:74:LEU:HD13	2.03	0.40
1:O1:31:ASP:OD1	1:O1:35:THR:OG1	2.28	0.40
3:P8:15:GLN:HG2	3:P8:156:ASN:OD1	2.21	0.40
2:R3:47:ARG:NH1	2:R3:84:ASP:CG	2.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:S9:105:LYS:N	3:S9:204:VAL:O	2.39	0.40
2:T3:5:LEU:O	2:T3:53:VAL:HG11	2.21	0.40
2:T3:31:LEU:HB3	2:T4:82:ASN:OD1	2.21	0.40
3:U8:8:TYR:HB3	3:U8:103:ARG:HD2	2.03	0.40
3:U8:51:VAL:HG13	3:U8:92:ILE:HG12	2.03	0.40
2:W2:54:LYS:NZ	2:W5:54:LYS:HG2	2.36	0.40
2:W5:2:ALA:HB1	2:W5:78:ARG:CZ	2.51	0.40
3:X8:95:LYS:HE3	3:X8:95:LYS:HB2	1.87	0.40
3:Y8:130:GLN:OE1	3:Y8:168:ASN:HB3	2.21	0.40
2:Z6:3:ASP:O	2:Z6:47:ARG:NH2	2.50	0.40
2:16:8:ILE:O	2:16:43:THR:HA	2.21	0.40
3:18:35:GLN:HE22	3:18:78:HIS:CE1	2.39	0.40
2:43:82:ASN:HD22	2:43:82:ASN:C	2.28	0.40
3:48:62:GLN:HA	3:48:63:PRO:HD3	1.86	0.40
3:A8:47:ALA:HB1	3:A8:50:ARG:HH12	1.86	0.40
2:B3:74:HIS:CG	2:B3:75:VAL:N	2.90	0.40
2:B5:29:VAL:HB	2:B5:46:VAL:CG1	2.51	0.40
2:B5:57:THR:O	2:B5:60:GLY:N	2.47	0.40
3:B8:52:THR:O	3:B8:56:LEU:HB2	2.22	0.40
3:C8:29:PHE:CZ	3:M8:120:TYR:HD1	2.39	0.40
3:C8:154:ALA:HB2	3:C8:198:ILE:HD11	2.03	0.40
2:D4:8:ILE:O	2:D4:43:THR:HA	2.22	0.40
3:E8:44:PRO:HB2	3:E8:46:ILE:HG13	2.02	0.40
3:F8:7:THR:CG2	3:F8:147:PRO:HG2	2.51	0.40
1:G1:57:TYR:HA	1:G1:78:ILE:HA	2.02	0.40
1:G1:74:VAL:HG23	1:W1:1:MET:SD	2.61	0.40
2:G2:47:ARG:HH22	2:G2:79:PRO:HG2	1.86	0.40
3:G8:35:GLN:HG2	3:G8:80:PHE:CG	2.57	0.40
3:G8:50:ARG:CD	3:G8:95:LYS:HD3	2.50	0.40
3:G9:88:ALA:O	3:G9:92:ILE:N	2.44	0.40
2:H6:4:ALA:N	2:H6:48:GLY:O	2.48	0.40
2:H6:13:PHE:HB2	2:H7:37:THR:HG21	2.03	0.40
2:I4:76:ILE:HG21	2:I4:79:PRO:HB3	2.04	0.40
3:I8:4:THR:O	3:I8:42:ILE:HG23	2.21	0.40
3:I8:122:THR:HG22	3:I8:134:ILE:HG22	2.02	0.40
1:J1:57:TYR:HA	1:J1:78:ILE:HA	2.04	0.40
2:J3:84:ASP:HB3	2:J3:91:ARG:O	2.21	0.40
2:J6:3:ASP:C	2:J6:47:ARG:HH12	2.30	0.40
3:J8:7:THR:HG23	3:J8:41:GLU:HB3	2.03	0.40
3:K8:123:GLN:HE21	3:K8:123:GLN:HB3	1.66	0.40
2:L4:8:ILE:HD12	2:L4:73:VAL:HG22	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L7:92:THR:O	2:L7:94:GLY:N	2.49	0.40
2:M5:20:ALA:O	2:M5:24:VAL:HG23	2.21	0.40
2:M6:76:ILE:HA	2:M6:77:PRO:HD3	1.94	0.40
2:M7:80:HIS:O	2:M7:83:VAL:N	2.54	0.40
3:M8:50:ARG:HB2	3:28:114:ILE:HD11	2.04	0.40
1:N1:26:LEU:HD12	1:N1:26:LEU:HA	1.87	0.40
2:N6:13:PHE:HB2	2:N7:37:THR:HG21	2.03	0.40
3:N8:11:LEU:HD23	3:N8:11:LEU:HA	1.72	0.40
3:N8:42:ILE:CD1	3:N8:96:LEU:HD11	2.49	0.40
3:N8:124:ILE:CG2	3:P8:66:GLN:HB3	2.51	0.40
2:O6:16:MET:O	2:O6:20:ALA:N	2.39	0.40
2:P5:12:GLY:HA2	2:P6:9:GLU:OE2	2.21	0.40
1:Q1:45:ASP:OD1	1:Q1:46:ALA:N	2.54	0.40
2:Q2:47:ARG:NH2	2:Q2:84:ASP:OD1	2.53	0.40
2:Q3:49:ASP:OD1	2:Q3:49:ASP:N	2.54	0.40
1:R1:28:ARG:NH2	1:R1:38:GLY:H	2.20	0.40
3:S8:63:PRO:HB3	3:S8:77:VAL:HG12	2.03	0.40
1:T1:68:VAL:C	1:T1:72:ARG:NH1	2.80	0.40
2:T4:8:ILE:O	2:T4:43:THR:HA	2.22	0.40
2:T4:53:VAL:O	2:T4:57:THR:OG1	2.30	0.40
3:T8:117:VAL:CG1	3:T8:121:GLN:HB3	2.52	0.40
2:V3:13:PHE:HB2	2:V4:37:THR:CG2	2.49	0.40
2:V6:76:ILE:HG21	2:V6:79:PRO:HB3	2.02	0.40
2:V7:16:MET:SD	2:V7:44:ALA:HB2	2.62	0.40
3:V8:79:HIS:CG	3:V8:80:PHE:H	2.39	0.40
3:V8:141:PHE:CZ	3:V8:143:LEU:HB2	2.56	0.40
2:X2:92:THR:HA	2:X2:93:PRO:HD3	1.95	0.40
2:X5:21:ASP:OD1	2:X5:25:LYS:HD2	2.21	0.40
1:Y1:2:VAL:HG23	1:Y1:57:TYR:CE1	2.56	0.40
2:Y5:7:ILE:HA	2:Y5:72:VAL:HG22	2.03	0.40
2:Y6:31:LEU:HD12	2:Y6:45:VAL:O	2.21	0.40
3:Z8:35:GLN:HG2	3:Z8:80:PHE:CD2	2.56	0.40
3:Z8:62:GLN:O	3:Z8:78:HIS:N	2.45	0.40
2:16:29:VAL:CG1	2:16:46:VAL:HB	2.51	0.40
3:18:37:SER:HA	3:18:78:HIS:HA	2.03	0.40
1:21:31:ASP:O	1:21:33:ASP:N	2.52	0.40
2:22:30:GLU:OE1	2:22:91:ARG:NH1	2.37	0.40
3:38:115:ARG:HA	3:38:139:SER:OG	2.22	0.40
2:46:3:ASP:O	2:46:47:ARG:NH1	2.54	0.40
3:48:141:PHE:O	3:48:179:TYR:HA	2.21	0.40
3:49:105:LYS:N	3:49:204:VAL:O	2.26	0.40

All (14) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X1:83:ASP:OD2	1:41:13:SER:OG[3_455]	1.82	0.38
2:M3:35:GLU:OE2	2:27:36:LYS:NZ[3_455]	1.86	0.34
1:M1:83:ASP:OD2	1:21:13:SER:OG[3_455]	1.93	0.27
1:T1:83:ASP:OD2	1:Y1:13:SER:OG[3_455]	1.93	0.27
2:X3:36:LYS:O	2:47:36:LYS:NZ[3_455]	1.96	0.24
2:K3:78:ARG:NH1	2:O7:27:ALA:O[3_455]	2.07	0.13
3:K8:50:ARG:NE	3:O8:112:GLN:OE1[3_455]	2.11	0.09
3:K8:49:ASN:OD1	3:O8:121:GLN:NE2[3_455]	2.12	0.08
1:K1:83:ASP:OD2	1:N1:13:SER:OG[3_455]	2.13	0.07
1:T1:1:MET:N	1:Y1:75:ASP:OD1[3_455]	2.14	0.06
3:O8:50:ARG:NE	3:18:112:GLN:OE1[3_455]	2.16	0.04
3:O8:49:ASN:OD1	3:18:121:GLN:NE2[3_455]	2.17	0.03
3:T8:49:ASN:OD1	3:Z8:121:GLN:NE2[3_455]	2.17	0.03
1:K1:1:MET:N	1:N1:75:ASP:OD1[3_455]	2.19	0.01

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 X-ray entries followed by that with respect to entries of similar resolution.

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	11	93/96 (97%)	80 (86%)	10 (11%)	3 (3%)	3	24
1	21	93/96 (97%)	79 (85%)	12 (13%)	2 (2%)	5	30
1	31	92/96 (96%)	77 (84%)	10 (11%)	5 (5%)	1	13
1	41	93/96 (97%)	77 (83%)	11 (12%)	5 (5%)	1	13
1	A1	93/96 (97%)	79 (85%)	11 (12%)	3 (3%)	3	24
1	B1	93/96 (97%)	78 (84%)	13 (14%)	2 (2%)	5	30
1	C1	93/96 (97%)	80 (86%)	12 (13%)	1 (1%)	11	44
1	D1	93/96 (97%)	79 (85%)	12 (13%)	2 (2%)	5	30
1	E1	93/96 (97%)	79 (85%)	10 (11%)	4 (4%)	2	18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F1	93/96 (97%)	80 (86%)	10 (11%)	3 (3%)	3	24
1	G1	93/96 (97%)	79 (85%)	13 (14%)	1 (1%)	11	44
1	H1	93/96 (97%)	80 (86%)	11 (12%)	2 (2%)	5	30
1	I1	93/96 (97%)	79 (85%)	11 (12%)	3 (3%)	3	24
1	J1	93/96 (97%)	79 (85%)	12 (13%)	2 (2%)	5	30
1	K1	93/96 (97%)	78 (84%)	10 (11%)	5 (5%)	1	13
1	L1	93/96 (97%)	79 (85%)	12 (13%)	2 (2%)	5	30
1	M1	93/96 (97%)	80 (86%)	11 (12%)	2 (2%)	5	30
1	N1	93/96 (97%)	79 (85%)	9 (10%)	5 (5%)	1	13
1	O1	93/96 (97%)	79 (85%)	11 (12%)	3 (3%)	3	24
1	P1	93/96 (97%)	80 (86%)	12 (13%)	1 (1%)	11	44
1	Q1	93/96 (97%)	79 (85%)	13 (14%)	1 (1%)	11	44
1	R1	93/96 (97%)	79 (85%)	12 (13%)	2 (2%)	5	30
1	S1	93/96 (97%)	80 (86%)	10 (11%)	3 (3%)	3	24
1	T1	93/96 (97%)	78 (84%)	11 (12%)	4 (4%)	2	18
1	U1	93/96 (97%)	78 (84%)	12 (13%)	3 (3%)	3	24
1	V1	93/96 (97%)	78 (84%)	14 (15%)	1 (1%)	11	44
1	W1	93/96 (97%)	79 (85%)	11 (12%)	3 (3%)	3	24
1	X1	93/96 (97%)	78 (84%)	11 (12%)	4 (4%)	2	18
1	Y1	93/96 (97%)	79 (85%)	11 (12%)	3 (3%)	3	24
1	Z1	93/96 (97%)	79 (85%)	10 (11%)	4 (4%)	2	18
2	12	92/99 (93%)	79 (86%)	8 (9%)	5 (5%)	1	13
2	13	90/99 (91%)	81 (90%)	7 (8%)	2 (2%)	5	30
2	14	92/99 (93%)	85 (92%)	6 (6%)	1 (1%)	11	44
2	15	91/99 (92%)	84 (92%)	5 (6%)	2 (2%)	5	30
2	16	90/99 (91%)	83 (92%)	7 (8%)	0	100	100
2	17	91/99 (92%)	86 (94%)	5 (6%)	0	100	100
2	22	92/99 (93%)	84 (91%)	6 (6%)	2 (2%)	5	30
2	23	90/99 (91%)	83 (92%)	6 (7%)	1 (1%)	11	44
2	24	92/99 (93%)	85 (92%)	6 (6%)	1 (1%)	11	44
2	25	91/99 (92%)	85 (93%)	6 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	26	90/99 (91%)	82 (91%)	8 (9%)	0	100	100
2	27	91/99 (92%)	84 (92%)	7 (8%)	0	100	100
2	32	92/99 (93%)	80 (87%)	7 (8%)	5 (5%)	1	13
2	33	90/99 (91%)	81 (90%)	7 (8%)	2 (2%)	5	30
2	34	92/99 (93%)	82 (89%)	7 (8%)	3 (3%)	3	23
2	35	91/99 (92%)	83 (91%)	8 (9%)	0	100	100
2	36	90/99 (91%)	82 (91%)	8 (9%)	0	100	100
2	37	91/99 (92%)	84 (92%)	7 (8%)	0	100	100
2	42	92/99 (93%)	80 (87%)	9 (10%)	3 (3%)	3	23
2	43	90/99 (91%)	80 (89%)	8 (9%)	2 (2%)	5	30
2	44	92/99 (93%)	85 (92%)	6 (6%)	1 (1%)	11	44
2	45	91/99 (92%)	82 (90%)	7 (8%)	2 (2%)	5	30
2	46	90/99 (91%)	82 (91%)	8 (9%)	0	100	100
2	47	91/99 (92%)	85 (93%)	6 (7%)	0	100	100
2	A2	90/99 (91%)	80 (89%)	8 (9%)	2 (2%)	5	30
2	A3	90/99 (91%)	82 (91%)	6 (7%)	2 (2%)	5	30
2	A4	91/99 (92%)	84 (92%)	6 (7%)	1 (1%)	11	44
2	A5	90/99 (91%)	83 (92%)	7 (8%)	0	100	100
2	A6	90/99 (91%)	82 (91%)	8 (9%)	0	100	100
2	A7	90/99 (91%)	85 (94%)	4 (4%)	1 (1%)	11	44
2	B2	89/99 (90%)	80 (90%)	7 (8%)	2 (2%)	5	30
2	B3	90/99 (91%)	82 (91%)	6 (7%)	2 (2%)	5	30
2	B4	90/99 (91%)	85 (94%)	4 (4%)	1 (1%)	11	44
2	B5	90/99 (91%)	84 (93%)	6 (7%)	0	100	100
2	B6	90/99 (91%)	82 (91%)	8 (9%)	0	100	100
2	B7	90/99 (91%)	85 (94%)	5 (6%)	0	100	100
2	C2	90/99 (91%)	79 (88%)	9 (10%)	2 (2%)	5	30
2	C3	90/99 (91%)	82 (91%)	6 (7%)	2 (2%)	5	30
2	C4	90/99 (91%)	84 (93%)	5 (6%)	1 (1%)	11	44
2	C5	90/99 (91%)	84 (93%)	6 (7%)	0	100	100
2	C6	90/99 (91%)	82 (91%)	8 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C7	91/99 (92%)	86 (94%)	5 (6%)	0	100	100
2	D2	91/99 (92%)	80 (88%)	9 (10%)	2 (2%)	5	30
2	D3	90/99 (91%)	81 (90%)	7 (8%)	2 (2%)	5	30
2	D4	90/99 (91%)	83 (92%)	6 (7%)	1 (1%)	11	44
2	D5	90/99 (91%)	85 (94%)	5 (6%)	0	100	100
2	D6	90/99 (91%)	81 (90%)	8 (9%)	1 (1%)	11	44
2	D7	91/99 (92%)	85 (93%)	6 (7%)	0	100	100
2	E2	92/99 (93%)	82 (89%)	8 (9%)	2 (2%)	5	30
2	E3	90/99 (91%)	81 (90%)	8 (9%)	1 (1%)	11	44
2	E4	92/99 (93%)	83 (90%)	8 (9%)	1 (1%)	11	44
2	E5	90/99 (91%)	86 (96%)	4 (4%)	0	100	100
2	E6	90/99 (91%)	82 (91%)	8 (9%)	0	100	100
2	E7	90/99 (91%)	86 (96%)	4 (4%)	0	100	100
2	F2	92/99 (93%)	82 (89%)	8 (9%)	2 (2%)	5	30
2	F3	90/99 (91%)	82 (91%)	6 (7%)	2 (2%)	5	30
2	F4	90/99 (91%)	84 (93%)	4 (4%)	2 (2%)	5	30
2	F5	90/99 (91%)	85 (94%)	5 (6%)	0	100	100
2	F6	90/99 (91%)	82 (91%)	8 (9%)	0	100	100
2	F7	91/99 (92%)	85 (93%)	6 (7%)	0	100	100
2	G2	90/99 (91%)	80 (89%)	8 (9%)	2 (2%)	5	30
2	G3	90/99 (91%)	79 (88%)	8 (9%)	3 (3%)	3	23
2	G4	90/99 (91%)	84 (93%)	5 (6%)	1 (1%)	11	44
2	G5	89/99 (90%)	83 (93%)	6 (7%)	0	100	100
2	G6	90/99 (91%)	83 (92%)	7 (8%)	0	100	100
2	G7	90/99 (91%)	85 (94%)	5 (6%)	0	100	100
2	H2	90/99 (91%)	78 (87%)	10 (11%)	2 (2%)	5	30
2	H3	90/99 (91%)	83 (92%)	5 (6%)	2 (2%)	5	30
2	H4	91/99 (92%)	82 (90%)	7 (8%)	2 (2%)	5	30
2	H5	89/99 (90%)	84 (94%)	5 (6%)	0	100	100
2	H6	90/99 (91%)	82 (91%)	8 (9%)	0	100	100
2	H7	90/99 (91%)	86 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	I2	90/99 (91%)	79 (88%)	9 (10%)	2 (2%)	5	30
2	I3	89/99 (90%)	82 (92%)	5 (6%)	2 (2%)	5	30
2	I4	90/99 (91%)	84 (93%)	5 (6%)	1 (1%)	11	44
2	I5	90/99 (91%)	85 (94%)	5 (6%)	0	100	100
2	I6	90/99 (91%)	82 (91%)	8 (9%)	0	100	100
2	I7	90/99 (91%)	86 (96%)	4 (4%)	0	100	100
2	J2	90/99 (91%)	80 (89%)	8 (9%)	2 (2%)	5	30
2	J3	90/99 (91%)	82 (91%)	6 (7%)	2 (2%)	5	30
2	J4	90/99 (91%)	84 (93%)	5 (6%)	1 (1%)	11	44
2	J5	89/99 (90%)	83 (93%)	5 (6%)	1 (1%)	11	44
2	J6	90/99 (91%)	82 (91%)	8 (9%)	0	100	100
2	J7	90/99 (91%)	85 (94%)	5 (6%)	0	100	100
2	K2	90/99 (91%)	80 (89%)	8 (9%)	2 (2%)	5	30
2	K3	90/99 (91%)	81 (90%)	7 (8%)	2 (2%)	5	30
2	K4	90/99 (91%)	84 (93%)	5 (6%)	1 (1%)	11	44
2	K5	91/99 (92%)	83 (91%)	8 (9%)	0	100	100
2	K6	90/99 (91%)	82 (91%)	8 (9%)	0	100	100
2	K7	91/99 (92%)	86 (94%)	5 (6%)	0	100	100
2	L2	92/99 (93%)	83 (90%)	7 (8%)	2 (2%)	5	30
2	L3	90/99 (91%)	81 (90%)	7 (8%)	2 (2%)	5	30
2	L4	90/99 (91%)	84 (93%)	5 (6%)	1 (1%)	11	44
2	L5	90/99 (91%)	84 (93%)	6 (7%)	0	100	100
2	L6	90/99 (91%)	81 (90%)	9 (10%)	0	100	100
2	L7	91/99 (92%)	86 (94%)	5 (6%)	0	100	100
2	M2	91/99 (92%)	80 (88%)	9 (10%)	2 (2%)	5	30
2	M3	90/99 (91%)	82 (91%)	6 (7%)	2 (2%)	5	30
2	M4	90/99 (91%)	83 (92%)	6 (7%)	1 (1%)	11	44
2	M5	91/99 (92%)	82 (90%)	8 (9%)	1 (1%)	11	44
2	M6	89/99 (90%)	81 (91%)	8 (9%)	0	100	100
2	M7	90/99 (91%)	85 (94%)	5 (6%)	0	100	100
2	N2	90/99 (91%)	82 (91%)	7 (8%)	1 (1%)	11	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	N3	89/99 (90%)	81 (91%)	5 (6%)	3 (3%)	3	23
2	N4	90/99 (91%)	84 (93%)	5 (6%)	1 (1%)	11	44
2	N5	91/99 (92%)	82 (90%)	5 (6%)	4 (4%)	2	17
2	N6	89/99 (90%)	81 (91%)	8 (9%)	0	100	100
2	N7	90/99 (91%)	85 (94%)	5 (6%)	0	100	100
2	O2	92/99 (93%)	81 (88%)	7 (8%)	4 (4%)	2	18
2	O3	90/99 (91%)	81 (90%)	6 (7%)	3 (3%)	3	23
2	O4	92/99 (93%)	86 (94%)	5 (5%)	1 (1%)	11	44
2	O5	91/99 (92%)	85 (93%)	6 (7%)	0	100	100
2	O6	90/99 (91%)	81 (90%)	9 (10%)	0	100	100
2	O7	91/99 (92%)	85 (93%)	6 (7%)	0	100	100
2	P2	92/99 (93%)	80 (87%)	9 (10%)	3 (3%)	3	23
2	P3	90/99 (91%)	81 (90%)	7 (8%)	2 (2%)	5	30
2	P4	92/99 (93%)	86 (94%)	5 (5%)	1 (1%)	11	44
2	P5	91/99 (92%)	84 (92%)	7 (8%)	0	100	100
2	P6	90/99 (91%)	82 (91%)	8 (9%)	0	100	100
2	P7	89/99 (90%)	84 (94%)	4 (4%)	1 (1%)	11	44
2	Q2	92/99 (93%)	80 (87%)	9 (10%)	3 (3%)	3	23
2	Q3	90/99 (91%)	81 (90%)	7 (8%)	2 (2%)	5	30
2	Q4	92/99 (93%)	86 (94%)	5 (5%)	1 (1%)	11	44
2	Q5	91/99 (92%)	83 (91%)	8 (9%)	0	100	100
2	Q6	90/99 (91%)	81 (90%)	9 (10%)	0	100	100
2	Q7	91/99 (92%)	85 (93%)	6 (7%)	0	100	100
2	R2	92/99 (93%)	80 (87%)	8 (9%)	4 (4%)	2	18
2	R3	90/99 (91%)	81 (90%)	7 (8%)	2 (2%)	5	30
2	R4	92/99 (93%)	85 (92%)	6 (6%)	1 (1%)	11	44
2	R5	91/99 (92%)	83 (91%)	7 (8%)	1 (1%)	11	44
2	R6	90/99 (91%)	78 (87%)	7 (8%)	5 (6%)	1	13
2	R7	91/99 (92%)	86 (94%)	4 (4%)	1 (1%)	11	44
2	S2	92/99 (93%)	81 (88%)	7 (8%)	4 (4%)	2	18
2	S3	90/99 (91%)	82 (91%)	6 (7%)	2 (2%)	5	30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	S4	92/99 (93%)	85 (92%)	6 (6%)	1 (1%)	11	44
2	S5	91/99 (92%)	84 (92%)	7 (8%)	0	100	100
2	S6	90/99 (91%)	82 (91%)	8 (9%)	0	100	100
2	S7	91/99 (92%)	86 (94%)	5 (6%)	0	100	100
2	T2	92/99 (93%)	81 (88%)	9 (10%)	2 (2%)	5	30
2	T3	90/99 (91%)	81 (90%)	7 (8%)	2 (2%)	5	30
2	T4	92/99 (93%)	84 (91%)	5 (5%)	3 (3%)	3	23
2	T5	91/99 (92%)	86 (94%)	3 (3%)	2 (2%)	5	30
2	T6	90/99 (91%)	82 (91%)	8 (9%)	0	100	100
2	T7	91/99 (92%)	87 (96%)	4 (4%)	0	100	100
2	U2	92/99 (93%)	80 (87%)	10 (11%)	2 (2%)	5	30
2	U3	90/99 (91%)	83 (92%)	6 (7%)	1 (1%)	11	44
2	U4	92/99 (93%)	85 (92%)	6 (6%)	1 (1%)	11	44
2	U5	91/99 (92%)	85 (93%)	5 (6%)	1 (1%)	11	44
2	U6	90/99 (91%)	83 (92%)	7 (8%)	0	100	100
2	U7	91/99 (92%)	85 (93%)	6 (7%)	0	100	100
2	V2	92/99 (93%)	81 (88%)	8 (9%)	3 (3%)	3	23
2	V3	90/99 (91%)	82 (91%)	6 (7%)	2 (2%)	5	30
2	V4	92/99 (93%)	84 (91%)	6 (6%)	2 (2%)	5	30
2	V5	91/99 (92%)	86 (94%)	5 (6%)	0	100	100
2	V6	90/99 (91%)	81 (90%)	8 (9%)	1 (1%)	11	44
2	V7	91/99 (92%)	85 (93%)	6 (7%)	0	100	100
2	W2	92/99 (93%)	81 (88%)	8 (9%)	3 (3%)	3	23
2	W3	90/99 (91%)	81 (90%)	7 (8%)	2 (2%)	5	30
2	W4	92/99 (93%)	83 (90%)	6 (6%)	3 (3%)	3	23
2	W5	91/99 (92%)	83 (91%)	8 (9%)	0	100	100
2	W6	90/99 (91%)	81 (90%)	9 (10%)	0	100	100
2	W7	91/99 (92%)	85 (93%)	6 (7%)	0	100	100
2	X2	92/99 (93%)	80 (87%)	10 (11%)	2 (2%)	5	30
2	X3	90/99 (91%)	81 (90%)	7 (8%)	2 (2%)	5	30
2	X4	92/99 (93%)	86 (94%)	5 (5%)	1 (1%)	11	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	X5	91/99 (92%)	84 (92%)	7 (8%)	0	100	100
2	X6	90/99 (91%)	82 (91%)	8 (9%)	0	100	100
2	X7	91/99 (92%)	86 (94%)	5 (6%)	0	100	100
2	Y2	92/99 (93%)	81 (88%)	8 (9%)	3 (3%)	3	23
2	Y3	90/99 (91%)	83 (92%)	5 (6%)	2 (2%)	5	30
2	Y4	92/99 (93%)	83 (90%)	8 (9%)	1 (1%)	11	44
2	Y5	90/99 (91%)	82 (91%)	6 (7%)	2 (2%)	5	30
2	Y6	90/99 (91%)	83 (92%)	7 (8%)	0	100	100
2	Y7	91/99 (92%)	85 (93%)	6 (7%)	0	100	100
2	Z2	92/99 (93%)	80 (87%)	8 (9%)	4 (4%)	2	18
2	Z3	90/99 (91%)	81 (90%)	7 (8%)	2 (2%)	5	30
2	Z4	92/99 (93%)	83 (90%)	7 (8%)	2 (2%)	5	30
2	Z5	91/99 (92%)	84 (92%)	6 (7%)	1 (1%)	11	44
2	Z6	90/99 (91%)	82 (91%)	8 (9%)	0	100	100
2	Z7	91/99 (92%)	84 (92%)	7 (8%)	0	100	100
3	18	201/212 (95%)	174 (87%)	22 (11%)	5 (2%)	4	28
3	19	194/212 (92%)	183 (94%)	10 (5%)	1 (0%)	24	58
3	28	201/212 (95%)	174 (87%)	26 (13%)	1 (0%)	24	58
3	29	201/212 (95%)	187 (93%)	13 (6%)	1 (0%)	24	58
3	38	201/212 (95%)	174 (87%)	25 (12%)	2 (1%)	12	45
3	39	201/212 (95%)	187 (93%)	14 (7%)	0	100	100
3	48	201/212 (95%)	174 (87%)	23 (11%)	4 (2%)	6	32
3	49	201/212 (95%)	188 (94%)	12 (6%)	1 (0%)	24	58
3	A8	201/212 (95%)	168 (84%)	28 (14%)	5 (2%)	4	28
3	A9	201/212 (95%)	190 (94%)	11 (6%)	0	100	100
3	B8	201/212 (95%)	175 (87%)	23 (11%)	3 (2%)	8	37
3	B9	201/212 (95%)	185 (92%)	16 (8%)	0	100	100
3	C8	201/212 (95%)	172 (86%)	27 (13%)	2 (1%)	12	45
3	C9	201/212 (95%)	187 (93%)	14 (7%)	0	100	100
3	D8	201/212 (95%)	172 (86%)	28 (14%)	1 (0%)	24	58
3	D9	201/212 (95%)	185 (92%)	15 (8%)	1 (0%)	24	58

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	E8	201/212 (95%)	173 (86%)	24 (12%)	4 (2%)	6	32
3	E9	201/212 (95%)	190 (94%)	11 (6%)	0	100	100
3	F8	201/212 (95%)	173 (86%)	24 (12%)	4 (2%)	6	32
3	F9	201/212 (95%)	189 (94%)	12 (6%)	0	100	100
3	G8	201/212 (95%)	173 (86%)	24 (12%)	4 (2%)	6	32
3	G9	201/212 (95%)	185 (92%)	15 (8%)	1 (0%)	24	58
3	H8	201/212 (95%)	172 (86%)	27 (13%)	2 (1%)	12	45
3	H9	201/212 (95%)	188 (94%)	11 (6%)	2 (1%)	12	45
3	I8	201/212 (95%)	174 (87%)	26 (13%)	1 (0%)	24	58
3	I9	201/212 (95%)	187 (93%)	14 (7%)	0	100	100
3	J8	201/212 (95%)	168 (84%)	30 (15%)	3 (2%)	8	37
3	J9	201/212 (95%)	189 (94%)	12 (6%)	0	100	100
3	K8	201/212 (95%)	175 (87%)	25 (12%)	1 (0%)	24	58
3	K9	201/212 (95%)	188 (94%)	12 (6%)	1 (0%)	24	58
3	L8	201/212 (95%)	173 (86%)	26 (13%)	2 (1%)	12	45
3	L9	201/212 (95%)	187 (93%)	13 (6%)	1 (0%)	24	58
3	M8	201/212 (95%)	173 (86%)	25 (12%)	3 (2%)	8	37
3	M9	201/212 (95%)	186 (92%)	12 (6%)	3 (2%)	8	37
3	N8	201/212 (95%)	171 (85%)	26 (13%)	4 (2%)	6	32
3	N9	201/212 (95%)	185 (92%)	16 (8%)	0	100	100
3	O8	201/212 (95%)	173 (86%)	27 (13%)	1 (0%)	24	58
3	O9	201/212 (95%)	188 (94%)	13 (6%)	0	100	100
3	P8	201/212 (95%)	172 (86%)	27 (13%)	2 (1%)	12	45
3	P9	201/212 (95%)	186 (92%)	14 (7%)	1 (0%)	24	58
3	Q8	201/212 (95%)	173 (86%)	27 (13%)	1 (0%)	24	58
3	Q9	201/212 (95%)	188 (94%)	13 (6%)	0	100	100
3	R8	201/212 (95%)	171 (85%)	26 (13%)	4 (2%)	6	32
3	R9	201/212 (95%)	182 (90%)	16 (8%)	3 (2%)	8	37
3	S8	201/212 (95%)	173 (86%)	27 (13%)	1 (0%)	24	58
3	S9	201/212 (95%)	189 (94%)	12 (6%)	0	100	100
3	T8	201/212 (95%)	175 (87%)	21 (10%)	5 (2%)	4	28

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	T9	201/212 (95%)	191 (95%)	10 (5%)	0	100	100
3	U8	201/212 (95%)	173 (86%)	25 (12%)	3 (2%)	8	37
3	U9	201/212 (95%)	189 (94%)	12 (6%)	0	100	100
3	V8	201/212 (95%)	172 (86%)	27 (13%)	2 (1%)	12	45
3	V9	201/212 (95%)	187 (93%)	14 (7%)	0	100	100
3	W8	201/212 (95%)	173 (86%)	23 (11%)	5 (2%)	4	28
3	W9	201/212 (95%)	188 (94%)	13 (6%)	0	100	100
3	X8	201/212 (95%)	174 (87%)	26 (13%)	1 (0%)	24	58
3	X9	201/212 (95%)	186 (92%)	14 (7%)	1 (0%)	24	58
3	Y8	201/212 (95%)	171 (85%)	27 (13%)	3 (2%)	8	37
3	Y9	201/212 (95%)	186 (92%)	15 (8%)	0	100	100
3	Z8	201/212 (95%)	170 (85%)	28 (14%)	3 (2%)	8	37
3	Z9	201/212 (95%)	185 (92%)	15 (8%)	1 (0%)	24	58
All	All	31147/33420 (93%)	28065 (90%)	2692 (9%)	390 (1%)	9	40

All (390) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A1	70	ASN
2	A2	91	ARG
2	A3	11	ARG
1	B1	70	ASN
2	B2	91	ARG
2	B3	11	ARG
2	B3	91	ARG
2	C2	91	ARG
2	C3	11	ARG
1	D1	70	ASN
2	D2	91	ARG
2	D3	12	ARG
1	E1	70	ASN
2	E2	91	ARG
2	E3	91	ARG
1	F1	70	ASN
1	F1	71	ASN
2	F2	91	ARG
2	F3	11	ARG

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Mol	Chain	Res	Type
2	F3	91	ARG
1	G1	70	ASN
2	G2	91	ARG
2	G3	11	ARG
2	G3	91	ARG
3	G9	98	VAL
1	H1	70	ASN
2	H2	91	ARG
2	H3	11	ARG
2	H3	91	ARG
1	I1	70	ASN
2	I2	91	ARG
2	I3	11	ARG
2	I3	91	ARG
1	J1	70	ASN
2	J2	91	ARG
2	J3	11	ARG
2	J3	91	ARG
2	J5	41	TYR
1	K1	70	ASN
2	K2	91	ARG
2	K3	11	ARG
2	K3	91	ARG
1	L1	70	ASN
2	L2	91	ARG
2	L3	11	ARG
2	L3	91	ARG
1	M1	70	ASN
2	M3	11	ARG
3	M9	98	VAL
1	N1	70	ASN
1	N1	71	ASN
2	N3	11	ARG
1	O1	70	ASN
2	O2	91	ARG
2	O3	11	ARG
2	O3	91	ARG
1	P1	70	ASN
2	P2	91	ARG
2	P3	11	ARG
2	P3	91	ARG
1	Q1	70	ASN

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Mol	Chain	Res	Type
2	Q2	91	ARG
2	Q3	11	ARG
2	Q3	91	ARG
1	R1	70	ASN
2	R2	91	ARG
2	R3	11	ARG
2	R3	91	ARG
2	R6	65	GLU
2	R6	71	VAL
1	S1	70	ASN
2	S2	91	ARG
2	S3	11	ARG
2	S3	91	ARG
1	T1	70	ASN
2	T2	91	ARG
2	T3	11	ARG
2	T3	91	ARG
1	U1	68	VAL
1	U1	70	ASN
2	U2	91	ARG
2	U3	91	ARG
1	V1	70	ASN
2	V2	91	ARG
2	V3	11	ARG
2	V3	91	ARG
1	W1	70	ASN
2	W2	91	ARG
2	W3	11	ARG
2	W3	91	ARG
1	X1	3	LEU
1	X1	70	ASN
2	X2	91	ARG
2	X3	11	ARG
2	X3	91	ARG
1	Y1	70	ASN
2	Y2	91	ARG
2	Y3	11	ARG
2	Y3	91	ARG
1	Z1	70	ASN
2	Z2	91	ARG
2	Z3	11	ARG
2	Z3	91	ARG

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Mol	Chain	Res	Type
1	11	70	ASN
2	12	69	GLU
2	12	91	ARG
2	13	11	ARG
2	13	91	ARG
1	21	70	ASN
1	21	71	ASN
2	22	91	ARG
2	23	91	ARG
1	31	70	ASN
2	32	91	ARG
2	33	11	ARG
2	33	91	ARG
1	41	70	ASN
2	42	91	ARG
2	43	11	ARG
2	43	91	ARG
2	45	31	LEU
2	45	32	ILE
2	A3	91	ARG
3	A8	138	GLU
1	C1	67	GLU
2	C3	91	ARG
2	D3	92	ARG
1	E1	3	LEU
1	E1	67	GLU
3	F8	129	SER
2	G3	48	GLY
2	H4	3	ASP
2	I4	77	PRO
1	L1	71	ASN
2	M3	91	ARG
2	M5	90	GLY
2	N5	48	GLY
1	O1	71	ASN
2	O3	3	ASP
2	R6	66	ARG
2	R6	70	VAL
3	R9	94	ASP
2	T5	41	TYR
1	U1	67	GLU
1	W1	67	GLU

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Mol	Chain	Res	Type
2	W2	93	PRO
1	Y1	71	ASN
2	Y5	47	GLY
1	Z1	71	ASN
2	Z2	93	PRO
2	Z4	94	GLY
1	11	67	GLU
2	15	90	GLY
1	31	73	PRO
1	31	74	VAL
2	34	10	VAL
1	41	3	LEU
1	41	67	GLU
1	A1	67	GLU
2	A4	77	PRO
1	B1	67	GLU
2	B4	77	PRO
1	D1	68	VAL
2	D4	77	PRO
2	E2	70	VAL
3	E8	61	VAL
3	E8	129	SER
2	F2	70	VAL
2	F4	3	ASP
2	G4	77	PRO
3	H8	129	SER
1	I1	71	ASN
1	J1	71	ASN
2	J4	77	PRO
1	K1	33	ASP
1	K1	67	GLU
3	L9	98	VAL
2	M4	77	PRO
1	N1	67	GLU
2	N2	70	VAL
2	N3	91	ARG
2	N5	49	ASP
2	O2	70	VAL
2	O2	93	PRO
2	Q2	93	PRO
2	R6	68	GLY
1	S1	71	ASN

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Mol	Chain	Res	Type
2	S2	94	GLY
1	T1	67	GLU
2	T4	3	ASP
2	U2	70	VAL
2	U4	77	PRO
2	V6	3	ASP
1	W1	71	ASN
2	W4	77	PRO
2	X4	77	PRO
1	Y1	67	GLU
2	Y4	77	PRO
2	12	93	PRO
2	12	94	GLY
2	14	77	PRO
2	24	77	PRO
2	32	94	GLY
2	34	3	ASP
2	44	77	PRO
3	48	129	SER
2	A2	70	VAL
3	A8	129	SER
2	B2	70	VAL
3	B8	61	VAL
2	C4	77	PRO
3	C8	61	VAL
2	D6	3	ASP
2	E4	77	PRO
3	F8	61	VAL
2	G2	70	VAL
3	G8	138	GLU
2	H4	77	PRO
3	H8	61	VAL
2	I2	70	VAL
2	J2	70	VAL
2	K2	70	VAL
2	K4	77	PRO
2	L2	70	VAL
2	M2	93	PRO
2	N4	77	PRO
3	N8	129	SER
1	O1	80	ALA
2	O4	77	PRO

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Mol	Chain	Res	Type
2	P2	93	PRO
2	P4	77	PRO
2	Q2	70	VAL
1	R1	67	GLU
2	R2	70	VAL
1	S1	67	GLU
2	S2	70	VAL
2	S4	77	PRO
2	T2	70	VAL
2	V2	93	PRO
3	V8	61	VAL
3	W8	129	SER
1	X1	67	GLU
2	Y2	70	VAL
2	Y5	48	ASP
3	Y8	129	SER
1	Z1	67	GLU
2	Z2	94	GLY
2	Z4	77	PRO
2	22	70	VAL
2	32	70	VAL
2	32	93	PRO
1	41	71	ASN
2	42	93	PRO
3	A8	33	PRO
2	C2	70	VAL
2	D2	70	VAL
3	E8	138	GLU
1	F1	61	SER
3	F8	138	GLU
3	G8	61	VAL
3	G8	129	SER
1	H1	71	ASN
2	H2	70	VAL
1	I1	67	GLU
3	J8	129	SER
2	L4	77	PRO
2	M2	70	VAL
3	M8	129	SER
3	M9	97	GLU
2	N3	49	ASP
3	N8	61	VAL

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Mol	Chain	Res	Type
2	P2	70	VAL
3	P8	61	VAL
2	Q4	77	PRO
2	R2	93	PRO
2	R2	94	GLY
3	R8	138	GLU
2	T4	94	GLY
3	T8	61	VAL
3	T8	129	SER
3	T8	138	GLU
2	V2	70	VAL
2	V4	77	PRO
2	W2	70	VAL
3	W8	61	VAL
3	W8	138	GLU
1	X1	71	ASN
2	X2	70	VAL
2	Z2	70	VAL
3	Z8	61	VAL
3	Z9	97	GLU
2	12	70	VAL
1	31	71	ASN
2	32	3	ASP
2	42	70	VAL
3	48	138	GLU
2	A7	4	ALA
3	B8	129	SER
3	D8	61	VAL
2	F4	77	PRO
3	H9	125	ILE
3	J8	61	VAL
3	J8	138	GLU
1	K1	65	GLN
1	M1	71	ASN
2	N5	91	ARG
3	N8	138	GLU
2	R5	91	ARG
2	R7	4	ALA
3	R9	93	LEU
2	S2	3	ASP
2	T5	93	PRO
2	U5	93	PRO

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Mol	Chain	Res	Type
2	V4	94	GLY
2	W4	93	PRO
3	W8	63	PRO
3	X8	61	VAL
3	Y8	61	VAL
3	Y8	138	GLU
3	Z8	129	SER
3	18	20	THR
3	18	129	SER
3	28	61	VAL
1	31	67	GLU
1	E1	68	VAL
3	H9	98	VAL
3	L8	61	VAL
3	M8	61	VAL
2	O2	94	GLY
3	Q8	61	VAL
2	R4	77	PRO
3	R9	125	ILE
3	S8	61	VAL
3	W8	167	VAL
1	11	68	VAL
3	18	61	VAL
3	38	61	VAL
3	48	61	VAL
1	A1	68	VAL
3	C8	63	PRO
3	I8	61	VAL
3	K8	61	VAL
3	O8	61	VAL
3	P9	125	ILE
3	R8	61	VAL
2	T4	77	PRO
2	W4	94	GLY
1	41	68	VAL
3	A8	61	VAL
3	B8	63	PRO
3	D9	98	VAL
1	K1	68	VAL
3	K9	125	ILE
3	P8	63	PRO
3	X9	125	ILE

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Mol	Chain	Res	Type
3	19	125	ILE
2	34	77	PRO
3	E8	63	PRO
3	L8	63	PRO
3	M8	167	VAL
3	M9	125	ILE
1	N1	68	VAL
2	N5	93	PRO
3	N8	63	PRO
3	R8	63	PRO
1	T1	32	PRO
1	T1	68	VAL
3	T8	63	PRO
3	T8	167	VAL
3	U8	61	VAL
3	U8	63	PRO
3	U8	167	VAL
3	V8	63	PRO
2	Y2	93	PRO
2	Z5	93	PRO
2	15	93	PRO
3	48	63	PRO
3	49	98	VAL
3	A8	63	PRO
3	F8	167	VAL
3	G8	63	PRO
1	N1	32	PRO
2	P7	76	ARG
3	R8	167	VAL
1	Z1	68	VAL
3	Z8	63	PRO
3	18	63	PRO
3	18	167	VAL
3	29	125	ILE
3	38	167	VAL

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 X-ray entries followed by that with respect to entries of similar resolution.

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	11	73/74 (99%)	73 (100%)	0	100	100
1	21	73/74 (99%)	73 (100%)	0	100	100
1	31	72/74 (97%)	72 (100%)	0	100	100
1	41	73/74 (99%)	73 (100%)	0	100	100
1	A1	73/74 (99%)	73 (100%)	0	100	100
1	B1	73/74 (99%)	73 (100%)	0	100	100
1	C1	73/74 (99%)	73 (100%)	0	100	100
1	D1	73/74 (99%)	73 (100%)	0	100	100
1	E1	73/74 (99%)	73 (100%)	0	100	100
1	F1	73/74 (99%)	73 (100%)	0	100	100
1	G1	73/74 (99%)	73 (100%)	0	100	100
1	H1	73/74 (99%)	73 (100%)	0	100	100
1	I1	73/74 (99%)	73 (100%)	0	100	100
1	J1	73/74 (99%)	73 (100%)	0	100	100
1	K1	73/74 (99%)	73 (100%)	0	100	100
1	L1	73/74 (99%)	73 (100%)	0	100	100
1	M1	73/74 (99%)	73 (100%)	0	100	100
1	N1	73/74 (99%)	73 (100%)	0	100	100
1	O1	73/74 (99%)	73 (100%)	0	100	100
1	P1	73/74 (99%)	73 (100%)	0	100	100
1	Q1	73/74 (99%)	73 (100%)	0	100	100
1	R1	73/74 (99%)	73 (100%)	0	100	100
1	S1	73/74 (99%)	73 (100%)	0	100	100
1	T1	73/74 (99%)	73 (100%)	0	100	100
1	U1	73/74 (99%)	73 (100%)	0	100	100
1	V1	73/74 (99%)	73 (100%)	0	100	100
1	W1	73/74 (99%)	72 (99%)	1 (1%)	59	72
1	X1	73/74 (99%)	73 (100%)	0	100	100
1	Y1	73/74 (99%)	73 (100%)	0	100	100
1	Z1	73/74 (99%)	73 (100%)	0	100	100
2	12	64/68 (94%)	64 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	13	63/68 (93%)	63 (100%)	0	100	100
2	14	64/68 (94%)	64 (100%)	0	100	100
2	15	63/68 (93%)	63 (100%)	0	100	100
2	16	63/68 (93%)	63 (100%)	0	100	100
2	17	63/68 (93%)	63 (100%)	0	100	100
2	22	64/68 (94%)	64 (100%)	0	100	100
2	23	63/68 (93%)	63 (100%)	0	100	100
2	24	64/68 (94%)	64 (100%)	0	100	100
2	25	63/68 (93%)	63 (100%)	0	100	100
2	26	63/68 (93%)	63 (100%)	0	100	100
2	27	63/68 (93%)	63 (100%)	0	100	100
2	32	64/68 (94%)	64 (100%)	0	100	100
2	33	63/68 (93%)	63 (100%)	0	100	100
2	34	64/68 (94%)	64 (100%)	0	100	100
2	35	63/68 (93%)	63 (100%)	0	100	100
2	36	63/68 (93%)	62 (98%)	1 (2%)	55	70
2	37	63/68 (93%)	62 (98%)	1 (2%)	55	70
2	42	64/68 (94%)	64 (100%)	0	100	100
2	43	63/68 (93%)	63 (100%)	0	100	100
2	44	64/68 (94%)	63 (98%)	1 (2%)	55	70
2	45	63/68 (93%)	63 (100%)	0	100	100
2	46	63/68 (93%)	63 (100%)	0	100	100
2	47	63/68 (93%)	63 (100%)	0	100	100
2	A2	63/68 (93%)	63 (100%)	0	100	100
2	A3	63/68 (93%)	63 (100%)	0	100	100
2	A4	63/68 (93%)	63 (100%)	0	100	100
2	A5	63/68 (93%)	63 (100%)	0	100	100
2	A6	63/68 (93%)	63 (100%)	0	100	100
2	A7	63/68 (93%)	63 (100%)	0	100	100
2	B2	62/68 (91%)	62 (100%)	0	100	100
2	B3	63/68 (93%)	63 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B4	63/68 (93%)	63 (100%)	0	100	100
2	B5	63/68 (93%)	63 (100%)	0	100	100
2	B6	63/68 (93%)	63 (100%)	0	100	100
2	B7	63/68 (93%)	63 (100%)	0	100	100
2	C2	63/68 (93%)	63 (100%)	0	100	100
2	C3	63/68 (93%)	63 (100%)	0	100	100
2	C4	63/68 (93%)	63 (100%)	0	100	100
2	C5	63/68 (93%)	63 (100%)	0	100	100
2	C6	63/68 (93%)	63 (100%)	0	100	100
2	C7	63/68 (93%)	63 (100%)	0	100	100
2	D2	63/68 (93%)	63 (100%)	0	100	100
2	D3	63/68 (93%)	63 (100%)	0	100	100
2	D4	63/68 (93%)	63 (100%)	0	100	100
2	D5	63/68 (93%)	63 (100%)	0	100	100
2	D6	63/68 (93%)	63 (100%)	0	100	100
2	D7	63/68 (93%)	63 (100%)	0	100	100
2	E2	64/68 (94%)	64 (100%)	0	100	100
2	E3	63/68 (93%)	62 (98%)	1 (2%)	55	70
2	E4	64/68 (94%)	64 (100%)	0	100	100
2	E5	63/68 (93%)	63 (100%)	0	100	100
2	E6	63/68 (93%)	63 (100%)	0	100	100
2	E7	63/68 (93%)	62 (98%)	1 (2%)	55	70
2	F2	64/68 (94%)	63 (98%)	1 (2%)	55	70
2	F3	63/68 (93%)	63 (100%)	0	100	100
2	F4	63/68 (93%)	63 (100%)	0	100	100
2	F5	63/68 (93%)	63 (100%)	0	100	100
2	F6	63/68 (93%)	63 (100%)	0	100	100
2	F7	63/68 (93%)	63 (100%)	0	100	100
2	G2	63/68 (93%)	63 (100%)	0	100	100
2	G3	63/68 (93%)	63 (100%)	0	100	100
2	G4	63/68 (93%)	63 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	G5	63/68 (93%)	63 (100%)	0	100	100
2	G6	63/68 (93%)	63 (100%)	0	100	100
2	G7	63/68 (93%)	63 (100%)	0	100	100
2	H2	63/68 (93%)	63 (100%)	0	100	100
2	H3	63/68 (93%)	63 (100%)	0	100	100
2	H4	63/68 (93%)	63 (100%)	0	100	100
2	H5	63/68 (93%)	63 (100%)	0	100	100
2	H6	63/68 (93%)	63 (100%)	0	100	100
2	H7	63/68 (93%)	63 (100%)	0	100	100
2	I2	63/68 (93%)	63 (100%)	0	100	100
2	I3	63/68 (93%)	63 (100%)	0	100	100
2	I4	63/68 (93%)	62 (98%)	1 (2%)	55	70
2	I5	63/68 (93%)	63 (100%)	0	100	100
2	I6	63/68 (93%)	63 (100%)	0	100	100
2	I7	63/68 (93%)	63 (100%)	0	100	100
2	J2	63/68 (93%)	63 (100%)	0	100	100
2	J3	63/68 (93%)	63 (100%)	0	100	100
2	J4	63/68 (93%)	63 (100%)	0	100	100
2	J5	63/68 (93%)	63 (100%)	0	100	100
2	J6	63/68 (93%)	63 (100%)	0	100	100
2	J7	63/68 (93%)	63 (100%)	0	100	100
2	K2	63/68 (93%)	63 (100%)	0	100	100
2	K3	63/68 (93%)	63 (100%)	0	100	100
2	K4	63/68 (93%)	63 (100%)	0	100	100
2	K5	63/68 (93%)	63 (100%)	0	100	100
2	K6	63/68 (93%)	63 (100%)	0	100	100
2	K7	63/68 (93%)	63 (100%)	0	100	100
2	L2	64/68 (94%)	64 (100%)	0	100	100
2	L3	63/68 (93%)	63 (100%)	0	100	100
2	L4	63/68 (93%)	63 (100%)	0	100	100
2	L5	63/68 (93%)	63 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	L6	63/68 (93%)	63 (100%)	0	100	100
2	L7	63/68 (93%)	63 (100%)	0	100	100
2	M2	63/68 (93%)	63 (100%)	0	100	100
2	M3	63/68 (93%)	63 (100%)	0	100	100
2	M4	63/68 (93%)	63 (100%)	0	100	100
2	M5	63/68 (93%)	63 (100%)	0	100	100
2	M6	63/68 (93%)	63 (100%)	0	100	100
2	M7	63/68 (93%)	63 (100%)	0	100	100
2	N2	63/68 (93%)	63 (100%)	0	100	100
2	N3	63/68 (93%)	63 (100%)	0	100	100
2	N4	63/68 (93%)	63 (100%)	0	100	100
2	N5	63/68 (93%)	63 (100%)	0	100	100
2	N6	63/68 (93%)	63 (100%)	0	100	100
2	N7	63/68 (93%)	63 (100%)	0	100	100
2	O2	64/68 (94%)	64 (100%)	0	100	100
2	O3	63/68 (93%)	63 (100%)	0	100	100
2	O4	64/68 (94%)	64 (100%)	0	100	100
2	O5	63/68 (93%)	63 (100%)	0	100	100
2	O6	63/68 (93%)	63 (100%)	0	100	100
2	O7	63/68 (93%)	63 (100%)	0	100	100
2	P2	64/68 (94%)	64 (100%)	0	100	100
2	P3	63/68 (93%)	63 (100%)	0	100	100
2	P4	64/68 (94%)	64 (100%)	0	100	100
2	P5	63/68 (93%)	63 (100%)	0	100	100
2	P6	63/68 (93%)	63 (100%)	0	100	100
2	P7	62/68 (91%)	62 (100%)	0	100	100
2	Q2	64/68 (94%)	64 (100%)	0	100	100
2	Q3	63/68 (93%)	63 (100%)	0	100	100
2	Q4	64/68 (94%)	64 (100%)	0	100	100
2	Q5	63/68 (93%)	63 (100%)	0	100	100
2	Q6	63/68 (93%)	63 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	Q7	63/68 (93%)	63 (100%)	0	100	100
2	R2	64/68 (94%)	64 (100%)	0	100	100
2	R3	63/68 (93%)	63 (100%)	0	100	100
2	R4	64/68 (94%)	64 (100%)	0	100	100
2	R5	63/68 (93%)	63 (100%)	0	100	100
2	R6	63/68 (93%)	63 (100%)	0	100	100
2	R7	63/68 (93%)	62 (98%)	1 (2%)	55	70
2	S2	64/68 (94%)	64 (100%)	0	100	100
2	S3	63/68 (93%)	63 (100%)	0	100	100
2	S4	64/68 (94%)	63 (98%)	1 (2%)	55	70
2	S5	63/68 (93%)	63 (100%)	0	100	100
2	S6	63/68 (93%)	63 (100%)	0	100	100
2	S7	63/68 (93%)	63 (100%)	0	100	100
2	T2	64/68 (94%)	64 (100%)	0	100	100
2	T3	63/68 (93%)	63 (100%)	0	100	100
2	T4	64/68 (94%)	64 (100%)	0	100	100
2	T5	63/68 (93%)	63 (100%)	0	100	100
2	T6	63/68 (93%)	63 (100%)	0	100	100
2	T7	63/68 (93%)	62 (98%)	1 (2%)	55	70
2	U2	64/68 (94%)	64 (100%)	0	100	100
2	U3	63/68 (93%)	63 (100%)	0	100	100
2	U4	64/68 (94%)	64 (100%)	0	100	100
2	U5	63/68 (93%)	63 (100%)	0	100	100
2	U6	63/68 (93%)	63 (100%)	0	100	100
2	U7	63/68 (93%)	63 (100%)	0	100	100
2	V2	64/68 (94%)	64 (100%)	0	100	100
2	V3	63/68 (93%)	63 (100%)	0	100	100
2	V4	64/68 (94%)	64 (100%)	0	100	100
2	V5	63/68 (93%)	63 (100%)	0	100	100
2	V6	63/68 (93%)	63 (100%)	0	100	100
2	V7	63/68 (93%)	63 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	W2	64/68 (94%)	64 (100%)	0	100	100
2	W3	63/68 (93%)	63 (100%)	0	100	100
2	W4	64/68 (94%)	64 (100%)	0	100	100
2	W5	63/68 (93%)	63 (100%)	0	100	100
2	W6	63/68 (93%)	63 (100%)	0	100	100
2	W7	63/68 (93%)	63 (100%)	0	100	100
2	X2	64/68 (94%)	64 (100%)	0	100	100
2	X3	63/68 (93%)	63 (100%)	0	100	100
2	X4	64/68 (94%)	64 (100%)	0	100	100
2	X5	63/68 (93%)	62 (98%)	1 (2%)	55	70
2	X6	63/68 (93%)	63 (100%)	0	100	100
2	X7	63/68 (93%)	63 (100%)	0	100	100
2	Y2	64/68 (94%)	64 (100%)	0	100	100
2	Y3	63/68 (93%)	63 (100%)	0	100	100
2	Y4	64/68 (94%)	64 (100%)	0	100	100
2	Y5	63/68 (93%)	63 (100%)	0	100	100
2	Y6	63/68 (93%)	63 (100%)	0	100	100
2	Y7	63/68 (93%)	62 (98%)	1 (2%)	55	70
2	Z2	64/68 (94%)	64 (100%)	0	100	100
2	Z3	63/68 (93%)	63 (100%)	0	100	100
2	Z4	64/68 (94%)	64 (100%)	0	100	100
2	Z5	63/68 (93%)	63 (100%)	0	100	100
2	Z6	63/68 (93%)	63 (100%)	0	100	100
2	Z7	63/68 (93%)	63 (100%)	0	100	100
3	18	155/164 (94%)	155 (100%)	0	100	100
3	28	155/164 (94%)	155 (100%)	0	100	100
3	38	155/164 (94%)	155 (100%)	0	100	100
3	48	155/164 (94%)	155 (100%)	0	100	100
3	A8	155/164 (94%)	155 (100%)	0	100	100
3	B8	155/164 (94%)	155 (100%)	0	100	100
3	C8	155/164 (94%)	155 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	D8	155/164 (94%)	155 (100%)	0	100	100
3	E8	155/164 (94%)	155 (100%)	0	100	100
3	F8	155/164 (94%)	155 (100%)	0	100	100
3	G8	155/164 (94%)	155 (100%)	0	100	100
3	H8	155/164 (94%)	155 (100%)	0	100	100
3	I8	155/164 (94%)	155 (100%)	0	100	100
3	J8	155/164 (94%)	155 (100%)	0	100	100
3	K8	155/164 (94%)	155 (100%)	0	100	100
3	L8	155/164 (94%)	155 (100%)	0	100	100
3	M8	155/164 (94%)	155 (100%)	0	100	100
3	N8	155/164 (94%)	155 (100%)	0	100	100
3	O8	155/164 (94%)	155 (100%)	0	100	100
3	P8	155/164 (94%)	155 (100%)	0	100	100
3	Q8	155/164 (94%)	155 (100%)	0	100	100
3	R8	155/164 (94%)	155 (100%)	0	100	100
3	S8	155/164 (94%)	155 (100%)	0	100	100
3	T8	155/164 (94%)	155 (100%)	0	100	100
3	U8	155/164 (94%)	155 (100%)	0	100	100
3	V8	155/164 (94%)	155 (100%)	0	100	100
3	W8	155/164 (94%)	155 (100%)	0	100	100
3	X8	155/164 (94%)	155 (100%)	0	100	100
3	Y8	155/164 (94%)	155 (100%)	0	100	100
3	Z8	155/164 (94%)	155 (100%)	0	100	100
All	All	18213/19380 (94%)	18200 (100%)	13 (0%)	88	87

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E3	89	LEU
2	E7	43	THR
2	F2	67	VAL
2	I4	24	VAL
2	R7	29	VAL
2	S4	57	THR

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Mol	Chain	Res	Type
2	T7	50	VAL
1	W1	19	ILE
2	X5	42	VAL
2	Y7	43	THR
2	36	57	THR
2	37	43	THR
2	44	57	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (84) such sidechains are listed below:

Mol	Chain	Res	Type
1	A1	65	GLN
3	A8	121	GLN
3	A8	130	GLN
1	C1	65	GLN
3	C8	15	GLN
3	C8	35	GLN
3	C8	107	GLN
3	C8	130	GLN
2	D5	74	HIS
3	D8	17	GLN
3	D8	62	GLN
3	D8	78	HIS
3	D8	121	GLN
3	E8	78	HIS
3	E8	121	GLN
1	G1	70	ASN
3	G8	49	ASN
3	G8	66	GLN
3	G8	121	GLN
2	I4	82	ASN
3	I8	15	GLN
3	I8	126	ASN
2	J4	82	ASN
3	J8	17	GLN
3	J8	107	GLN
3	K8	62	GLN
3	K8	78	HIS
3	K8	107	GLN
3	K8	121	GLN
3	L8	17	GLN
2	M5	61	GLN

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Mol	Chain	Res	Type
3	M8	62	GLN
3	M8	78	HIS
3	M8	121	GLN
1	N1	65	GLN
3	N8	66	GLN
3	N8	107	GLN
3	N8	126	ASN
1	O1	65	GLN
2	O4	82	ASN
3	O8	123	GLN
1	P1	65	GLN
3	P8	78	HIS
3	P8	130	GLN
3	Q8	17	GLN
3	Q8	35	GLN
3	Q8	121	GLN
3	Q8	130	GLN
3	R8	78	HIS
3	R8	121	GLN
2	S4	82	ASN
3	S8	107	GLN
3	S8	126	ASN
3	T8	130	GLN
1	U1	65	GLN
3	U8	17	GLN
3	U8	107	GLN
3	V8	17	GLN
3	V8	130	GLN
1	W1	65	GLN
3	W8	17	GLN
3	W8	121	GLN
3	W8	123	GLN
3	W8	156	ASN
3	X8	78	HIS
3	Z8	17	GLN
3	Z8	35	GLN
3	Z8	107	GLN
3	Z8	130	GLN
3	Z8	156	ASN
1	11	65	GLN
2	14	82	ASN
3	18	78	HIS

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Mol	Chain	Res	Type
3	18	107	GLN
3	28	17	GLN
3	28	62	GLN
3	28	78	HIS
3	28	126	ASN
3	28	130	GLN
3	28	156	ASN
3	28	168	ASN
1	31	65	GLN
3	48	121	GLN
3	48	156	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	11	95/96 (98%)	0.61	3 (3%)	50	28	65, 89, 126, 149	0
1	21	95/96 (98%)	0.51	5 (5%)	32	18	49, 75, 109, 126	0
1	31	94/96 (97%)	0.67	4 (4%)	40	21	64, 91, 139, 160	0
1	41	95/96 (98%)	0.58	3 (3%)	50	28	57, 84, 118, 140	0
1	A1	95/96 (98%)	0.72	5 (5%)	32	18	61, 83, 112, 131	0
1	B1	95/96 (98%)	0.63	5 (5%)	32	18	63, 87, 122, 134	0
1	C1	95/96 (98%)	0.41	3 (3%)	50	28	63, 89, 115, 132	0
1	D1	95/96 (98%)	0.58	5 (5%)	32	18	60, 86, 114, 130	0
1	E1	95/96 (98%)	0.51	4 (4%)	40	21	53, 87, 115, 136	0
1	F1	95/96 (98%)	0.78	3 (3%)	50	28	71, 94, 123, 140	0
1	G1	95/96 (98%)	0.63	5 (5%)	32	18	76, 94, 126, 159	0
1	H1	95/96 (98%)	0.64	7 (7%)	20	13	63, 91, 130, 148	0
1	I1	95/96 (98%)	0.64	6 (6%)	26	16	67, 89, 125, 137	0
1	J1	95/96 (98%)	0.66	4 (4%)	40	21	63, 88, 123, 151	0
1	K1	95/96 (98%)	0.53	3 (3%)	50	28	55, 80, 112, 131	0
1	L1	95/96 (98%)	0.52	3 (3%)	50	28	52, 79, 109, 120	0
1	M1	95/96 (98%)	0.53	3 (3%)	50	28	55, 79, 111, 122	0
1	N1	95/96 (98%)	0.45	4 (4%)	40	21	54, 80, 110, 118	0
1	O1	95/96 (98%)	0.62	4 (4%)	40	21	66, 91, 126, 147	0
1	P1	95/96 (98%)	0.64	5 (5%)	32	18	65, 91, 116, 137	0
1	Q1	95/96 (98%)	0.64	5 (5%)	32	18	62, 89, 125, 150	0
1	R1	95/96 (98%)	0.63	3 (3%)	50	28	70, 95, 124, 145	0
1	S1	95/96 (98%)	0.66	6 (6%)	26	16	57, 94, 118, 139	0
1	T1	95/96 (98%)	0.58	7 (7%)	20	13	55, 82, 110, 128	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	U1	95/96 (98%)	0.45	4 (4%)	40	21	54, 82, 111, 126	0
1	V1	95/96 (98%)	0.65	5 (5%)	32	18	72, 94, 124, 138	0
1	W1	95/96 (98%)	0.64	7 (7%)	20	13	73, 94, 126, 135	0
1	X1	95/96 (98%)	0.46	3 (3%)	50	28	54, 80, 110, 120	0
1	Y1	95/96 (98%)	0.51	4 (4%)	40	21	50, 82, 112, 134	0
1	Z1	95/96 (98%)	0.65	4 (4%)	40	21	66, 92, 123, 141	0
2	12	94/99 (94%)	0.30	1 (1%)	78	52	58, 82, 113, 128	0
2	13	92/99 (92%)	0.41	3 (3%)	49	27	58, 82, 110, 131	0
2	14	94/99 (94%)	0.33	4 (4%)	40	21	54, 80, 113, 150	0
2	15	93/99 (93%)	0.33	1 (1%)	78	52	54, 81, 112, 140	0
2	16	92/99 (92%)	0.31	1 (1%)	78	52	58, 79, 111, 132	0
2	17	93/99 (93%)	0.39	3 (3%)	50	28	57, 81, 114, 128	0
2	22	94/99 (94%)	0.31	2 (2%)	63	36	47, 71, 103, 133	0
2	23	92/99 (92%)	0.36	3 (3%)	49	27	45, 76, 104, 115	0
2	24	94/99 (94%)	0.21	0	100	100	39, 70, 102, 124	0
2	25	93/99 (93%)	0.22	1 (1%)	78	52	44, 70, 99, 131	0
2	26	92/99 (92%)	0.28	1 (1%)	78	52	43, 73, 99, 119	0
2	27	93/99 (93%)	0.32	3 (3%)	50	28	54, 74, 107, 123	0
2	32	94/99 (94%)	0.31	2 (2%)	63	36	61, 81, 111, 135	0
2	33	92/99 (92%)	0.39	3 (3%)	49	27	48, 84, 113, 129	0
2	34	94/99 (94%)	0.30	1 (1%)	78	52	57, 81, 113, 137	0
2	35	93/99 (93%)	0.28	1 (1%)	78	52	65, 83, 113, 121	0
2	36	92/99 (92%)	0.31	3 (3%)	49	27	63, 85, 110, 122	0
2	37	93/99 (93%)	0.39	5 (5%)	31	18	58, 79, 113, 124	0
2	42	94/99 (94%)	0.29	0	100	100	49, 76, 105, 134	0
2	43	92/99 (92%)	0.41	3 (3%)	49	27	54, 80, 113, 131	0
2	44	94/99 (94%)	0.29	3 (3%)	50	28	58, 81, 111, 147	0
2	45	93/99 (93%)	0.29	2 (2%)	62	35	59, 82, 111, 140	0
2	46	92/99 (92%)	0.31	3 (3%)	49	27	54, 77, 101, 115	0
2	47	93/99 (93%)	0.24	2 (2%)	62	35	53, 76, 108, 123	0
2	A2	92/99 (92%)	0.45	3 (3%)	49	27	59, 82, 109, 121	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
2	A3	92/99 (92%)	0.37	0	100 100	56, 84, 110, 128	0
2	A4	93/99 (93%)	0.45	3 (3%)	50 28	55, 85, 112, 142	0
2	A5	92/99 (92%)	0.36	6 (6%)	25 15	54, 85, 111, 126	0
2	A6	92/99 (92%)	0.44	2 (2%)	62 35	60, 86, 112, 122	0
2	A7	92/99 (92%)	0.46	3 (3%)	49 27	54, 84, 112, 128	0
2	B2	91/99 (91%)	0.27	2 (2%)	62 35	54, 73, 105, 125	0
2	B3	92/99 (92%)	0.38	2 (2%)	62 35	51, 81, 103, 123	0
2	B4	92/99 (92%)	0.30	1 (1%)	78 52	57, 77, 107, 116	0
2	B5	92/99 (92%)	0.39	1 (1%)	78 52	58, 82, 109, 123	0
2	B6	92/99 (92%)	0.37	3 (3%)	49 27	58, 77, 105, 116	0
2	B7	92/99 (92%)	0.42	3 (3%)	49 27	57, 80, 104, 114	0
2	C2	92/99 (92%)	0.28	0	100 100	53, 77, 104, 114	0
2	C3	92/99 (92%)	0.32	2 (2%)	62 35	63, 81, 113, 122	0
2	C4	92/99 (92%)	0.18	1 (1%)	78 52	54, 75, 100, 122	0
2	C5	92/99 (92%)	0.29	1 (1%)	78 52	55, 79, 105, 121	0
2	C6	92/99 (92%)	0.28	1 (1%)	78 52	50, 76, 106, 120	0
2	C7	93/99 (93%)	0.30	1 (1%)	78 52	54, 75, 102, 131	0
2	D2	93/99 (93%)	0.28	0	100 100	50, 78, 111, 118	0
2	D3	92/99 (92%)	0.49	1 (1%)	78 52	60, 84, 112, 123	0
2	D4	92/99 (92%)	0.35	0	100 100	54, 80, 108, 121	0
2	D5	92/99 (92%)	0.26	1 (1%)	78 52	60, 83, 109, 133	0
2	D6	92/99 (92%)	0.38	3 (3%)	49 27	45, 76, 104, 122	0
2	D7	93/99 (93%)	0.39	2 (2%)	62 35	48, 77, 108, 119	0
2	E2	94/99 (94%)	0.35	4 (4%)	40 21	58, 80, 112, 128	0
2	E3	92/99 (92%)	0.49	3 (3%)	49 27	68, 87, 112, 124	0
2	E4	94/99 (94%)	0.27	1 (1%)	78 52	61, 82, 114, 128	0
2	E5	92/99 (92%)	0.37	3 (3%)	49 27	59, 83, 108, 131	0
2	E6	92/99 (92%)	0.38	4 (4%)	40 21	63, 81, 105, 122	0
2	E7	92/99 (92%)	0.28	1 (1%)	78 52	53, 81, 109, 125	0
2	F2	94/99 (94%)	0.38	1 (1%)	78 52	66, 87, 116, 135	0
2	F3	92/99 (92%)	0.43	5 (5%)	31 18	66, 87, 116, 127	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
2	F4	92/99 (92%)	0.27	2 (2%) 62 35	64, 83, 111, 130	0
2	F5	92/99 (92%)	0.38	1 (1%) 78 52	67, 86, 109, 129	0
2	F6	92/99 (92%)	0.31	1 (1%) 78 52	62, 83, 108, 118	0
2	F7	93/99 (93%)	0.31	2 (2%) 62 35	62, 84, 111, 131	0
2	G2	92/99 (92%)	0.50	4 (4%) 40 21	65, 90, 113, 121	0
2	G3	92/99 (92%)	0.47	3 (3%) 49 27	63, 88, 119, 129	0
2	G4	92/99 (92%)	0.44	4 (4%) 40 21	60, 86, 113, 127	0
2	G5	91/99 (91%)	0.36	1 (1%) 78 52	65, 84, 111, 127	0
2	G6	92/99 (92%)	0.43	2 (2%) 62 35	66, 87, 110, 126	0
2	G7	92/99 (92%)	0.39	3 (3%) 49 27	55, 83, 122, 137	0
2	H2	92/99 (92%)	0.39	1 (1%) 78 52	58, 79, 104, 111	0
2	H3	92/99 (92%)	0.39	2 (2%) 62 35	58, 84, 117, 126	0
2	H4	93/99 (93%)	0.34	1 (1%) 78 52	57, 83, 112, 135	0
2	H5	91/99 (91%)	0.43	4 (4%) 39 21	59, 84, 112, 121	0
2	H6	92/99 (92%)	0.42	1 (1%) 78 52	58, 82, 105, 121	0
2	H7	92/99 (92%)	0.39	4 (4%) 40 21	61, 83, 108, 127	0
2	I2	92/99 (92%)	0.38	1 (1%) 78 52	54, 81, 107, 123	0
2	I3	91/99 (91%)	0.35	4 (4%) 39 21	64, 85, 109, 130	0
2	I4	92/99 (92%)	0.34	2 (2%) 62 35	58, 83, 106, 117	0
2	I5	92/99 (92%)	0.54	4 (4%) 40 21	59, 87, 115, 125	0
2	I6	92/99 (92%)	0.39	3 (3%) 49 27	60, 87, 111, 121	0
2	I7	92/99 (92%)	0.46	3 (3%) 49 27	62, 83, 107, 131	0
2	J2	92/99 (92%)	0.38	1 (1%) 78 52	65, 84, 110, 125	0
2	J3	92/99 (92%)	0.42	3 (3%) 49 27	59, 81, 112, 123	0
2	J4	92/99 (92%)	0.27	1 (1%) 78 52	59, 79, 109, 119	0
2	J5	91/99 (91%)	0.33	2 (2%) 62 35	51, 78, 107, 121	0
2	J6	92/99 (92%)	0.37	1 (1%) 78 52	51, 81, 105, 123	0
2	J7	92/99 (92%)	0.22	1 (1%) 78 52	56, 80, 103, 121	0
2	K2	92/99 (92%)	0.37	2 (2%) 62 35	43, 79, 106, 119	0
2	K3	92/99 (92%)	0.32	3 (3%) 49 27	60, 83, 115, 134	0
2	K4	92/99 (92%)	0.17	3 (3%) 49 27	50, 77, 108, 120	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
2	K5	93/99 (93%)	0.33	2 (2%) 62 35	42, 80, 102, 136	0
2	K6	92/99 (92%)	0.34	4 (4%) 40 21	53, 78, 104, 119	0
2	K7	93/99 (93%)	0.29	1 (1%) 78 52	50, 78, 112, 121	0
2	L2	94/99 (94%)	0.37	0 100 100	46, 78, 105, 126	0
2	L3	92/99 (92%)	0.37	2 (2%) 62 35	52, 80, 112, 126	0
2	L4	92/99 (92%)	0.25	2 (2%) 62 35	53, 79, 101, 116	0
2	L5	92/99 (92%)	0.22	2 (2%) 62 35	54, 76, 107, 128	0
2	L6	92/99 (92%)	0.33	3 (3%) 49 27	53, 79, 105, 135	0
2	L7	93/99 (93%)	0.38	2 (2%) 62 35	47, 71, 93, 116	0
2	M2	93/99 (93%)	0.30	1 (1%) 78 52	47, 69, 94, 107	0
2	M3	92/99 (92%)	0.28	2 (2%) 62 35	54, 76, 108, 121	0
2	M4	92/99 (92%)	0.20	0 100 100	44, 75, 94, 122	0
2	M5	93/99 (93%)	0.33	2 (2%) 62 35	48, 71, 99, 122	0
2	M6	91/99 (91%)	0.27	2 (2%) 62 35	50, 71, 99, 114	0
2	M7	92/99 (92%)	0.39	2 (2%) 62 35	49, 75, 105, 123	0
2	N2	92/99 (92%)	0.17	2 (2%) 62 35	50, 71, 100, 114	0
2	N3	91/99 (91%)	0.42	4 (4%) 39 21	42, 76, 101, 133	0
2	N4	92/99 (92%)	0.24	2 (2%) 62 35	50, 73, 100, 121	0
2	N5	93/99 (93%)	0.35	4 (4%) 40 21	57, 75, 105, 115	0
2	N6	91/99 (91%)	0.29	1 (1%) 78 52	55, 76, 98, 106	0
2	N7	92/99 (92%)	0.24	1 (1%) 78 52	50, 75, 106, 118	0
2	O2	94/99 (94%)	0.33	2 (2%) 63 36	62, 84, 117, 131	0
2	O3	92/99 (92%)	0.37	1 (1%) 78 52	56, 81, 114, 124	0
2	O4	94/99 (94%)	0.22	3 (3%) 50 28	56, 83, 114, 130	0
2	O5	93/99 (93%)	0.29	2 (2%) 62 35	59, 85, 113, 130	0
2	O6	92/99 (92%)	0.24	2 (2%) 62 35	57, 78, 103, 122	0
2	O7	93/99 (93%)	0.43	3 (3%) 50 28	63, 81, 106, 121	0
2	P2	94/99 (94%)	0.35	1 (1%) 78 52	59, 84, 115, 130	0
2	P3	92/99 (92%)	0.37	4 (4%) 40 21	56, 82, 112, 122	0
2	P4	94/99 (94%)	0.20	0 100 100	53, 82, 112, 128	0
2	P5	93/99 (93%)	0.51	2 (2%) 62 35	55, 82, 113, 123	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
2	P6	92/99 (92%)	0.36	2 (2%)	62 35	59, 82, 108, 117	0
2	P7	91/99 (91%)	0.46	2 (2%)	62 35	49, 79, 110, 114	0
2	Q2	94/99 (94%)	0.51	5 (5%)	32 18	51, 83, 118, 129	0
2	Q3	92/99 (92%)	0.50	5 (5%)	31 18	62, 83, 107, 129	0
2	Q4	94/99 (94%)	0.36	3 (3%)	50 28	56, 84, 109, 133	0
2	Q5	93/99 (93%)	0.41	0	100 100	61, 82, 113, 119	0
2	Q6	92/99 (92%)	0.27	4 (4%)	40 21	56, 82, 112, 123	0
2	Q7	93/99 (93%)	0.47	4 (4%)	40 21	63, 85, 115, 130	0
2	R2	94/99 (94%)	0.28	3 (3%)	50 28	61, 83, 110, 144	0
2	R3	92/99 (92%)	0.47	3 (3%)	49 27	51, 82, 113, 126	0
2	R4	94/99 (94%)	0.33	2 (2%)	63 36	56, 82, 116, 143	0
2	R5	93/99 (93%)	0.30	3 (3%)	50 28	62, 86, 115, 143	0
2	R6	92/99 (92%)	0.44	3 (3%)	49 27	62, 87, 115, 132	0
2	R7	93/99 (93%)	0.42	2 (2%)	62 35	62, 82, 114, 127	0
2	S2	94/99 (94%)	0.46	2 (2%)	63 36	53, 84, 112, 139	0
2	S3	92/99 (92%)	0.46	2 (2%)	62 35	65, 83, 116, 123	0
2	S4	94/99 (94%)	0.30	1 (1%)	78 52	65, 83, 105, 152	0
2	S5	93/99 (93%)	0.51	4 (4%)	40 21	34, 83, 108, 117	0
2	S6	92/99 (92%)	0.38	1 (1%)	78 52	46, 81, 107, 119	0
2	S7	93/99 (93%)	0.38	1 (1%)	78 52	51, 79, 108, 123	0
2	T2	94/99 (94%)	0.50	2 (2%)	63 36	45, 72, 105, 155	0
2	T3	92/99 (92%)	0.46	2 (2%)	62 35	46, 78, 108, 137	0
2	T4	94/99 (94%)	0.18	2 (2%)	63 36	53, 78, 113, 141	0
2	T5	93/99 (93%)	0.39	2 (2%)	62 35	40, 75, 103, 125	0
2	T6	92/99 (92%)	0.39	5 (5%)	31 18	53, 80, 108, 124	0
2	T7	93/99 (93%)	0.38	3 (3%)	50 28	54, 79, 109, 125	0
2	U2	94/99 (94%)	0.30	1 (1%)	78 52	42, 71, 101, 121	0
2	U3	92/99 (92%)	0.45	3 (3%)	49 27	57, 86, 117, 129	0
2	U4	94/99 (94%)	0.44	5 (5%)	32 18	46, 76, 112, 127	0
2	U5	93/99 (93%)	0.25	1 (1%)	78 52	60, 77, 110, 131	0
2	U6	92/99 (92%)	0.33	2 (2%)	62 35	55, 76, 98, 109	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
2	U7	93/99 (93%)	0.54	8 (8%)	16 11	44, 79, 110, 136	0
2	V2	94/99 (94%)	0.44	2 (2%)	63 36	59, 85, 112, 136	0
2	V3	92/99 (92%)	0.40	3 (3%)	49 27	56, 80, 109, 126	0
2	V4	94/99 (94%)	0.44	1 (1%)	78 52	60, 82, 106, 125	0
2	V5	93/99 (93%)	0.55	1 (1%)	78 52	55, 85, 112, 124	0
2	V6	92/99 (92%)	0.39	2 (2%)	62 35	57, 79, 107, 117	0
2	V7	93/99 (93%)	0.33	0	100 100	60, 79, 102, 116	0
2	W2	94/99 (94%)	0.36	1 (1%)	78 52	61, 87, 116, 125	0
2	W3	92/99 (92%)	0.55	3 (3%)	49 27	63, 87, 117, 134	0
2	W4	94/99 (94%)	0.30	4 (4%)	40 21	62, 84, 110, 157	0
2	W5	93/99 (93%)	0.37	5 (5%)	31 18	60, 84, 114, 142	0
2	W6	92/99 (92%)	0.32	4 (4%)	40 21	64, 83, 107, 131	0
2	W7	93/99 (93%)	0.39	2 (2%)	62 35	47, 79, 108, 134	0
2	X2	94/99 (94%)	0.39	3 (3%)	50 28	51, 76, 107, 137	0
2	X3	92/99 (92%)	0.38	2 (2%)	62 35	52, 80, 112, 128	0
2	X4	94/99 (94%)	0.22	3 (3%)	50 28	46, 76, 109, 129	0
2	X5	93/99 (93%)	0.41	5 (5%)	31 18	51, 80, 107, 137	0
2	X6	92/99 (92%)	0.28	3 (3%)	49 27	57, 80, 101, 132	0
2	X7	93/99 (93%)	0.35	3 (3%)	50 28	57, 79, 108, 121	0
2	Y2	94/99 (94%)	0.32	3 (3%)	50 28	58, 78, 109, 122	0
2	Y3	92/99 (92%)	0.54	3 (3%)	49 27	52, 82, 105, 125	0
2	Y4	94/99 (94%)	0.42	6 (6%)	25 15	44, 83, 113, 133	0
2	Y5	92/99 (92%)	0.44	2 (2%)	62 35	50, 75, 104, 130	0
2	Y6	92/99 (92%)	0.40	2 (2%)	62 35	49, 80, 103, 119	0
2	Y7	93/99 (93%)	0.36	3 (3%)	50 28	55, 81, 105, 128	0
2	Z2	94/99 (94%)	0.29	1 (1%)	78 52	58, 82, 113, 130	0
2	Z3	92/99 (92%)	0.42	4 (4%)	40 21	62, 85, 111, 126	0
2	Z4	94/99 (94%)	0.20	2 (2%)	63 36	60, 80, 110, 141	0
2	Z5	93/99 (93%)	0.25	1 (1%)	78 52	59, 82, 114, 122	0
2	Z6	92/99 (92%)	0.30	1 (1%)	78 52	57, 81, 112, 129	0
2	Z7	93/99 (93%)	0.48	4 (4%)	40 21	55, 74, 106, 123	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
3	18	203/212 (95%)	1.43	46 (22%)	2	2	71, 120, 149, 157	0
3	19	198/212 (93%)	2.31	103 (52%)	0	0	121, 155, 174, 192	0
3	28	203/212 (95%)	1.37	44 (21%)	2	2	68, 116, 146, 163	0
3	29	203/212 (95%)	1.70	68 (33%)	1	1	106, 145, 172, 190	0
3	38	203/212 (95%)	1.50	54 (26%)	1	2	72, 120, 152, 175	0
3	39	203/212 (95%)	2.31	116 (57%)	0	0	124, 156, 176, 190	0
3	48	203/212 (95%)	1.33	39 (19%)	3	3	73, 117, 147, 161	0
3	49	203/212 (95%)	1.96	86 (42%)	0	1	110, 149, 171, 189	0
3	A8	203/212 (95%)	1.34	42 (20%)	2	3	76, 121, 149, 163	0
3	A9	203/212 (95%)	2.21	105 (51%)	0	1	118, 156, 177, 196	0
3	B8	203/212 (95%)	1.50	57 (28%)	1	2	73, 116, 145, 172	0
3	B9	203/212 (95%)	2.20	110 (54%)	0	0	103, 148, 172, 194	0
3	C8	203/212 (95%)	1.36	44 (21%)	2	2	74, 115, 147, 170	0
3	C9	203/212 (95%)	1.91	82 (40%)	0	1	100, 147, 171, 203	0
3	D8	203/212 (95%)	1.52	53 (26%)	1	2	79, 115, 144, 172	0
3	D9	203/212 (95%)	2.14	104 (51%)	0	1	111, 145, 170, 181	0
3	E8	203/212 (95%)	1.51	54 (26%)	1	2	85, 124, 152, 168	0
3	E9	203/212 (95%)	2.05	94 (46%)	0	1	115, 156, 177, 184	0
3	F8	203/212 (95%)	1.48	56 (27%)	1	2	71, 125, 155, 178	0
3	F9	203/212 (95%)	2.36	123 (60%)	0	0	116, 157, 181, 202	0
3	G8	203/212 (95%)	1.43	51 (25%)	1	2	74, 122, 150, 184	0
3	G9	203/212 (95%)	2.33	123 (60%)	0	0	124, 159, 180, 197	0
3	H8	203/212 (95%)	1.54	57 (28%)	1	2	68, 121, 150, 161	0
3	H9	203/212 (95%)	2.19	101 (49%)	0	1	111, 156, 178, 194	0
3	I8	203/212 (95%)	1.48	55 (27%)	1	2	84, 121, 150, 171	0
3	I9	203/212 (95%)	2.25	115 (56%)	0	0	112, 156, 177, 195	0
3	J8	203/212 (95%)	1.40	53 (26%)	1	2	72, 118, 145, 168	0
3	J9	203/212 (95%)	2.09	105 (51%)	0	1	105, 149, 173, 188	0
3	K8	203/212 (95%)	1.43	48 (23%)	2	2	72, 119, 148, 167	0
3	K9	203/212 (95%)	2.05	101 (49%)	0	1	113, 152, 172, 197	0
3	L8	203/212 (95%)	1.28	41 (20%)	3	3	73, 116, 146, 165	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
3	L9	203/212 (95%)	2.04	90 (44%)	0	1	109, 150, 173, 191	0
3	M8	203/212 (95%)	1.37	40 (19%)	3	3	68, 114, 148, 168	0
3	M9	203/212 (95%)	1.78	69 (33%)	1	1	105, 145, 174, 181	0
3	N8	203/212 (95%)	1.50	48 (23%)	2	2	62, 117, 152, 164	0
3	N9	203/212 (95%)	2.01	98 (48%)	0	1	103, 150, 175, 189	0
3	O8	203/212 (95%)	1.39	47 (23%)	2	2	80, 118, 150, 183	0
3	O9	203/212 (95%)	2.18	106 (52%)	0	0	111, 154, 178, 188	0
3	P8	203/212 (95%)	1.39	45 (22%)	2	2	76, 117, 141, 155	0
3	P9	203/212 (95%)	2.06	100 (49%)	0	1	119, 149, 173, 195	0
3	Q8	203/212 (95%)	1.42	51 (25%)	1	2	71, 121, 152, 172	0
3	Q9	203/212 (95%)	2.19	108 (53%)	0	0	113, 157, 183, 201	0
3	R8	203/212 (95%)	1.46	45 (22%)	2	2	70, 122, 152, 174	0
3	R9	203/212 (95%)	2.23	114 (56%)	0	0	116, 157, 177, 185	0
3	S8	203/212 (95%)	1.48	57 (28%)	1	2	78, 121, 149, 172	0
3	S9	203/212 (95%)	2.17	101 (49%)	0	1	122, 156, 176, 186	0
3	T8	203/212 (95%)	1.58	61 (30%)	1	2	68, 114, 149, 169	0
3	T9	203/212 (95%)	2.46	119 (58%)	0	0	109, 153, 179, 195	0
3	U8	203/212 (95%)	1.48	56 (27%)	1	2	73, 118, 150, 162	0
3	U9	203/212 (95%)	2.21	105 (51%)	0	1	100, 153, 175, 188	0
3	V8	203/212 (95%)	1.42	49 (24%)	2	2	75, 118, 149, 166	0
3	V9	203/212 (95%)	2.04	98 (48%)	0	1	108, 148, 170, 179	0
3	W8	203/212 (95%)	1.40	44 (21%)	2	2	80, 121, 148, 167	0
3	W9	203/212 (95%)	2.15	109 (53%)	0	0	112, 155, 178, 190	0
3	X8	203/212 (95%)	1.40	50 (24%)	2	2	77, 116, 149, 165	0
3	X9	203/212 (95%)	1.97	91 (44%)	0	1	107, 150, 175, 195	0
3	Y8	203/212 (95%)	1.43	52 (25%)	1	2	66, 118, 153, 163	0
3	Y9	203/212 (95%)	2.05	93 (45%)	0	1	114, 151, 175, 184	0
3	Z8	203/212 (95%)	1.52	59 (29%)	1	2	74, 121, 151, 167	0
3	Z9	203/212 (95%)	2.22	112 (55%)	0	0	115, 155, 175, 184	0
All	All	31689/33420 (94%)	0.93	5092 (16%)	4	4	34, 95, 163, 203	0

All (5092) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	19	84	GLU	8.1
3	Z9	84	GLU	7.4
3	T9	61	VAL	7.3
3	G9	123	GLN	6.7
3	J9	17	GLN	6.6
3	G9	84	GLU	6.6
3	I8	17	GLN	6.6
3	39	17	GLN	6.6
3	U8	66	GLN	6.5
3	19	123	GLN	6.5
3	J9	35	GLN	6.4
3	T8	66	GLN	6.4
3	Z9	16	PRO	6.4
3	L9	27	ARG	6.3
3	W9	123	GLN	6.3
3	D9	61	VAL	6.3
3	Q9	136	PRO	6.2
3	D8	66	GLN	6.2
3	E9	27	ARG	6.2
3	S9	27	ARG	6.2
3	E8	136	PRO	6.1
3	S8	73	GLY	6.0
3	K8	66	GLN	6.0
3	S8	66	GLN	6.0
3	19	150	TYR	6.0
3	18	72	TYR	6.0
3	39	136	PRO	5.9
3	O9	64	ALA	5.9
3	H9	52	THR	5.8
3	G8	44	PRO	5.8
3	P9	84	GLU	5.8
3	D8	129	SER	5.8
3	G8	136	PRO	5.8
3	C9	61	VAL	5.8
3	R9	59	THR	5.8
3	K9	27	ARG	5.8
3	Y8	44	PRO	5.8
3	19	17	GLN	5.7
3	R9	84	GLU	5.7
3	K9	123	GLN	5.7
3	T8	44	PRO	5.7
3	H9	147	PRO	5.6
3	O9	88	ALA	5.6

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Mol	Chain	Res	Type	RSRZ
3	U8	136	PRO	5.6
3	F9	17	GLN	5.6
3	O8	66	GLN	5.6
3	T9	123	GLN	5.6
3	W9	17	GLN	5.6
3	B9	84	GLU	5.6
3	V8	66	GLN	5.6
3	H9	101	GLU	5.6
3	N8	17	GLN	5.6
3	Q8	66	GLN	5.6
3	Z9	61	VAL	5.6
3	Y8	66	GLN	5.5
3	T9	145	THR	5.5
3	L9	64	ALA	5.5
3	Z8	44	PRO	5.5
3	19	64	ALA	5.5
3	F8	44	PRO	5.5
3	F9	35	GLN	5.4
3	T9	117	VAL	5.4
3	Q9	17	GLN	5.4
3	X8	66	GLN	5.4
3	J9	119	ALA	5.4
3	19	52	THR	5.4
3	X9	64	ALA	5.4
3	19	101	GLU	5.4
3	E9	145	THR	5.4
3	T9	43	ALA	5.4
3	49	147	PRO	5.4
3	I8	132	MET	5.4
3	D9	66	GLN	5.4
3	G8	66	GLN	5.4
3	U9	16	PRO	5.3
3	X9	150	TYR	5.3
3	39	163	ASN	5.3
3	U9	32	VAL	5.3
3	V9	17	GLN	5.3
3	19	100	GLU	5.3
3	T9	150	TYR	5.3
3	K9	163	ASN	5.3
3	D9	136	PRO	5.2
3	T9	179	TYR	5.2
3	A9	48	ILE	5.2

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Mol	Chain	Res	Type	RSRZ
3	A9	61	VAL	5.2
3	F8	17	GLN	5.2
3	W9	64	ALA	5.2
3	Y9	63	PRO	5.2
3	F9	123	GLN	5.2
3	S9	17	GLN	5.2
3	B9	61	VAL	5.2
3	X9	61	VAL	5.2
3	G9	16	PRO	5.2
3	D8	34	GLY	5.2
3	T9	64	ALA	5.2
3	C9	147	PRO	5.2
3	M8	44	PRO	5.2
3	18	43	ALA	5.2
3	I9	136	PRO	5.2
3	O8	44	PRO	5.2
3	V8	3	ILE	5.2
3	U9	72	TYR	5.2
3	U9	163	ASN	5.1
3	X9	147	PRO	5.1
3	19	118	GLU	5.1
3	C8	66	GLN	5.1
3	I9	64	ALA	5.1
3	N8	66	GLN	5.1
3	49	17	GLN	5.1
3	39	156	ASN	5.1
3	P9	33	PRO	5.1
3	J8	73	GLY	5.1
3	S9	186	GLU	5.1
3	F8	66	GLN	5.1
3	F9	63	PRO	5.1
3	A9	119	ALA	5.1
3	Q9	205	ALA	5.1
3	39	64	ALA	5.1
3	L9	123	GLN	5.1
3	U9	67	VAL	5.1
3	U9	85	VAL	5.1
3	X9	84	GLU	5.0
3	N9	78	HIS	5.0
3	O9	108	VAL	5.0
3	F8	73	GLY	5.0
3	A8	66	GLN	5.0

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Mol	Chain	Res	Type	RSRZ
3	G9	64	ALA	5.0
3	V8	73	GLY	5.0
3	J9	84	GLU	5.0
3	O9	27	ARG	5.0
3	39	149	GLY	5.0
3	H8	32	VAL	5.0
3	B8	73	GLY	4.9
3	Y9	151	ALA	4.9
3	G8	72	TYR	4.9
3	I8	44	PRO	4.9
3	X8	44	PRO	4.9
3	49	27	ARG	4.9
3	I9	116	ALA	4.9
3	B9	100	GLU	4.9
3	A9	52	THR	4.9
3	D9	16	PRO	4.9
3	E9	16	PRO	4.9
3	X8	3	ILE	4.9
3	H9	16	PRO	4.9
3	P9	123	GLN	4.9
3	Q9	123	GLN	4.9
3	U9	64	ALA	4.9
3	29	163	ASN	4.9
3	19	51	VAL	4.9
3	Q9	84	GLU	4.9
3	H8	72	TYR	4.9
3	Z9	72	TYR	4.9
3	W9	79	HIS	4.9
3	I9	150	TYR	4.9
3	D9	27	ARG	4.9
2	R3	2	ALA	4.9
3	W8	44	PRO	4.9
3	Y9	147	PRO	4.9
3	I9	123	GLN	4.9
3	V8	17	GLN	4.9
3	29	17	GLN	4.9
3	P9	76	GLU	4.8
3	B8	66	GLN	4.8
3	Q8	73	GLY	4.8
3	19	27	ARG	4.8
3	D9	52	THR	4.8
3	F9	20	THR	4.8

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Mol	Chain	Res	Type	RSRZ
3	F9	130	GLN	4.8
3	Q8	17	GLN	4.8
3	T9	149	GLY	4.8
3	P9	27	ARG	4.8
3	F9	119	ALA	4.8
3	J9	136	PRO	4.8
3	T9	33	PRO	4.8
3	Z8	136	PRO	4.8
1	H1	61	SER	4.8
3	E9	144	GLU	4.8
3	P9	100	GLU	4.8
3	L9	88	ALA	4.8
3	U9	20	THR	4.8
3	H9	123	GLN	4.8
3	L8	66	GLN	4.8
3	R8	66	GLN	4.8
3	T8	136	PRO	4.8
3	Z8	66	GLN	4.8
3	39	63	PRO	4.8
3	N9	61	VAL	4.8
3	H9	27	ARG	4.8
3	F8	3	ILE	4.8
3	D9	116	ALA	4.8
3	Z9	64	ALA	4.8
3	Z9	66	GLN	4.8
3	A9	15	GLN	4.7
3	28	3	ILE	4.7
3	B9	13	ALA	4.7
3	C9	64	ALA	4.7
3	G9	136	PRO	4.7
3	V9	15	GLN	4.7
3	28	68	VAL	4.7
3	R9	51	VAL	4.7
3	B8	34	GLY	4.7
3	U9	123	GLN	4.7
3	G9	31	PRO	4.7
3	19	136	PRO	4.7
3	U9	27	ARG	4.7
3	39	119	ALA	4.7
3	Z9	17	GLN	4.7
3	D8	44	PRO	4.7
3	Y9	163	ASN	4.7

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Mol	Chain	Res	Type	RSRZ
3	G9	88	ALA	4.7
3	T9	100	GLU	4.7
3	L9	72	TYR	4.7
3	R9	123	GLN	4.7
3	C9	163	ASN	4.7
3	X8	163	ASN	4.7
3	F9	186	GLU	4.7
3	K9	64	ALA	4.7
3	N9	64	ALA	4.7
3	Q9	100	GLU	4.7
3	M8	66	GLN	4.7
3	K8	44	PRO	4.6
3	28	44	PRO	4.6
3	T9	135	LEU	4.6
3	A9	32	VAL	4.6
3	J8	3	ILE	4.6
3	M9	61	VAL	4.6
3	M9	64	ALA	4.6
3	T9	67	VAL	4.6
3	X9	119	ALA	4.6
3	W8	66	GLN	4.6
3	Z8	132	MET	4.6
3	T9	17	GLN	4.6
3	A9	34	GLY	4.6
3	L9	29	PHE	4.6
3	N8	44	PRO	4.6
3	49	78	HIS	4.6
3	R9	81	ASP	4.6
3	X9	48	ILE	4.6
3	L9	174	ALA	4.6
3	V9	101	GLU	4.6
3	49	186	GLU	4.6
3	39	52	THR	4.6
3	J9	156	ASN	4.6
3	U9	156	ASN	4.6
3	K9	29	PHE	4.6
3	B8	129	SER	4.6
3	U8	73	GLY	4.6
3	38	132	MET	4.6
3	H8	66	GLN	4.6
3	18	66	GLN	4.6
3	49	123	GLN	4.6

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Mol	Chain	Res	Type	RSRZ
3	V9	84	GLU	4.6
3	W9	84	GLU	4.6
3	Q8	44	PRO	4.6
3	T8	111	HIS	4.6
3	19	82	GLN	4.5
3	O9	186	GLU	4.5
3	G9	147	PRO	4.5
3	O9	16	PRO	4.5
1	31	88	GLY	4.5
3	B9	138	GLU	4.5
3	T9	144	GLU	4.5
3	29	84	GLU	4.5
3	A8	44	PRO	4.5
3	F9	136	PRO	4.5
3	A9	88	ALA	4.5
3	P8	66	GLN	4.5
3	W9	130	GLN	4.5
3	E9	163	ASN	4.5
3	F9	16	PRO	4.5
3	N8	72	TYR	4.5
3	X9	136	PRO	4.5
3	Y9	136	PRO	4.5
3	28	192	GLU	4.5
3	N8	94	ASP	4.5
3	Y8	43	ALA	4.5
3	I8	66	GLN	4.5
3	M9	123	GLN	4.5
3	Z9	35	GLN	4.5
3	A9	27	ARG	4.5
3	F9	122	THR	4.5
3	H9	149	GLY	4.5
3	B9	33	PRO	4.5
3	G9	138	GLU	4.5
3	W8	39	TRP	4.5
3	28	72	TYR	4.5
3	A9	85	VAL	4.5
3	I9	32	VAL	4.5
3	F9	198	ILE	4.5
3	S8	17	GLN	4.5
3	T9	118	GLU	4.5
3	D9	65	VAL	4.5
3	Y9	61	VAL	4.5

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Mol	Chain	Res	Type	RSRZ
3	29	61	VAL	4.5
3	J9	123	GLN	4.4
3	T9	137	GLY	4.4
3	L9	186	GLU	4.4
3	19	156	ASN	4.4
3	A9	53	ASP	4.4
3	C9	65	VAL	4.4
3	S9	134	ILE	4.4
3	Y9	27	ARG	4.4
3	48	17	GLN	4.4
3	B8	44	PRO	4.4
3	D9	43	ALA	4.4
3	G9	119	ALA	4.4
3	H9	55	ALA	4.4
3	J9	116	ALA	4.4
3	S8	12	ASP	4.4
3	T9	78	HIS	4.4
3	X8	73	GLY	4.4
3	Z8	34	GLY	4.4
3	E9	150	TYR	4.4
3	B9	85	VAL	4.4
3	S9	68	VAL	4.4
3	L9	6	ARG	4.4
3	N9	123	GLN	4.4
3	Z8	17	GLN	4.4
3	G9	52	THR	4.4
3	R9	16	PRO	4.4
3	39	147	PRO	4.4
3	L9	41	GLU	4.4
3	Y9	60	LYS	4.4
3	K9	28	GLY	4.4
3	I9	31	PRO	4.4
3	Y8	136	PRO	4.4
3	M9	6	ARG	4.4
3	Y8	30	LEU	4.4
3	O9	116	ALA	4.4
3	H9	146	GLN	4.4
3	R9	17	GLN	4.4
3	T9	15	GLN	4.4
3	J9	52	THR	4.4
3	28	73	GLY	4.4
3	U9	48	ILE	4.4

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Mol	Chain	Res	Type	RSRZ
3	U8	172	TYR	4.3
3	39	27	ARG	4.3
3	E9	123	GLN	4.3
3	G9	29	PHE	4.3
3	L9	28	GLY	4.3
3	M8	30	LEU	4.3
3	G8	32	VAL	4.3
3	R8	43	ALA	4.3
3	Y9	64	ALA	4.3
3	C9	66	GLN	4.3
3	E8	66	GLN	4.3
3	S9	35	GLN	4.3
3	K8	28	GLY	4.3
3	I9	28	GLY	4.3
3	E9	33	PRO	4.3
3	V9	16	PRO	4.3
3	39	78	HIS	4.3
3	I9	144	GLU	4.3
3	O8	128	ASN	4.3
3	49	43	ALA	4.3
3	X9	17	GLN	4.3
3	M8	3	ILE	4.3
3	T9	28	GLY	4.3
3	V8	149	GLY	4.3
3	49	149	GLY	4.3
3	A9	16	PRO	4.3
3	V9	106	PRO	4.3
3	29	106	PRO	4.3
3	I9	67	VAL	4.3
3	V9	53	ASP	4.3
2	Y5	68	GLU	4.3
3	F8	26	ALA	4.3
3	H9	158	ALA	4.3
3	I8	71	ALA	4.3
3	Y8	72	TYR	4.3
3	18	172	TYR	4.3
3	U8	3	ILE	4.3
3	39	123	GLN	4.3
3	I9	103	ARG	4.3
3	U9	7	THR	4.3
3	F9	78	HIS	4.3
1	11	61	SER	4.3

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Mol	Chain	Res	Type	RSRZ
2	W3	2	ALA	4.3
3	H9	186	GLU	4.3
3	S9	64	ALA	4.3
3	Z9	47	ALA	4.3
3	D9	156	ASN	4.3
3	C8	17	GLN	4.3
3	Q9	122	THR	4.3
3	39	59	THR	4.3
3	M8	72	TYR	4.3
3	19	94	ASP	4.3
3	R8	30	LEU	4.3
3	48	172	TYR	4.3
3	S8	132	MET	4.2
3	T9	156	ASN	4.2
3	38	66	GLN	4.2
3	U9	110	THR	4.2
3	D8	67	VAL	4.2
3	F8	32	VAL	4.2
3	H9	31	PRO	4.2
3	I9	33	PRO	4.2
3	L9	147	PRO	4.2
3	V9	175	PHE	4.2
3	N8	3	ILE	4.2
3	Y9	46	ILE	4.2
3	19	88	ALA	4.2
3	S9	78	HIS	4.2
3	S9	150	TYR	4.2
3	H9	17	GLN	4.2
3	D8	73	GLY	4.2
3	K8	73	GLY	4.2
3	K8	32	VAL	4.2
3	R9	136	PRO	4.2
3	X9	30	LEU	4.2
2	U3	2	ALA	4.2
3	N9	119	ALA	4.2
3	P9	88	ALA	4.2
3	Y8	133	MET	4.2
3	C9	72	TYR	4.2
3	C9	84	GLU	4.2
3	S9	123	GLN	4.2
3	B9	141	PHE	4.2
3	G9	61	VAL	4.2

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Mol	Chain	Res	Type	RSRZ
3	R8	3	ILE	4.2
3	Q9	88	ALA	4.2
2	46	49	ASP	4.2
3	C9	53	ASP	4.2
3	M8	28	GLY	4.2
3	N8	20	THR	4.2
3	T9	21	PHE	4.2
3	38	3	ILE	4.2
3	C8	44	PRO	4.2
3	H9	136	PRO	4.2
3	28	136	PRO	4.2
3	V9	64	ALA	4.2
3	W9	47	ALA	4.2
3	E8	172	TYR	4.2
3	G9	150	TYR	4.2
3	M9	84	GLU	4.2
3	T9	27	ARG	4.2
3	Y9	179	TYR	4.2
3	E9	78	HIS	4.2
3	J9	78	HIS	4.2
3	X9	60	LYS	4.2
3	W9	126	ASN	4.2
3	T9	5	LEU	4.2
3	O9	52	THR	4.2
3	R9	149	GLY	4.2
3	Y8	137	GLY	4.2
3	48	3	ILE	4.2
3	48	73	GLY	4.2
3	B8	32	VAL	4.2
3	T8	32	VAL	4.2
3	O8	132	MET	4.2
3	Q9	16	PRO	4.2
3	F9	116	ALA	4.2
3	F9	150	TYR	4.2
3	O8	179	TYR	4.2
3	K8	3	ILE	4.2
3	Q9	134	ILE	4.2
3	F9	53	ASP	4.1
3	T8	131	GLY	4.1
3	Y9	149	GLY	4.1
3	Z8	73	GLY	4.1
2	L3	2	ALA	4.1

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Mol	Chain	Res	Type	RSRZ
3	D9	58	ALA	4.1
3	Z9	116	ALA	4.1
3	Z9	123	GLN	4.1
3	Y9	134	ILE	4.1
3	C8	73	GLY	4.1
3	F9	51	VAL	4.1
3	S8	45	GLY	4.1
3	Z8	137	GLY	4.1
3	N9	106	PRO	4.1
3	19	33	PRO	4.1
2	27	2	ALA	4.1
3	19	116	ALA	4.1
3	G9	15	GLN	4.1
3	I9	17	GLN	4.1
3	L9	121	GLN	4.1
3	O8	17	GLN	4.1
3	Y9	141	PHE	4.1
3	29	35	GLN	4.1
3	A8	32	VAL	4.1
3	H9	65	VAL	4.1
3	T9	7	THR	4.1
3	19	163	ASN	4.1
1	W1	61	SER	4.1
3	T9	60	LYS	4.1
3	N8	136	PRO	4.1
3	V9	136	PRO	4.1
3	B9	17	GLN	4.1
3	K9	15	GLN	4.1
3	X8	17	GLN	4.1
3	Q9	138	GLU	4.1
3	I9	156	ASN	4.1
3	P8	149	GLY	4.1
1	G1	61	SER	4.1
3	F9	27	ARG	4.1
3	X9	27	ARG	4.1
3	49	16	PRO	4.1
3	49	64	ALA	4.1
2	36	49	ASP	4.1
3	I9	80	PHE	4.1
3	D8	17	GLN	4.1
3	N9	17	GLN	4.1
3	R8	39	TRP	4.1

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Mol	Chain	Res	Type	RSRZ
2	U5	69	GLU	4.1
3	C9	68	VAL	4.1
3	M8	73	GLY	4.1
3	R8	34	GLY	4.1
3	G9	27	ARG	4.1
3	R9	63	PRO	4.1
3	39	120	TYR	4.1
3	H8	137	GLY	4.1
3	19	122	THR	4.1
3	S9	49	ASN	4.1
3	B9	116	ALA	4.1
3	D9	64	ALA	4.1
3	H9	64	ALA	4.1
3	P8	132	MET	4.0
3	P9	95	LYS	4.0
3	38	17	GLN	4.0
3	L9	84	GLU	4.0
3	M8	74	LEU	4.0
3	O9	51	VAL	4.0
3	39	169	VAL	4.0
3	D8	28	GLY	4.0
3	H8	131	GLY	4.0
3	M8	45	GLY	4.0
3	N9	122	THR	4.0
3	F8	136	PRO	4.0
3	F9	141	PHE	4.0
3	N8	43	ALA	4.0
3	W8	71	ALA	4.0
3	R8	44	PRO	4.0
3	29	16	PRO	4.0
3	O9	17	GLN	4.0
3	D9	150	TYR	4.0
3	E9	61	VAL	4.0
3	K8	72	TYR	4.0
3	L8	100	GLU	4.0
3	R8	72	TYR	4.0
3	U9	61	VAL	4.0
3	W9	67	VAL	4.0
3	X8	32	VAL	4.0
3	X9	120	TYR	4.0
3	Y9	85	VAL	4.0
3	B9	52	THR	4.0

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Mol	Chain	Res	Type	RSRZ
3	G9	4	THR	4.0
3	Y8	134	ILE	4.0
3	C8	71	ALA	4.0
3	G9	156	ASN	4.0
3	X9	163	ASN	4.0
3	L8	136	PRO	4.0
3	V8	136	PRO	4.0
3	B9	78	HIS	4.0
3	19	78	HIS	4.0
3	A9	17	GLN	4.0
3	Y9	35	GLN	4.0
3	M9	72	TYR	4.0
3	Z9	76	GLU	4.0
3	38	172	TYR	4.0
3	F8	149	GLY	4.0
3	W8	34	GLY	4.0
3	T8	132	MET	4.0
3	28	132	MET	4.0
3	39	88	ALA	4.0
3	R9	33	PRO	4.0
3	F9	15	GLN	4.0
3	Y9	123	GLN	4.0
1	U1	61	SER	4.0
3	B8	192	GLU	4.0
3	Q8	172	TYR	4.0
3	R9	12	ASP	4.0
3	39	118	GLU	4.0
3	49	101	GLU	4.0
3	49	134	ILE	4.0
3	39	55	ALA	4.0
3	19	79	HIS	4.0
3	Z9	121	GLN	4.0
3	H9	61	VAL	4.0
2	A2	9	GLU	4.0
3	P9	7	THR	4.0
3	U9	120	TYR	4.0
3	V9	100	GLU	4.0
3	Y9	168	ASN	4.0
3	K8	70	ARG	4.0
3	Q9	50	ARG	4.0
3	S9	121	GLN	4.0
3	Y8	17	GLN	4.0

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Mol	Chain	Res	Type	RSRZ
3	E8	65	VAL	3.9
3	F8	68	VAL	3.9
3	Q9	186	GLU	3.9
3	19	20	THR	3.9
3	L9	43	ALA	3.9
3	M9	88	ALA	3.9
3	J9	163	ASN	3.9
3	19	171	PRO	3.9
3	48	136	PRO	3.9
3	P9	51	VAL	3.9
3	F8	132	MET	3.9
3	H8	132	MET	3.9
3	Y9	21	PHE	3.9
3	J9	7	THR	3.9
3	Q9	150	TYR	3.9
3	T8	34	GLY	3.9
3	V8	72	TYR	3.9
3	R9	181	ALA	3.9
3	39	116	ALA	3.9
3	D8	39	TRP	3.9
3	W9	81	ASP	3.9
3	Z9	136	PRO	3.9
3	49	62	GLN	3.9
3	E8	32	VAL	3.9
3	M9	32	VAL	3.9
3	S9	108	VAL	3.9
3	H8	172	TYR	3.9
3	Z9	59	THR	3.9
3	49	28	GLY	3.9
3	E8	39	TRP	3.9
3	B9	16	PRO	3.9
3	J8	44	PRO	3.9
3	A9	134	ILE	3.9
3	P9	163	ASN	3.9
3	N8	30	LEU	3.9
3	W8	30	LEU	3.9
1	41	61	SER	3.9
3	K9	122	THR	3.9
3	M9	59	THR	3.9
3	S8	72	TYR	3.9
3	X8	72	TYR	3.9
3	U8	44	PRO	3.9

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Mol	Chain	Res	Type	RSRZ
3	F8	133	MET	3.9
3	L8	133	MET	3.9
3	P9	35	GLN	3.9
3	39	166	LEU	3.9
3	Z9	79	HIS	3.9
3	O8	73	GLY	3.9
3	T9	52	THR	3.9
3	A9	84	GLU	3.9
3	A9	172	TYR	3.9
3	P9	138	GLU	3.9
3	U9	47	ALA	3.9
3	N8	24	LYS	3.9
3	H8	133	MET	3.9
3	P8	44	PRO	3.9
3	S9	136	PRO	3.9
3	38	44	PRO	3.9
3	49	63	PRO	3.9
3	E9	17	GLN	3.9
3	Q8	32	VAL	3.9
3	S8	67	VAL	3.9
3	X9	85	VAL	3.9
3	18	32	VAL	3.9
3	P9	20	THR	3.9
2	R5	69	GLU	3.8
2	X5	69	GLU	3.8
3	G9	101	GLU	3.8
3	I8	172	TYR	3.8
3	L8	172	TYR	3.8
3	S9	100	GLU	3.8
3	T9	41	GLU	3.8
3	28	74	LEU	3.8
3	H8	136	PRO	3.8
3	19	16	PRO	3.8
3	E9	156	ASN	3.8
3	F9	24	LYS	3.8
2	37	2	ALA	3.8
3	H8	43	ALA	3.8
3	H8	149	GLY	3.8
3	T9	20	THR	3.8
3	U9	155	ALA	3.8
3	49	6	ARG	3.8
3	J8	30	LEU	3.8

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Mol	Chain	Res	Type	RSRZ
3	V8	172	TYR	3.8
3	C9	136	PRO	3.8
3	M8	17	GLN	3.8
3	T8	68	VAL	3.8
3	48	66	GLN	3.8
3	C8	70	ARG	3.8
3	I9	190	ALA	3.8
3	W9	36	ALA	3.8
3	X8	30	LEU	3.8
3	29	64	ALA	3.8
2	H4	69	GLU	3.8
3	D9	41	GLU	3.8
3	E9	80	PHE	3.8
3	J9	41	GLU	3.8
3	E8	44	PRO	3.8
3	T9	136	PRO	3.8
3	19	147	PRO	3.8
3	O9	123	GLN	3.8
3	49	32	VAL	3.8
3	I9	128	ASN	3.8
3	K8	163	ASN	3.8
3	G9	81	ASP	3.8
3	A8	149	GLY	3.8
3	B9	43	ALA	3.8
3	I9	155	ALA	3.8
3	R8	179	TYR	3.8
3	N9	16	PRO	3.8
1	21	68	VAL	3.8
3	G9	32	VAL	3.8
3	H8	67	VAL	3.8
3	U9	107	GLN	3.8
3	F9	49	ASN	3.8
3	Z8	74	LEU	3.8
3	18	30	LEU	3.8
3	38	39	TRP	3.8
3	Q9	27	ARG	3.8
3	M8	132	MET	3.8
3	W8	132	MET	3.8
3	A8	20	THR	3.8
3	A9	64	ALA	3.8
3	N9	53	ASP	3.8
3	Y9	52	THR	3.8

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Mol	Chain	Res	Type	RSRZ
3	49	53	ASP	3.8
3	J9	138	GLU	3.8
3	K9	84	GLU	3.8
3	B9	15	GLN	3.8
3	C9	32	VAL	3.8
3	W8	68	VAL	3.8
3	D9	128	ASN	3.8
3	T9	163	ASN	3.8
3	N8	73	GLY	3.8
3	W9	116	ALA	3.8
3	19	203	GLY	3.8
2	K5	69	GLU	3.8
3	A9	72	TYR	3.8
3	B9	186	GLU	3.8
3	D9	186	GLU	3.8
3	Q8	72	TYR	3.8
3	T8	72	TYR	3.8
3	A8	67	VAL	3.8
3	A9	33	PRO	3.8
3	K9	147	PRO	3.8
3	Q9	31	PRO	3.8
3	V8	68	VAL	3.8
3	G9	17	GLN	3.7
3	H8	3	ILE	3.7
3	H9	92	ILE	3.7
3	K9	130	GLN	3.7
3	S9	15	GLN	3.7
1	21	61	SER	3.7
3	W8	129	SER	3.7
3	A9	47	ALA	3.7
3	H9	28	GLY	3.7
3	I9	196	ALA	3.7
3	P8	73	GLY	3.7
3	Z9	58	ALA	3.7
3	E9	4	THR	3.7
3	H9	96	LEU	3.7
3	O9	84	GLU	3.7
3	Q9	135	LEU	3.7
3	M8	136	PRO	3.7
3	P9	16	PRO	3.7
3	S8	65	VAL	3.7
3	W8	136	PRO	3.7

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Mol	Chain	Res	Type	RSRZ
3	T9	37	SER	3.7
3	28	66	GLN	3.7
2	B7	62	ARG	3.7
3	A8	133	MET	3.7
3	S8	133	MET	3.7
3	M8	163	ASN	3.7
3	R9	163	ASN	3.7
3	S9	126	ASN	3.7
3	S9	163	ASN	3.7
3	W9	163	ASN	3.7
3	C9	149	GLY	3.7
3	P9	116	ALA	3.7
3	T9	151	ALA	3.7
3	N9	52	THR	3.7
3	D9	32	VAL	3.7
3	E8	3	ILE	3.7
3	U9	53	ASP	3.7
3	I9	84	GLU	3.7
3	K8	157	GLU	3.7
3	N9	138	GLU	3.7
3	R8	68	VAL	3.7
3	U9	192	GLU	3.7
3	W9	144	GLU	3.7
3	18	179	TYR	3.7
3	X9	123	GLN	3.7
3	T9	79	HIS	3.7
3	W8	133	MET	3.7
3	Y9	6	ARG	3.7
3	L9	163	ASN	3.7
2	X3	2	ALA	3.7
3	H9	119	ALA	3.7
3	Q9	158	ALA	3.7
3	S9	116	ALA	3.7
3	19	119	ALA	3.7
3	I9	122	THR	3.7
3	38	149	GLY	3.7
3	U9	134	ILE	3.7
3	A9	67	VAL	3.7
3	A9	123	GLN	3.7
3	B9	123	GLN	3.7
3	C8	136	PRO	3.7
3	P8	81	ASP	3.7

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Mol	Chain	Res	Type	RSRZ
3	S8	136	PRO	3.7
3	19	44	PRO	3.7
3	38	72	TYR	3.7
3	H8	17	GLN	3.7
3	B9	128	ASN	3.7
3	E9	14	LEU	3.7
3	F9	163	ASN	3.7
3	R8	26	ALA	3.7
3	J9	61	VAL	3.7
3	P8	133	MET	3.7
3	A9	130	GLN	3.7
3	G9	33	PRO	3.7
3	N9	150	TYR	3.7
3	S8	27	ARG	3.7
3	N9	186	GLU	3.7
3	T9	62	GLN	3.7
3	U9	33	PRO	3.7
3	V9	147	PRO	3.7
3	49	183	SER	3.7
3	19	81	ASP	3.7
3	O8	30	LEU	3.7
3	P9	119	ALA	3.7
3	Q9	151	ALA	3.7
3	S9	149	GLY	3.7
3	E8	133	MET	3.7
3	E9	51	VAL	3.7
1	A1	61	SER	3.7
3	B8	136	PRO	3.7
3	E9	35	GLN	3.7
3	L8	130	GLN	3.7
3	M9	35	GLN	3.7
3	R8	17	GLN	3.7
3	R9	44	PRO	3.7
3	V9	35	GLN	3.7
3	Y9	100	GLU	3.7
3	Z8	192	GLU	3.7
2	14	49	ASP	3.7
3	B9	11	LEU	3.7
3	J9	81	ASP	3.7
3	C9	46	ILE	3.6
3	L9	55	ALA	3.6
3	M9	47	ALA	3.6

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Mol	Chain	Res	Type	RSRZ
3	N9	13	ALA	3.6
3	E9	20	THR	3.6
3	F8	137	GLY	3.6
3	G9	28	GLY	3.6
3	N8	137	GLY	3.6
3	C9	27	ARG	3.6
3	V8	67	VAL	3.6
3	39	117	VAL	3.6
3	A9	150	TYR	3.6
3	E9	63	PRO	3.6
3	N9	147	PRO	3.6
3	O9	35	GLN	3.6
3	R9	121	GLN	3.6
3	F8	179	TYR	3.6
3	K9	72	TYR	3.6
3	Y9	150	TYR	3.6
3	Z9	33	PRO	3.6
3	39	16	PRO	3.6
3	F9	96	LEU	3.6
3	R9	118	GLU	3.6
2	I3	49	ASP	3.6
2	Q6	49	ASP	3.6
3	F9	81	ASP	3.6
3	G9	134	ILE	3.6
3	P8	3	ILE	3.6
3	T8	3	ILE	3.6
3	Z9	81	ASP	3.6
3	F9	55	ALA	3.6
3	K9	165	HIS	3.6
3	Z9	88	ALA	3.6
3	G9	20	THR	3.6
3	G9	163	ASN	3.6
3	O9	20	THR	3.6
3	O9	163	ASN	3.6
3	Z9	20	THR	3.6
3	L9	67	VAL	3.6
3	Z9	6	ARG	3.6
3	O9	141	PHE	3.6
3	A8	30	LEU	3.6
3	M9	17	GLN	3.6
3	M9	147	PRO	3.6
3	P9	136	PRO	3.6

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Mol	Chain	Res	Type	RSRZ
3	U9	147	PRO	3.6
3	39	146	GLN	3.6
3	C9	100	GLU	3.6
3	H8	76	GLU	3.6
3	O9	179	TYR	3.6
3	Q9	101	GLU	3.6
3	W8	192	GLU	3.6
3	39	69	GLU	3.6
3	F9	92	ILE	3.6
3	B9	64	ALA	3.6
3	V9	119	ALA	3.6
3	K9	78	HIS	3.6
3	O8	34	GLY	3.6
3	B9	126	ASN	3.6
3	N8	163	ASN	3.6
3	Q9	128	ASN	3.6
3	Z9	60	LYS	3.6
3	Z9	65	VAL	3.6
3	W9	66	GLN	3.6
3	X9	31	PRO	3.6
3	C8	3	ILE	3.6
3	D9	84	GLU	3.6
3	H9	48	ILE	3.6
3	I8	3	ILE	3.6
3	F9	36	ALA	3.6
3	X8	71	ALA	3.6
3	Q8	81	ASP	3.6
3	D8	68	VAL	3.6
3	O9	49	ASN	3.6
3	Q9	163	ASN	3.6
3	S9	117	VAL	3.6
3	38	65	VAL	3.6
3	A9	147	PRO	3.6
3	C9	39	TRP	3.6
3	O9	66	GLN	3.6
3	S9	33	PRO	3.6
2	M7	69	GLU	3.6
3	C8	72	TYR	3.6
3	F9	100	GLU	3.6
3	G8	172	TYR	3.6
3	D8	133	MET	3.6
2	T7	2	ALA	3.6

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Mol	Chain	Res	Type	RSRZ
3	A9	193	ALA	3.6
3	K9	55	ALA	3.6
3	19	127	ARG	3.6
2	N3	49	ASP	3.6
3	E9	52	THR	3.6
3	G9	78	HIS	3.6
3	P9	32	VAL	3.6
3	Z9	67	VAL	3.6
3	49	79	HIS	3.6
3	49	117	VAL	3.6
1	R1	61	SER	3.6
3	C9	156	ASN	3.6
3	P9	156	ASN	3.6
3	C9	17	GLN	3.6
3	E9	121	GLN	3.6
3	49	15	GLN	3.6
3	D9	33	PRO	3.6
3	O9	147	PRO	3.6
3	P9	31	PRO	3.6
3	W9	44	PRO	3.6
3	H9	120	TYR	3.6
3	J8	72	TYR	3.6
3	U8	72	TYR	3.6
3	19	76	GLU	3.6
2	G3	2	ALA	3.6
3	Z8	26	ALA	3.6
1	K1	88	GLY	3.6
3	Y8	28	GLY	3.6
3	T9	63	PRO	3.5
3	W9	16	PRO	3.5
3	D9	100	GLU	3.5
3	G9	120	TYR	3.5
3	S9	118	GLU	3.5
3	T9	138	GLU	3.5
3	C9	116	ALA	3.5
3	G8	149	GLY	3.5
3	J9	34	GLY	3.5
3	Q9	52	THR	3.5
3	G8	3	ILE	3.5
3	M9	183	SER	3.5
3	S8	42	ILE	3.5
3	39	128	ASN	3.5

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Mol	Chain	Res	Type	RSRZ
3	X9	146	GLN	3.5
3	18	17	GLN	3.5
3	38	35	GLN	3.5
3	B9	136	PRO	3.5
3	V8	44	PRO	3.5
3	G8	74	LEU	3.5
3	H8	179	TYR	3.5
2	W6	2	ALA	3.5
2	13	2	ALA	3.5
3	R9	64	ALA	3.5
3	W9	158	ALA	3.5
3	Z8	71	ALA	3.5
3	H9	91	THR	3.5
3	N9	169	VAL	3.5
3	38	32	VAL	3.5
3	B9	156	ASN	3.5
3	G8	111	HIS	3.5
2	R4	49	ASP	3.5
3	C8	81	ASP	3.5
3	J9	53	ASP	3.5
3	T8	35	GLN	3.5
3	U9	35	GLN	3.5
3	P8	136	PRO	3.5
3	Z9	27	ARG	3.5
3	F9	184	GLU	3.5
3	H8	71	ALA	3.5
3	M9	87	ALA	3.5
3	U9	55	ALA	3.5
3	39	157	GLU	3.5
3	B9	91	THR	3.5
3	C8	201	VAL	3.5
3	F9	68	VAL	3.5
3	H9	59	THR	3.5
3	O9	68	VAL	3.5
3	Q9	51	VAL	3.5
3	S9	61	VAL	3.5
3	48	132	MET	3.5
3	F8	30	LEU	3.5
3	L9	17	GLN	3.5
3	P9	17	GLN	3.5
3	U9	17	GLN	3.5
3	Y9	128	ASN	3.5

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Mol	Chain	Res	Type	RSRZ
3	B8	177	ARG	3.5
3	J9	6	ARG	3.5
3	M9	99	ARG	3.5
3	D9	174	ALA	3.5
3	I9	186	GLU	3.5
3	J9	36	ALA	3.5
3	H8	39	TRP	3.5
3	49	192	GLU	3.5
3	V9	46	ILE	3.5
3	G8	65	VAL	3.5
3	N8	32	VAL	3.5
3	O9	28	GLY	3.5
3	18	68	VAL	3.5
3	B9	20	THR	3.5
3	W9	122	THR	3.5
3	K8	30	LEU	3.5
3	K9	49	ASN	3.5
3	M9	163	ASN	3.5
3	N9	136	PRO	3.5
3	S9	53	ASP	3.5
3	T9	12	ASP	3.5
3	E8	72	TYR	3.5
3	I9	119	ALA	3.5
3	T9	116	ALA	3.5
3	F8	192	GLU	3.5
3	T9	134	ILE	3.5
3	D9	117	VAL	3.5
3	D9	137	GLY	3.5
3	P8	129	SER	3.5
3	T8	4	THR	3.5
3	U9	52	THR	3.5
3	W9	20	THR	3.5
3	Y9	20	THR	3.5
3	28	129	SER	3.5
3	F9	66	GLN	3.5
3	Q9	35	GLN	3.5
3	X9	35	GLN	3.5
3	F9	126	ASN	3.5
3	Q8	175	PHE	3.5
3	Y9	156	ASN	3.5
2	R4	2	ALA	3.4
3	O9	119	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
3	O9	134	ILE	3.4
3	R9	119	ALA	3.4
3	T9	196	ALA	3.4
3	A8	72	TYR	3.4
3	K9	150	TYR	3.4
3	O9	72	TYR	3.4
3	T8	172	TYR	3.4
2	Y4	58	GLU	3.4
3	B9	118	GLU	3.4
3	H9	84	GLU	3.4
3	N9	84	GLU	3.4
3	W9	76	GLU	3.4
3	39	195	GLU	3.4
3	F9	39	TRP	3.4
3	I8	67	VAL	3.4
3	V8	32	VAL	3.4
3	28	65	VAL	3.4
3	C8	30	LEU	3.4
3	O9	109	MET	3.4
3	S9	28	GLY	3.4
3	T9	176	GLY	3.4
3	V8	74	LEU	3.4
3	L9	59	THR	3.4
3	J8	66	GLN	3.4
3	U9	193	ALA	3.4
3	O9	120	TYR	3.4
3	W8	172	TYR	3.4
3	F9	67	VAL	3.4
3	M9	100	GLU	3.4
3	W8	41	GLU	3.4
3	Z8	94	ASP	3.4
3	48	30	LEU	3.4
3	N8	25	THR	3.4
3	R9	20	THR	3.4
3	18	39	TRP	3.4
3	G9	175	PHE	3.4
3	29	27	ARG	3.4
3	I9	15	GLN	3.4
3	H9	63	PRO	3.4
3	I8	95	LYS	3.4
3	T9	168	ASN	3.4
3	A9	158	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
3	39	197	ALA	3.4
3	H9	32	VAL	3.4
3	Q9	8	TYR	3.4
3	R9	204	VAL	3.4
3	U8	67	VAL	3.4
3	X8	179	TYR	3.4
3	39	186	GLU	3.4
3	N9	20	THR	3.4
3	H8	130	GLN	3.4
3	28	17	GLN	3.4
3	I9	187	ILE	3.4
3	A9	136	PRO	3.4
3	B9	63	PRO	3.4
3	H9	163	ASN	3.4
3	K9	156	ASN	3.4
3	18	163	ASN	3.4
3	L9	154	ALA	3.4
3	N8	13	ALA	3.4
3	S9	119	ALA	3.4
3	T9	119	ALA	3.4
3	28	71	ALA	3.4
3	48	133	MET	3.4
3	Q9	78	HIS	3.4
3	18	65	VAL	3.4
3	48	67	VAL	3.4
3	J8	172	TYR	3.4
3	P9	97	GLU	3.4
3	T9	90	SER	3.4
3	Z8	179	TYR	3.4
3	G9	144	GLU	3.4
3	39	84	GLU	3.4
3	Y9	145	THR	3.4
3	G8	39	TRP	3.4
3	O9	15	GLN	3.4
3	T8	17	GLN	3.4
3	D8	74	LEU	3.4
3	R8	33	PRO	3.4
3	R8	133	MET	3.4
3	O8	71	ALA	3.4
3	O9	151	ALA	3.4
3	P9	162	ALA	3.4
3	W9	191	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
3	Y9	197	ALA	3.4
3	A9	169	VAL	3.4
3	R8	32	VAL	3.4
3	L9	78	HIS	3.4
3	U9	78	HIS	3.4
3	B9	72	TYR	3.4
3	P8	72	TYR	3.4
3	R9	195	GLU	3.4
3	J9	122	THR	3.4
3	39	127	ARG	3.4
3	X8	24	LYS	3.4
3	I9	134	ILE	3.4
3	L9	15	GLN	3.4
3	38	133	MET	3.4
3	I8	136	PRO	3.4
3	J9	16	PRO	3.4
3	49	136	PRO	3.4
2	A7	2	ALA	3.4
2	V5	2	ALA	3.4
3	G9	36	ALA	3.4
3	G9	151	ALA	3.4
3	K8	71	ALA	3.4
3	M9	116	ALA	3.4
3	T9	58	ALA	3.4
3	X8	26	ALA	3.4
3	A9	49	ASN	3.4
3	B9	163	ASN	3.4
3	L9	126	ASN	3.4
3	U8	65	VAL	3.4
3	Y9	32	VAL	3.4
3	E9	120	TYR	3.4
3	I8	72	TYR	3.4
3	49	172	TYR	3.4
3	C8	184	GLU	3.3
3	C9	186	GLU	3.3
3	D9	149	GLY	3.3
3	K8	149	GLY	3.3
3	U8	28	GLY	3.3
3	29	100	GLU	3.3
3	O9	48	ILE	3.3
3	Z8	3	ILE	3.3
2	I4	49	ASP	3.3

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Mol	Chain	Res	Type	RSRZ
2	R6	49	ASP	3.3
3	D9	130	GLN	3.3
3	I9	53	ASP	3.3
3	R9	35	GLN	3.3
3	V8	133	MET	3.3
3	F9	88	ALA	3.3
3	T9	147	PRO	3.3
3	U9	19	ALA	3.3
3	Z9	55	ALA	3.3
3	C8	32	VAL	3.3
3	C8	68	VAL	3.3
3	D9	152	VAL	3.3
3	E8	163	ASN	3.3
3	G9	49	ASN	3.3
3	N8	67	VAL	3.3
3	49	156	ASN	3.3
3	I9	27	ARG	3.3
3	Z9	103	ARG	3.3
3	O9	195	GLU	3.3
3	U9	28	GLY	3.3
3	48	72	TYR	3.3
3	G8	184	GLU	3.3
3	I9	69	GLU	3.3
3	T9	91	THR	3.3
3	X9	135	LEU	3.3
3	Y9	144	GLU	3.3
3	Q9	66	GLN	3.3
3	Y8	132	MET	3.3
3	A9	94	ASP	3.3
3	F8	39	TRP	3.3
3	O9	53	ASP	3.3
3	F9	43	ALA	3.3
3	H9	116	ALA	3.3
3	J9	64	ALA	3.3
3	Q8	33	PRO	3.3
3	I9	117	VAL	3.3
3	Z9	32	VAL	3.3
3	28	67	VAL	3.3
3	A9	50	ARG	3.3
3	D9	6	ARG	3.3
3	P9	49	ASN	3.3
3	R9	3	ILE	3.3

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Mol	Chain	Res	Type	RSRZ
2	X5	39	GLY	3.3
3	X8	45	GLY	3.3
3	49	72	TYR	3.3
3	O9	165	HIS	3.3
3	C8	133	MET	3.3
3	B8	15	GLN	3.3
3	E9	62	GLN	3.3
3	A9	12	ASP	3.3
2	X4	2	ALA	3.3
2	X7	2	ALA	3.3
3	K9	16	PRO	3.3
3	T8	106	PRO	3.3
3	T9	197	ALA	3.3
3	Y9	55	ALA	3.3
3	H8	68	VAL	3.3
3	T9	85	VAL	3.3
3	18	67	VAL	3.3
3	39	32	VAL	3.3
3	D9	163	ASN	3.3
3	F9	48	ILE	3.3
3	G9	168	ASN	3.3
1	J1	34	GLY	3.3
3	J8	149	GLY	3.3
2	N3	69	GLU	3.3
3	H8	192	GLU	3.3
3	H9	7	THR	3.3
3	I9	20	THR	3.3
3	X9	144	GLU	3.3
3	19	109	MET	3.3
3	29	20	THR	3.3
3	B9	107	GLN	3.3
3	C9	123	GLN	3.3
3	H9	82	GLN	3.3
3	Y9	15	GLN	3.3
3	39	62	GLN	3.3
2	D7	2	ALA	3.3
3	E9	147	PRO	3.3
3	I9	16	PRO	3.3
3	Q9	64	ALA	3.3
3	B9	32	VAL	3.3
3	O8	67	VAL	3.3
3	Z9	53	ASP	3.3

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Mol	Chain	Res	Type	RSRZ
3	C8	129	SER	3.3
3	E9	48	ILE	3.3
3	G9	48	ILE	3.3
3	H8	129	SER	3.3
3	M9	156	ASN	3.3
3	39	49	ASN	3.3
2	G2	39	GLY	3.3
3	A8	172	TYR	3.3
3	D8	72	TYR	3.3
3	S9	122	THR	3.3
3	U8	179	TYR	3.3
2	N5	58	GLU	3.3
3	E9	100	GLU	3.3
3	J9	76	GLU	3.3
3	X9	186	GLU	3.3
3	I9	107	GLN	3.3
3	J9	165	HIS	3.3
3	M9	78	HIS	3.3
3	G9	43	ALA	3.3
3	K9	19	ALA	3.3
3	Q8	26	ALA	3.3
3	R9	205	ALA	3.3
3	U8	71	ALA	3.3
3	A8	136	PRO	3.3
3	C9	16	PRO	3.3
3	F9	106	PRO	3.3
3	O9	65	VAL	3.3
3	P9	164	VAL	3.3
3	Q9	32	VAL	3.3
3	Q9	147	PRO	3.3
3	S9	16	PRO	3.3
3	V8	39	TRP	3.3
3	W9	3	ILE	3.3
3	W9	85	VAL	3.3
3	29	44	PRO	3.3
3	H9	202	SER	3.3
3	E8	132	MET	3.3
3	J8	132	MET	3.3
3	H9	131	GLY	3.3
3	A9	122	THR	3.3
3	H9	150	TYR	3.3
3	P8	172	TYR	3.3

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Mol	Chain	Res	Type	RSRZ
3	P9	122	THR	3.3
3	Q9	72	TYR	3.3
3	S9	52	THR	3.3
3	Z9	4	THR	3.3
3	39	145	THR	3.3
3	49	20	THR	3.3
2	I6	69	GLU	3.3
3	P8	17	GLN	3.3
3	V9	123	GLN	3.3
3	29	123	GLN	3.3
3	E8	30	LEU	3.2
3	B9	99	ARG	3.2
3	G9	197	ALA	3.2
3	M8	70	ARG	3.2
3	P9	64	ALA	3.2
3	R9	191	ALA	3.2
3	S8	71	ALA	3.2
3	T9	181	ALA	3.2
3	U9	22	ILE	3.2
3	X9	88	ALA	3.2
3	Z9	119	ALA	3.2
3	Z9	193	ALA	3.2
1	S1	61	SER	3.2
3	J8	65	VAL	3.2
3	U9	106	PRO	3.2
3	V9	33	PRO	3.2
2	I6	49	ASP	3.2
3	J8	133	MET	3.2
3	39	53	ASP	3.2
1	Z1	88	GLY	3.2
3	A8	137	GLY	3.2
3	B9	176	GLY	3.2
3	W9	49	ASN	3.2
3	C9	150	TYR	3.2
3	U9	150	TYR	3.2
3	Z8	72	TYR	3.2
3	19	4	THR	3.2
3	E9	118	GLU	3.2
3	R9	184	GLU	3.2
3	T9	130	GLN	3.2
3	B9	27	ARG	3.2
3	I8	165	HIS	3.2

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Mol	Chain	Res	Type	RSRZ
3	O9	103	ARG	3.2
3	U9	127	ARG	3.2
3	19	50	ARG	3.2
3	C9	119	ALA	3.2
3	L8	43	ALA	3.2
3	L9	189	ALA	3.2
3	T8	43	ALA	3.2
3	T9	88	ALA	3.2
3	W9	190	ALA	3.2
3	29	54	ALA	3.2
3	C8	67	VAL	3.2
3	E9	136	PRO	3.2
1	G1	75	ASP	3.2
2	T6	49	ASP	3.2
2	U7	84	ASP	3.2
3	G9	60	LYS	3.2
3	J8	12	ASP	3.2
3	V9	12	ASP	3.2
3	C8	149	GLY	3.2
3	E8	73	GLY	3.2
3	M8	149	GLY	3.2
3	B8	110	THR	3.2
3	C8	179	TYR	3.2
3	V8	179	TYR	3.2
3	Y8	172	TYR	3.2
2	Q3	69	GLU	3.2
3	H9	157	GLU	3.2
3	M9	101	GLU	3.2
3	O9	130	GLN	3.2
3	S8	159	GLU	3.2
3	S9	144	GLU	3.2
3	U9	80	PHE	3.2
3	Y9	107	GLN	3.2
3	18	41	GLU	3.2
3	Q9	6	ARG	3.2
2	32	2	ALA	3.2
3	I9	191	ALA	3.2
3	J9	164	VAL	3.2
3	M8	71	ALA	3.2
3	P9	54	ALA	3.2
3	T9	169	VAL	3.2
3	W9	162	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
3	39	61	VAL	3.2
3	39	85	VAL	3.2
3	48	44	PRO	3.2
1	F1	45	ASP	3.2
3	G8	30	LEU	3.2
3	G8	45	GLY	3.2
3	J8	137	GLY	3.2
3	Q9	12	ASP	3.2
3	Q9	156	ASN	3.2
3	U8	34	GLY	3.2
3	Z8	45	GLY	3.2
3	B9	130	GLN	3.2
3	F8	172	TYR	3.2
3	L9	150	TYR	3.2
3	S8	172	TYR	3.2
3	19	15	GLN	3.2
3	A9	118	GLU	3.2
3	R9	27	ARG	3.2
3	V9	76	GLU	3.2
3	39	115	ARG	3.2
3	D8	71	ALA	3.2
3	H9	51	VAL	3.2
3	O8	32	VAL	3.2
3	Q8	129	SER	3.2
3	38	68	VAL	3.2
3	48	68	VAL	3.2
3	W9	31	PRO	3.2
3	W9	63	PRO	3.2
3	R9	135	LEU	3.2
3	T9	74	LEU	3.2
3	I9	149	GLY	3.2
3	V9	149	GLY	3.2
3	D9	4	THR	3.2
3	F9	21	PHE	3.2
3	K9	128	ASN	3.2
3	L8	175	PHE	3.2
3	N9	141	PHE	3.2
3	Q8	20	THR	3.2
3	T9	122	THR	3.2
3	Z9	110	THR	3.2
3	49	163	ASN	3.2
2	44	49	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
3	B9	179	TYR	3.2
3	D9	17	GLN	3.2
3	G9	130	GLN	3.2
3	G9	146	GLN	3.2
3	I9	35	GLN	3.2
3	I9	72	TYR	3.2
3	J9	72	TYR	3.2
3	L8	72	TYR	3.2
3	M8	27	ARG	3.2
3	28	172	TYR	3.2
3	A9	184	GLU	3.2
3	I9	195	GLU	3.2
3	J9	100	GLU	3.2
3	L9	76	GLU	3.2
3	Q9	195	GLU	3.2
3	J8	32	VAL	3.2
3	L9	61	VAL	3.2
3	L9	196	ALA	3.2
3	Q8	205	ALA	3.2
3	W9	109	MET	3.2
3	Z9	169	VAL	3.2
3	18	71	ALA	3.2
3	39	185	ALA	3.2
1	I1	61	SER	3.2
3	A9	183	SER	3.2
3	G9	183	SER	3.2
3	B8	33	PRO	3.2
3	P9	147	PRO	3.2
3	S9	147	PRO	3.2
3	V9	63	PRO	3.2
3	19	31	PRO	3.2
3	J8	74	LEU	3.2
3	R9	14	LEU	3.2
3	C8	28	GLY	3.2
3	F9	134	ILE	3.2
3	I8	39	TRP	3.2
3	U9	39	TRP	3.2
3	29	80	PHE	3.2
3	I9	126	ASN	3.2
3	J9	59	THR	3.2
3	N9	27	ARG	3.2
3	T9	49	ASN	3.2

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Mol	Chain	Res	Type	RSRZ
3	X9	52	THR	3.2
3	B8	17	GLN	3.2
2	J4	49	ASP	3.2
3	D8	188	ASP	3.2
3	I9	81	ASP	3.2
3	Y8	179	TYR	3.2
3	D8	157	GLU	3.2
3	G9	118	GLU	3.2
3	N8	133	MET	3.2
3	P9	144	GLU	3.2
3	Q9	41	GLU	3.2
3	V9	41	GLU	3.2
3	V9	138	GLU	3.2
3	V9	157	GLU	3.2
3	Z8	41	GLU	3.2
3	49	157	GLU	3.2
3	A9	151	ALA	3.2
3	C9	88	ALA	3.2
3	Q9	204	VAL	3.2
3	S9	43	ALA	3.2
3	T9	36	ALA	3.2
3	V8	108	VAL	3.2
3	Y9	88	ALA	3.2
3	19	185	ALA	3.2
3	39	87	ALA	3.2
3	39	151	ALA	3.2
3	48	65	VAL	3.2
3	L9	31	PRO	3.2
3	T9	16	PRO	3.2
3	18	136	PRO	3.2
3	Y8	111	HIS	3.2
1	W1	88	GLY	3.1
3	D8	45	GLY	3.1
3	C9	52	THR	3.1
3	F9	6	ARG	3.1
3	S8	28	GLY	3.1
3	H8	20	THR	3.1
3	T8	110	THR	3.1
3	49	59	THR	3.1
3	J9	15	GLN	3.1
3	W9	156	ASN	3.1
3	28	163	ASN	3.1

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Mol	Chain	Res	Type	RSRZ
3	B8	172	TYR	3.1
3	W8	179	TYR	3.1
3	19	72	TYR	3.1
3	C9	101	GLU	3.1
3	E8	184	GLU	3.1
3	N9	144	GLU	3.1
3	R8	184	GLU	3.1
3	S9	184	GLU	3.1
3	W9	195	GLU	3.1
3	Z9	144	GLU	3.1
3	C8	43	ALA	3.1
3	F9	205	ALA	3.1
3	K8	26	ALA	3.1
3	N9	151	ALA	3.1
3	O8	43	ALA	3.1
3	T9	65	VAL	3.1
3	W9	88	ALA	3.1
3	Z8	67	VAL	3.1
3	Z9	71	ALA	3.1
3	49	67	VAL	3.1
3	49	158	ALA	3.1
3	L8	30	LEU	3.1
3	F9	171	PRO	3.1
3	A8	80	PHE	3.1
3	A8	134	ILE	3.1
3	K8	134	ILE	3.1
3	G9	149	GLY	3.1
3	J8	70	ARG	3.1
3	R8	70	ARG	3.1
3	Z8	27	ARG	3.1
3	D8	132	MET	3.1
3	D9	122	THR	3.1
3	L8	17	GLN	3.1
3	M8	39	TRP	3.1
3	S9	66	GLN	3.1
3	28	130	GLN	3.1
3	S9	156	ASN	3.1
3	A9	120	TYR	3.1
3	S9	179	TYR	3.1
2	Q7	2	ALA	3.1
3	A9	205	ALA	3.1
3	B9	167	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
3	D9	26	ALA	3.1
3	I8	65	VAL	3.1
3	J8	100	GLU	3.1
3	K9	54	ALA	3.1
3	O9	138	GLU	3.1
3	P8	43	ALA	3.1
3	P9	41	GLU	3.1
3	R8	192	GLU	3.1
3	S8	192	GLU	3.1
3	U8	32	VAL	3.1
3	V8	71	ALA	3.1
3	19	61	VAL	3.1
3	29	55	ALA	3.1
3	39	138	GLU	3.1
2	W6	49	ASP	3.1
2	Y4	49	ASP	3.1
2	33	3	ASP	3.1
3	I9	12	ASP	3.1
3	T9	53	ASP	3.1
3	L8	3	ILE	3.1
3	L9	134	ILE	3.1
3	Q9	63	PRO	3.1
3	W9	92	ILE	3.1
3	39	124	ILE	3.1
3	N8	177	ARG	3.1
3	R9	165	HIS	3.1
1	Q1	88	GLY	3.1
3	H8	95	LYS	3.1
3	R9	28	GLY	3.1
3	S9	24	LYS	3.1
3	Y8	173	GLY	3.1
3	18	34	GLY	3.1
3	C9	7	THR	3.1
3	29	59	THR	3.1
3	U8	17	GLN	3.1
3	Z9	62	GLN	3.1
3	H8	74	LEU	3.1
3	O9	156	ASN	3.1
3	V9	168	ASN	3.1
1	E1	61	SER	3.1
3	B8	68	VAL	3.1
3	B9	185	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
3	E8	192	GLU	3.1
3	E9	190	ALA	3.1
3	G9	100	GLU	3.1
3	L9	54	ALA	3.1
3	L9	202	SER	3.1
3	R9	196	ALA	3.1
3	U8	98	VAL	3.1
3	Z9	117	VAL	3.1
3	19	8	TYR	3.1
3	M9	186	GLU	3.1
3	19	87	ALA	3.1
3	L9	136	PRO	3.1
3	49	33	PRO	3.1
3	K8	27	ARG	3.1
3	O8	27	ARG	3.1
3	Z9	70	ARG	3.1
3	I8	133	MET	3.1
3	A8	73	GLY	3.1
3	O9	149	GLY	3.1
3	V8	34	GLY	3.1
3	38	45	GLY	3.1
3	38	131	GLY	3.1
3	E9	15	GLN	3.1
3	H9	66	GLN	3.1
3	I9	14	LEU	3.1
3	J8	20	THR	3.1
3	Q9	7	THR	3.1
3	X9	59	THR	3.1
3	X9	122	THR	3.1
3	19	153	LEU	3.1
3	F8	67	VAL	3.1
3	G8	43	ALA	3.1
3	G9	202	SER	3.1
3	K9	67	VAL	3.1
3	O9	85	VAL	3.1
3	R9	72	TYR	3.1
3	T9	32	VAL	3.1
3	W9	168	ASN	3.1
3	M9	43	ALA	3.1
3	M9	190	ALA	3.1
3	U9	189	ALA	3.1
3	W9	72	TYR	3.1

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Mol	Chain	Res	Type	RSRZ
3	Z9	120	TYR	3.1
3	29	162	ALA	3.1
3	49	174	ALA	3.1
3	49	205	ALA	3.1
3	I9	100	GLU	3.1
3	J9	48	ILE	3.1
3	J9	186	GLU	3.1
3	W9	118	GLU	3.1
2	D6	49	ASP	3.1
2	Q2	49	ASP	3.1
2	13	49	ASP	3.1
3	D9	60	LYS	3.1
3	O8	136	PRO	3.1
3	O9	81	ASP	3.1
3	P9	44	PRO	3.1
3	Z9	127	ARG	3.1
2	G2	33	GLY	3.1
3	J9	14	LEU	3.1
3	38	34	GLY	3.1
3	J8	17	GLN	3.1
3	L9	66	GLN	3.1
3	Q9	15	GLN	3.1
3	V9	130	GLN	3.1
3	W9	35	GLN	3.1
3	X9	107	GLN	3.1
3	X9	145	THR	3.1
3	49	121	GLN	3.1
2	H3	2	ALA	3.1
2	H7	2	ALA	3.1
2	47	2	ALA	3.1
3	A9	156	ASN	3.1
3	B8	163	ASN	3.1
3	E9	19	ALA	3.1
3	F8	72	TYR	3.1
3	H9	72	TYR	3.1
3	I9	46	ILE	3.1
3	I9	158	ALA	3.1
3	N9	32	VAL	3.1
3	N9	116	ALA	3.1
3	N9	128	ASN	3.1
3	S9	67	VAL	3.1
3	V9	150	TYR	3.1

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Mol	Chain	Res	Type	RSRZ
3	W9	55	ALA	3.1
3	29	169	VAL	3.1
3	P8	179	TYR	3.1
3	T8	150	TYR	3.1
2	G6	69	GLU	3.1
2	U2	69	GLU	3.1
3	B9	144	GLU	3.1
3	K8	175	PHE	3.1
3	L9	21	PHE	3.1
3	M8	192	GLU	3.1
3	R9	41	GLU	3.1
3	N9	60	LYS	3.1
3	A8	177	ARG	3.1
3	C8	27	ARG	3.1
3	M9	16	PRO	3.1
3	V8	106	PRO	3.1
3	29	147	PRO	3.1
3	39	106	PRO	3.1
1	D1	90	ASP	3.1
3	A9	86	LEU	3.1
3	H9	81	ASP	3.1
3	S9	56	LEU	3.1
1	Y1	88	GLY	3.1
3	Q9	102	GLY	3.1
3	A9	78	HIS	3.1
3	C9	59	THR	3.1
3	F9	107	GLN	3.0
3	S9	20	THR	3.1
3	V8	62	GLN	3.0
3	19	107	GLN	3.0
3	19	146	GLN	3.0
3	I8	68	VAL	3.0
3	W9	61	VAL	3.0
3	38	67	VAL	3.0
3	A9	36	ALA	3.0
3	B8	205	ALA	3.0
3	V9	190	ALA	3.0
3	W8	205	ALA	3.0
3	Z9	158	ALA	3.0
3	A9	141	PHE	3.0
3	S8	179	TYR	3.0
2	I5	58	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
2	J5	69	GLU	3.0
2	L5	58	GLU	3.0
3	E9	195	GLU	3.0
3	I8	192	GLU	3.0
3	K9	186	GLU	3.0
3	U9	70	ARG	3.0
3	29	184	GLU	3.0
3	G9	44	PRO	3.0
3	M9	33	PRO	3.0
3	O9	136	PRO	3.0
3	T9	75	LEU	3.0
3	B9	12	ASP	3.0
3	P9	94	ASP	3.0
3	18	81	ASP	3.0
3	38	94	ASP	3.0
3	E9	28	GLY	3.0
3	T9	45	GLY	3.0
3	48	149	GLY	3.0
3	I9	52	THR	3.0
3	N9	107	GLN	3.0
3	O9	121	GLN	3.0
3	P9	52	THR	3.0
3	B8	111	HIS	3.0
3	Q8	111	HIS	3.0
3	U9	46	ILE	3.0
3	39	46	ILE	3.0
3	49	46	ILE	3.0
3	K9	108	VAL	3.0
3	39	167	VAL	3.0
3	A9	191	ALA	3.0
3	I9	189	ALA	3.0
3	J9	162	ALA	3.0
3	K9	154	ALA	3.0
3	P9	197	ALA	3.0
3	T9	19	ALA	3.0
3	U9	21	PHE	3.0
3	U9	43	ALA	3.0
3	G9	8	TYR	3.0
3	H9	156	ASN	3.0
3	J9	150	TYR	3.0
3	P8	39	TRP	3.0
3	Q8	39	TRP	3.0

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Mol	Chain	Res	Type	RSRZ
3	S9	72	TYR	3.0
2	W6	69	GLU	3.0
3	F9	118	GLU	3.0
3	I9	41	GLU	3.0
3	P8	30	LEU	3.0
3	Q8	30	LEU	3.0
3	Q8	96	LEU	3.0
3	Q8	192	GLU	3.0
3	U9	138	GLU	3.0
3	V8	132	MET	3.0
3	28	100	GLU	3.0
3	48	39	TRP	3.0
3	J9	33	PRO	3.0
3	Z9	63	PRO	3.0
2	A4	49	ASP	3.0
3	U9	12	ASP	3.0
3	Z9	28	GLY	3.0
3	D9	7	THR	3.0
3	O9	146	GLN	3.0
3	V9	146	GLN	3.0
3	W9	145	THR	3.0
3	P9	78	HIS	3.0
3	S9	65	VAL	3.0
3	V8	201	VAL	3.0
3	W9	202	SER	3.0
3	C9	58	ALA	3.0
3	E8	43	ALA	3.0
3	F8	71	ALA	3.0
3	H9	155	ALA	3.0
3	Q9	119	ALA	3.0
3	Q9	196	ALA	3.0
3	T9	174	ALA	3.0
3	29	116	ALA	3.0
3	48	71	ALA	3.0
3	F8	6	ARG	3.0
3	18	177	ARG	3.0
3	19	177	ARG	3.0
3	X9	128	ASN	3.0
3	19	179	TYR	3.0
3	28	133	MET	3.0
2	D3	59	GLU	3.0
2	Q4	69	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
2	Y4	69	GLU	3.0
3	D8	136	PRO	3.0
3	I9	147	PRO	3.0
3	L8	44	PRO	3.0
3	A9	28	GLY	3.0
3	F8	28	GLY	3.0
3	Y9	112	GLN	3.0
3	39	60	LYS	3.0
1	W1	75	ASP	3.0
2	S3	49	ASP	3.0
1	Q1	61	SER	3.0
3	H9	68	VAL	3.0
3	J9	37	SER	3.0
3	Q9	40	VAL	3.0
3	T8	175	PHE	3.0
3	U8	201	VAL	3.0
3	Z9	40	VAL	3.0
2	A4	2	ALA	3.0
2	R7	2	ALA	3.0
3	A9	43	ALA	3.0
3	D9	47	ALA	3.0
3	E9	54	ALA	3.0
3	L8	71	ALA	3.0
3	M9	54	ALA	3.0
3	P9	55	ALA	3.0
3	P9	75	LEU	3.0
3	Q8	71	ALA	3.0
3	R9	116	ALA	3.0
3	X9	116	ALA	3.0
3	H9	115	ARG	3.0
3	I8	70	ARG	3.0
3	P8	27	ARG	3.0
3	48	70	ARG	3.0
3	D8	172	TYR	3.0
3	H9	168	ASN	3.0
3	L9	49	ASN	3.0
3	19	120	TYR	3.0
2	Y3	58	GLU	3.0
2	15	69	GLU	3.0
3	F9	33	PRO	3.0
3	J8	39	TRP	3.0
3	T9	195	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
3	R8	136	PRO	3.0
3	D9	134	ILE	3.0
3	X9	46	ILE	3.0
3	C9	45	GLY	3.0
3	D9	173	GLY	3.0
3	Z8	28	GLY	3.0
3	D9	141	PHE	3.0
3	E8	15	GLN	3.0
1	B1	61	SER	3.0
3	H9	110	THR	3.0
3	V9	59	THR	3.0
3	X8	25	THR	3.0
3	Y8	20	THR	3.0
3	B9	51	VAL	3.0
3	O8	81	ASP	3.0
3	O9	135	LEU	3.0
3	P8	67	VAL	3.0
3	U8	30	LEU	3.0
3	Z8	96	LEU	3.0
3	19	32	VAL	3.0
2	P5	84	ASP	3.0
3	E8	119	ALA	3.0
3	E9	55	ALA	3.0
3	L8	132	MET	3.0
3	M8	133	MET	3.0
3	S9	6	ARG	3.0
3	V9	158	ALA	3.0
3	19	55	ALA	3.0
3	D9	78	HIS	3.0
3	B8	179	TYR	3.0
3	C8	163	ASN	3.0
3	M8	172	TYR	3.0
3	W9	179	TYR	3.0
2	D7	58	GLU	3.0
3	C9	195	GLU	3.0
3	X9	138	GLU	3.0
3	39	184	GLU	3.0
3	C9	33	PRO	3.0
3	F9	147	PRO	3.0
3	O9	92	ILE	3.0
3	B9	137	GLY	3.0
3	R8	28	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
3	S8	149	GLY	3.0
3	W9	131	GLY	3.0
3	A9	56	LEU	3.0
3	C9	15	GLN	3.0
3	D8	30	LEU	3.0
3	G9	5	LEU	3.0
3	H8	65	VAL	3.0
3	J9	146	GLN	3.0
3	Q9	146	GLN	3.0
3	X9	56	LEU	3.0
3	N8	65	VAL	3.0
3	Y8	65	VAL	3.0
3	Y8	68	VAL	3.0
3	Z8	68	VAL	3.0
3	Z9	202	SER	3.0
3	48	32	VAL	3.0
3	G9	6	ARG	3.0
3	B9	119	ALA	3.0
3	C9	55	ALA	3.0
3	C9	161	ALA	3.0
3	K9	116	ALA	3.0
3	Q9	190	ALA	3.0
3	39	161	ALA	3.0
3	I9	163	ASN	2.9
3	O9	150	TYR	2.9
3	V9	156	ASN	2.9
3	Z9	150	TYR	2.9
2	A5	69	GLU	2.9
2	L4	58	GLU	2.9
3	C9	44	PRO	2.9
3	D9	144	GLU	2.9
3	I9	184	GLU	2.9
3	J9	101	GLU	2.9
3	R9	144	GLU	2.9
3	U9	124	ILE	2.9
3	29	118	GLU	2.9
3	39	3	ILE	2.9
3	G9	135	LEU	2.9
3	B8	131	GLY	2.9
3	Y9	28	GLY	2.9
1	B1	13	SER	2.9
1	O1	61	SER	2.9

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Mol	Chain	Res	Type	RSRZ
3	D9	40	VAL	2.9
3	D9	68	VAL	2.9
3	G8	17	GLN	2.9
3	F9	70	ARG	2.9
3	I8	129	SER	2.9
3	K9	170	THR	2.9
3	L9	52	THR	2.9
3	Q9	121	GLN	2.9
3	R9	107	GLN	2.9
3	V9	68	VAL	2.9
3	V9	112	GLN	2.9
3	W8	146	GLN	2.9
3	39	204	VAL	2.9
3	49	52	THR	2.9
3	Z9	43	ALA	2.9
2	G4	49	ASP	2.9
3	K9	81	ASP	2.9
3	W9	53	ASP	2.9
3	G9	165	HIS	2.9
3	J8	42	ILE	2.9
3	U9	60	LYS	2.9
3	R9	179	TYR	2.9
3	Z8	172	TYR	2.9
3	Z9	48	ILE	2.9
3	K9	168	ASN	2.9
2	X2	69	GLU	2.9
3	Z8	97	GLU	2.9
3	19	138	GLU	2.9
3	R8	74	LEU	2.9
3	T9	141	PHE	2.9
3	Z9	141	PHE	2.9
3	19	166	LEU	2.9
3	C8	177	ARG	2.9
3	E8	182	GLY	2.9
3	K8	34	GLY	2.9
3	N8	28	GLY	2.9
3	R8	45	GLY	2.9
3	W8	27	ARG	2.9
3	Z9	149	GLY	2.9
3	18	45	GLY	2.9
3	K8	17	GLN	2.9
3	O8	68	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
3	P9	90	SER	2.9
3	S8	40	VAL	2.9
3	X9	32	VAL	2.9
3	X9	62	GLN	2.9
3	Z8	129	SER	2.9
3	Z9	90	SER	2.9
3	Z9	107	GLN	2.9
3	19	130	GLN	2.9
3	A8	43	ALA	2.9
3	R9	55	ALA	2.9
3	U9	71	ALA	2.9
3	W8	174	ALA	2.9
3	38	54	ALA	2.9
3	39	205	ALA	2.9
3	G9	114	ILE	2.9
2	Q4	49	ASP	2.9
2	22	49	ASP	2.9
3	J9	12	ASP	2.9
3	F8	165	HIS	2.9
3	G9	153	LEU	2.9
3	L9	79	HIS	2.9
3	P9	56	LEU	2.9
3	P9	63	PRO	2.9
3	Q9	69	GLU	2.9
3	S8	44	PRO	2.9
3	S9	195	GLU	2.9
3	U9	63	PRO	2.9
3	U9	126	ASN	2.9
3	39	38	LEU	2.9
2	D6	35	GLU	2.9
3	D9	195	GLU	2.9
3	E8	41	GLU	2.9
3	J9	29	PHE	2.9
3	K9	171	PRO	2.9
3	X9	141	PHE	2.9
3	G8	133	MET	2.9
1	I1	88	GLY	2.9
1	T1	61	SER	2.9
1	31	61	SER	2.9
3	38	27	ARG	2.9
3	A9	66	GLN	2.9
3	F9	112	GLN	2.9

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Mol	Chain	Res	Type	RSRZ
3	H9	62	GLN	2.9
3	J9	68	VAL	2.9
3	M9	130	GLN	2.9
3	N9	67	VAL	2.9
3	O9	164	VAL	2.9
3	P9	68	VAL	2.9
3	T8	204	VAL	2.9
3	W8	17	GLN	2.9
3	X8	35	GLN	2.9
3	Y9	17	GLN	2.9
3	Y9	130	GLN	2.9
3	I8	110	THR	2.9
3	L9	20	THR	2.9
3	D9	54	ALA	2.9
3	K9	158	ALA	2.9
3	M8	26	ALA	2.9
3	N9	181	ALA	2.9
3	R9	88	ALA	2.9
3	S8	26	ALA	2.9
3	U9	174	ALA	2.9
3	Y8	71	ALA	2.9
3	Z8	95	LYS	2.9
3	O9	198	ILE	2.9
3	Q8	42	ILE	2.9
3	S8	46	ILE	2.9
3	38	134	ILE	2.9
3	C8	74	LEU	2.9
3	G9	11	LEU	2.9
2	L6	49	ASP	2.9
3	F9	179	TYR	2.9
3	P9	120	TYR	2.9
3	S9	12	ASP	2.9
3	S9	120	TYR	2.9
3	U9	29	PHE	2.9
3	W9	21	PHE	2.9
3	A8	163	ASN	2.9
3	C9	78	HIS	2.9
3	F9	79	HIS	2.9
3	29	53	ASP	2.9
3	A9	100	GLU	2.9
3	D9	69	GLU	2.9
3	D9	192	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
3	H9	41	GLU	2.9
3	K8	133	MET	2.9
3	N9	33	PRO	2.9
3	P9	118	GLU	2.9
3	R9	97	GLU	2.9
3	R9	138	GLU	2.9
3	U8	133	MET	2.9
3	Z9	186	GLU	2.9
3	29	101	GLU	2.9
3	C9	6	ARG	2.9
3	T9	115	ARG	2.9
3	D9	67	VAL	2.9
3	F9	28	GLY	2.9
3	G8	73	GLY	2.9
3	G9	173	GLY	2.9
3	K8	15	GLN	2.9
3	N9	149	GLY	2.9
3	Q9	167	VAL	2.9
3	W9	164	VAL	2.9
3	19	202	SER	2.9
3	29	32	VAL	2.9
3	L9	60	LYS	2.9
3	Q9	59	THR	2.9
3	R9	52	THR	2.9
3	H9	154	ALA	2.9
3	R9	154	ALA	2.9
3	S8	43	ALA	2.9
3	S9	162	ALA	2.9
3	W9	151	ALA	2.9
3	29	161	ALA	2.9
3	D8	3	ILE	2.9
3	O9	187	ILE	2.9
3	O8	74	LEU	2.9
3	V8	30	LEU	2.9
3	49	21	PHE	2.9
2	B3	49	ASP	2.9
2	S6	49	ASP	2.9
3	K8	136	PRO	2.9
3	L9	63	PRO	2.9
3	R8	172	TYR	2.9
3	U9	172	TYR	2.9
3	V9	171	PRO	2.9

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Mol	Chain	Res	Type	RSRZ
3	W9	120	TYR	2.9
2	I3	69	GLU	2.9
3	A8	41	GLU	2.9
3	B8	79	HIS	2.9
3	F8	41	GLU	2.9
3	H9	100	GLU	2.9
3	O9	184	GLU	2.9
3	P8	128	ASN	2.9
3	P9	101	GLU	2.9
3	T8	79	HIS	2.9
3	T9	157	GLU	2.9
3	T9	184	GLU	2.9
3	X9	49	ASN	2.9
3	38	177	ARG	2.9
1	Y1	61	SER	2.9
3	A8	17	GLN	2.9
3	A9	62	GLN	2.9
3	A9	152	VAL	2.9
3	D8	32	VAL	2.9
3	O8	129	SER	2.9
3	P8	65	VAL	2.9
3	Y9	169	VAL	2.9
3	B8	39	TRP	2.9
3	O8	110	THR	2.9
3	W9	52	THR	2.9
3	Z8	39	TRP	2.9
3	B8	71	ALA	2.9
3	D9	119	ALA	2.9
3	S9	205	ALA	2.9
3	V9	197	ALA	2.9
3	W8	3	ILE	2.9
3	18	13	ALA	2.9
3	29	134	ILE	2.9
3	E8	135	LEU	2.9
3	T8	133	MET	2.9
3	D8	27	ARG	2.9
3	T9	72	TYR	2.9
3	T9	99	ARG	2.9
3	V9	72	TYR	2.9
2	C3	49	ASP	2.8
3	B9	53	ASP	2.8
3	K9	79	HIS	2.8

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Mol	Chain	Res	Type	RSRZ
3	P9	165	HIS	2.8
3	R9	79	HIS	2.8
3	N9	85	VAL	2.8
3	P9	61	VAL	2.8
3	S8	202	SER	2.8
3	S9	79	HIS	2.8
3	29	128	ASN	2.9
3	X9	12	ASP	2.8
3	39	159	GLU	2.9
2	X2	39	GLY	2.8
3	B9	131	GLY	2.8
3	F9	61	VAL	2.8
3	L8	28	GLY	2.8
3	M9	85	VAL	2.8
3	N8	68	VAL	2.8
3	U9	65	VAL	2.8
3	X8	67	VAL	2.8
3	Z8	65	VAL	2.8
3	49	65	VAL	2.8
3	D9	35	GLN	2.8
3	I9	130	GLN	2.8
3	N9	15	GLN	2.8
3	S8	3	ILE	2.8
3	U9	4	THR	2.8
3	Z9	3	ILE	2.8
3	B9	205	ALA	2.8
3	D9	71	ALA	2.8
3	F8	74	LEU	2.8
3	F9	75	LEU	2.8
3	F9	197	ALA	2.8
3	G9	116	ALA	2.8
3	I9	19	ALA	2.8
3	I9	181	ALA	2.8
3	Y9	135	LEU	2.8
3	Y9	193	ALA	2.8
3	Z9	122	THR	2.8
3	H9	80	PHE	2.8
3	I9	29	PHE	2.8
3	K9	127	ARG	2.8
3	S8	177	ARG	2.8
3	X8	177	ARG	2.8
3	B9	172	TYR	2.8

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Mol	Chain	Res	Type	RSRZ
3	J9	106	PRO	2.8
3	K9	136	PRO	2.8
3	Z9	179	TYR	2.8
3	29	60	LYS	2.8
2	F4	58	GLU	2.8
2	L6	69	GLU	2.8
3	A9	195	GLU	2.8
3	A9	200	SER	2.8
3	U9	183	SER	2.8
3	X9	118	GLU	2.8
3	39	51	VAL	2.8
2	C6	49	ASP	2.8
3	A9	35	GLN	2.8
3	J9	135	LEU	2.8
3	K9	35	GLN	2.8
3	K9	75	LEU	2.8
3	L9	82	GLN	2.8
3	P8	12	ASP	2.8
3	P9	45	GLY	2.8
3	Q8	137	GLY	2.8
3	Q9	34	GLY	2.8
3	S8	94	ASP	2.8
3	S9	34	GLY	2.8
3	U9	74	LEU	2.8
3	49	130	GLN	2.8
3	A9	196	ALA	2.8
3	I9	88	ALA	2.8
3	J8	43	ALA	2.8
3	L8	205	ALA	2.8
3	S9	47	ALA	2.8
3	49	162	ALA	2.8
3	O8	133	MET	2.8
3	R8	132	MET	2.8
3	S9	80	PHE	2.8
3	U9	109	MET	2.8
3	19	133	MET	2.8
3	E9	60	LYS	2.8
3	P9	6	ARG	2.8
3	J8	179	TYR	2.8
3	K8	179	TYR	2.8
3	Q9	120	TYR	2.8
3	B9	117	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
3	G9	198	ILE	2.8
3	L9	32	VAL	2.8
3	M8	65	VAL	2.8
3	N8	74	LEU	2.8
3	R8	129	SER	2.8
3	R8	163	ASN	2.8
3	V9	97	GLU	2.8
3	Y9	84	GLU	2.8
3	Z8	76	GLU	2.8
3	H9	78	HIS	2.8
3	M9	146	GLN	2.8
3	V9	79	HIS	2.8
1	H1	75	ASP	2.8
1	S1	49	ALA	2.8
3	A9	154	ALA	2.8
3	B9	94	ASP	2.8
3	E9	26	ALA	2.8
3	E9	119	ALA	2.8
3	J9	174	ALA	2.8
3	K9	181	ALA	2.8
3	R8	94	ASP	2.8
3	W9	170	THR	2.8
3	49	71	ALA	2.8
3	B8	141	PHE	2.8
3	X8	39	TRP	2.8
3	A8	27	ARG	2.8
3	P9	115	ARG	2.8
3	D9	44	PRO	2.8
3	I9	198	ILE	2.8
3	N9	72	TYR	2.8
3	T9	31	PRO	2.8
3	U8	134	ILE	2.8
3	W8	72	TYR	2.8
3	W9	134	ILE	2.8
3	B9	68	VAL	2.8
3	F9	65	VAL	2.8
3	K9	169	VAL	2.8
3	L8	129	SER	2.8
3	19	63	PRO	2.8
3	38	136	PRO	2.8
3	L8	201	VAL	2.8
3	M8	67	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
3	39	183	SER	2.8
3	49	51	VAL	2.8
2	M3	58	GLU	2.8
2	T7	58	GLU	2.8
3	C9	138	GLU	2.8
3	D9	123	GLN	2.8
3	F9	168	ASN	2.8
3	H9	118	GLU	2.8
3	J9	107	GLN	2.8
3	L8	73	GLY	2.8
3	N9	45	GLY	2.8
3	U9	49	ASN	2.8
3	V8	137	GLY	2.8
2	I6	2	ALA	2.8
3	B9	194	ALA	2.8
3	E9	170	THR	2.8
3	F8	43	ALA	2.8
3	H9	122	THR	2.8
3	J8	71	ALA	2.8
3	J9	54	ALA	2.8
3	L9	4	THR	2.8
3	L9	162	ALA	2.8
3	N9	145	THR	2.8
3	R9	26	ALA	2.8
3	U9	119	ALA	2.8
3	V9	20	THR	2.8
3	X9	4	THR	2.8
3	X9	174	ALA	2.8
3	Z9	21	PHE	2.8
3	39	20	THR	2.8
3	39	165	HIS	2.8
1	T1	90	ASP	2.8
2	E4	49	ASP	2.8
2	U6	49	ASP	2.8
2	U7	49	ASP	2.8
2	W4	49	ASP	2.8
3	O8	39	TRP	2.8
3	R9	6	ARG	2.8
3	Z9	74	LEU	2.8
3	E9	198	ILE	2.8
3	L9	48	ILE	2.8
3	N9	48	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
3	P9	92	ILE	2.8
3	Q8	3	ILE	2.8
3	Q9	3	ILE	2.8
3	S9	48	ILE	2.8
1	M1	61	SER	2.8
3	E9	32	VAL	2.8
3	I8	32	VAL	2.8
3	J9	31	PRO	2.8
3	K8	204	VAL	2.8
3	L9	106	PRO	2.8
3	Q9	65	VAL	2.8
3	U9	152	VAL	2.8
3	W9	136	PRO	2.8
3	V9	179	TYR	2.8
3	W9	172	TYR	2.8
2	T6	18	GLU	2.8
3	A9	144	GLU	2.8
3	D8	137	GLY	2.8
3	H9	15	GLN	2.8
3	I8	73	GLY	2.8
3	L9	89	GLY	2.8
3	L9	100	GLU	2.8
3	P9	69	GLU	2.8
3	Q9	76	GLU	2.8
3	Q9	118	GLU	2.8
3	S8	163	ASN	2.8
3	T8	130	GLN	2.8
3	T9	73	GLY	2.8
3	V9	144	GLU	2.8
3	W9	102	GLY	2.8
3	Z9	100	GLU	2.8
3	49	100	GLU	2.8
2	E5	2	ALA	2.8
3	G9	7	THR	2.8
3	G9	122	THR	2.8
3	K9	162	ALA	2.8
3	Q8	132	MET	2.8
3	T8	71	ALA	2.8
3	U8	13	ALA	2.8
3	X9	7	THR	2.8
2	A6	49	ASP	2.8
2	O4	49	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
2	R3	49	ASP	2.8
3	B8	94	ASP	2.8
3	J9	27	ARG	2.8
3	J9	103	ARG	2.8
3	T8	30	LEU	2.8
3	H9	46	ILE	2.8
3	T8	134	ILE	2.8
2	J3	93	PRO	2.8
3	F9	32	VAL	2.8
3	G9	51	VAL	2.8
3	H9	85	VAL	2.8
3	J8	68	VAL	2.8
3	O9	117	VAL	2.8
3	Q8	65	VAL	2.8
3	R8	67	VAL	2.8
3	R9	90	SER	2.8
3	V8	16	PRO	2.8
3	Y9	152	VAL	2.8
3	29	120	TYR	2.8
2	Q6	38	GLY	2.8
2	Q7	69	GLU	2.8
2	U4	68	GLY	2.8
3	A9	107	GLN	2.8
3	K9	144	GLU	2.8
3	N9	130	GLN	2.8
3	U8	132	MET	2.8
3	X8	133	MET	2.8
3	Z9	130	GLN	2.8
3	O9	26	ALA	2.8
3	U9	128	ASN	2.8
3	38	76	GLU	2.8
2	E7	2	ALA	2.8
3	D9	193	ALA	2.8
3	D9	196	ALA	2.8
3	F8	20	THR	2.8
3	F9	59	THR	2.8
3	K8	20	THR	2.8
3	N8	71	ALA	2.8
3	U9	196	ALA	2.8
3	V8	20	THR	2.8
3	Y8	25	THR	2.8
3	29	4	THR	2.8

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Mol	Chain	Res	Type	RSRZ
3	A9	79	HIS	2.7
3	F9	165	HIS	2.7
3	G9	79	HIS	2.7
3	G9	103	ARG	2.7
3	I9	50	ARG	2.7
3	49	74	LEU	2.7
1	E1	45	ASP	2.7
1	H1	45	ASP	2.7
1	21	90	ASP	2.7
2	R5	84	ASP	2.7
3	H9	3	ILE	2.7
3	K9	53	ASP	2.7
3	Q8	94	ASP	2.7
3	Q9	81	ASP	2.7
3	Q9	94	ASP	2.7
3	V8	42	ILE	2.7
3	19	198	ILE	2.7
3	S8	39	TRP	2.7
1	Z1	61	SER	2.7
3	D8	65	VAL	2.7
3	H9	106	PRO	2.7
3	L9	65	VAL	2.7
3	S8	129	SER	2.7
3	U9	40	VAL	2.7
3	Y9	31	PRO	2.7
3	F9	175	PHE	2.7
3	H9	60	LYS	2.7
3	N8	172	TYR	2.7
3	Z9	80	PHE	2.7
3	38	175	PHE	2.7
3	R9	82	GLN	2.7
3	49	150	TYR	2.7
2	I7	40	GLY	2.7
3	B8	116	ALA	2.7
3	B9	69	GLU	2.7
3	F9	64	ALA	2.7
3	G9	186	GLU	2.7
3	H8	159	GLU	2.7
3	O9	69	GLU	2.7
3	S9	157	GLU	2.7
3	T8	73	GLY	2.7
3	T8	192	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
3	T9	84	GLU	2.7
3	V9	55	ALA	2.7
3	V9	162	ALA	2.7
3	X9	100	GLU	2.7
3	39	28	GLY	2.7
3	J9	205	ALA	2.7
3	B9	145	THR	2.7
3	Y8	163	ASN	2.7
3	Z9	128	ASN	2.7
3	J9	115	ARG	2.7
3	M9	177	ARG	2.7
3	O9	96	LEU	2.7
3	R9	30	LEU	2.7
3	U9	75	LEU	2.7
3	U9	135	LEU	2.7
3	38	30	LEU	2.7
3	48	74	LEU	2.7
3	A8	111	HIS	2.7
2	P3	49	ASP	2.7
2	33	49	ASP	2.7
3	S9	81	ASP	2.7
3	U8	188	ASP	2.7
3	Y8	81	ASP	2.7
3	Z8	12	ASP	2.7
3	B9	204	VAL	2.7
3	X9	183	SER	2.7
3	B8	10	PHE	2.7
3	K8	132	MET	2.7
3	M9	44	PRO	2.7
3	N8	132	MET	2.7
3	Y8	32	VAL	2.7
3	V9	60	LYS	2.7
3	X9	16	PRO	2.7
3	39	175	PHE	2.7
1	V1	88	GLY	2.7
2	Z7	68	GLY	2.7
3	B9	35	GLN	2.7
3	D9	179	TYR	2.7
3	F9	72	TYR	2.7
3	G9	35	GLN	2.7
3	H9	130	GLN	2.7
3	I9	62	GLN	2.7

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Mol	Chain	Res	Type	RSRZ
2	W2	9	GLU	2.7
3	A9	185	ALA	2.7
3	A9	20	THR	2.7
3	E8	74	LEU	2.7
3	E9	138	GLU	2.7
3	G9	155	ALA	2.7
3	J8	159	GLU	2.7
3	J9	166	LEU	2.7
3	K9	189	ALA	2.7
3	N9	43	ALA	2.7
3	R9	185	ALA	2.7
3	S9	196	ALA	2.7
3	U8	45	GLY	2.7
3	X9	185	ALA	2.7
3	N9	7	THR	2.7
3	V9	52	THR	2.7
3	W9	97	GLU	2.7
3	Y8	100	GLU	2.7
3	C8	128	ASN	2.7
3	H9	6	ARG	2.7
3	28	70	ARG	2.7
3	29	52	THR	2.7
3	39	126	ASN	2.7
3	N9	134	ILE	2.7
2	E6	49	ASP	2.7
2	F4	49	ASP	2.7
3	A9	68	VAL	2.7
3	C8	39	TRP	2.7
3	B9	21	PHE	2.7
3	E8	29	PHE	2.7
3	E9	21	PHE	2.7
3	E9	117	VAL	2.7
3	I9	40	VAL	2.7
3	M9	60	LYS	2.7
3	N9	108	VAL	2.7
3	U8	80	PHE	2.7
3	U8	108	VAL	2.7
3	Z8	133	MET	2.7
3	B9	171	PRO	2.7
3	G9	171	PRO	2.7
3	L9	171	PRO	2.7
3	W8	33	PRO	2.7

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Mol	Chain	Res	Type	RSRZ
3	C9	146	GLN	2.7
2	D6	2	ALA	2.7
3	E8	13	ALA	2.7
3	E8	45	GLY	2.7
3	I9	166	LEU	2.7
3	S8	74	LEU	2.7
3	T9	86	LEU	2.7
3	U9	15	GLN	2.7
3	V9	166	LEU	2.7
3	F9	190	ALA	2.7
3	J9	191	ALA	2.7
3	L9	116	ALA	2.7
3	M9	119	ALA	2.7
3	N9	161	ALA	2.7
3	U9	194	ALA	2.7
3	19	172	TYR	2.7
3	29	119	ALA	2.7
2	W5	58	GLU	2.7
3	D9	59	THR	2.7
3	F9	101	GLU	2.7
3	G9	170	THR	2.7
3	H9	4	THR	2.7
3	R9	100	GLU	2.7
3	U8	100	GLU	2.7
3	I8	134	ILE	2.7
3	R9	187	ILE	2.7
3	U9	122	THR	2.7
3	49	91	THR	2.7
3	Z9	49	ASN	2.7
3	J8	24	LYS	2.7
3	W8	165	HIS	2.7
1	L1	61	SER	2.7
3	I9	139	SER	2.7
3	B8	65	VAL	2.7
3	E8	67	VAL	2.7
3	F9	152	VAL	2.7
3	I9	61	VAL	2.7
3	N9	68	VAL	2.7
3	O8	65	VAL	2.7
3	U9	169	VAL	2.7
3	W8	67	VAL	2.7
3	W9	32	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
3	W9	175	PHE	2.7
3	Y8	201	VAL	2.7
3	28	32	VAL	2.7
2	43	49	ASP	2.7
3	H8	94	ASP	2.7
3	K8	39	TRP	2.7
3	B8	106	PRO	2.7
3	H8	44	PRO	2.7
3	J9	63	PRO	2.7
3	S9	153	LEU	2.7
3	T9	171	PRO	2.7
3	18	44	PRO	2.7
3	19	106	PRO	2.7
3	K9	62	GLN	2.7
3	N9	62	GLN	2.7
2	K3	2	ALA	2.7
2	T3	2	ALA	2.7
2	Y3	2	ALA	2.7
3	E9	151	ALA	2.7
3	E9	174	ALA	2.7
3	I8	149	GLY	2.7
3	L9	158	ALA	2.7
3	L9	193	ALA	2.7
3	Q8	177	ARG	2.7
3	Q9	87	ALA	2.7
3	R9	151	ALA	2.7
3	S9	36	ALA	2.7
3	T8	70	ARG	2.7
3	U8	149	GLY	2.7
3	V9	6	ARG	2.7
3	49	116	ALA	2.7
3	B9	92	ILE	2.7
2	O2	9	GLU	2.7
2	X2	58	GLU	2.7
3	A9	4	THR	2.7
3	I9	138	GLU	2.7
3	K9	100	GLU	2.7
3	18	159	GLU	2.7
3	29	186	GLU	2.7
3	X9	156	ASN	2.7
1	S1	95	LYS	2.7
3	Z9	57	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
3	E9	29	PHE	2.7
3	F9	202	SER	2.7
3	K9	21	PHE	2.7
3	V9	78	HIS	2.7
3	V9	202	SER	2.7
3	D9	153	LEU	2.7
3	H8	30	LEU	2.7
3	H9	5	LEU	2.7
3	I8	135	LEU	2.7
3	O9	61	VAL	2.7
2	X6	49	ASP	2.7
3	A8	39	TRP	2.7
3	F9	62	GLN	2.7
3	G8	70	ARG	2.7
3	G8	94	ASP	2.7
3	J8	81	ASP	2.7
3	J9	94	ASP	2.7
3	P9	50	ARG	2.7
3	Q9	53	ASP	2.7
3	X9	63	PRO	2.7
3	39	39	TRP	2.7
1	31	34	GLY	2.7
2	S7	2	ALA	2.7
2	Z3	20	ALA	2.7
3	B9	150	TYR	2.7
3	C9	26	ALA	2.7
3	E9	3	ILE	2.7
3	O9	19	ALA	2.7
3	O9	71	ALA	2.7
3	P9	72	TYR	2.7
3	P9	150	TYR	2.7
3	Q9	149	GLY	2.7
3	R8	116	ALA	2.7
3	R9	150	TYR	2.7
3	S8	34	GLY	2.7
3	T9	87	ALA	2.7
3	U8	42	ILE	2.7
3	19	48	ILE	2.7
3	49	66	GLN	2.7
3	F9	87	ALA	2.7
3	F9	185	ALA	2.7
3	G9	54	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
3	U9	162	ALA	2.7
3	U9	197	ALA	2.7
3	W9	150	TYR	2.7
3	39	191	ALA	2.7
3	49	55	ALA	2.7
2	E5	58	GLU	2.7
3	B9	192	GLU	2.7
3	K9	145	THR	2.7
3	S9	7	THR	2.7
3	U9	195	GLU	2.7
3	V9	186	GLU	2.7
3	W9	159	GLU	2.7
3	Y9	192	GLU	2.7
3	H9	24	LYS	2.7
3	P8	95	LYS	2.7
3	P9	128	ASN	2.7
3	S9	60	LYS	2.7
3	Y9	126	ASN	2.7
3	49	126	ASN	2.7
3	N9	29	PHE	2.7
3	S9	141	PHE	2.7
1	C1	61	SER	2.7
1	P1	61	SER	2.7
3	B9	90	SER	2.7
3	H9	90	SER	2.7
3	T8	74	LEU	2.7
3	U8	74	LEU	2.7
3	39	90	SER	2.7
3	D9	51	VAL	2.6
3	G8	67	VAL	2.6
3	I9	165	HIS	2.6
3	X9	51	VAL	2.6
3	B9	31	PRO	2.6
3	C8	106	PRO	2.6
3	O8	134	ILE	2.6
3	O8	177	ARG	2.6
3	38	33	PRO	2.6
3	C9	35	GLN	2.6
3	C9	62	GLN	2.6
3	N8	39	TRP	2.6
2	A5	39	GLY	2.6
2	H2	49	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
2	K7	2	ALA	2.6
3	K8	81	ASP	2.6
3	L9	81	ASP	2.6
3	M8	131	GLY	2.6
3	N9	131	GLY	2.6
3	N9	197	ALA	2.6
3	Q9	116	ALA	2.6
3	R9	13	ALA	2.6
3	R9	54	ALA	2.6
3	T9	205	ALA	2.6
3	W8	13	ALA	2.6
3	Y8	174	ALA	2.6
3	Z8	64	ALA	2.6
3	19	54	ALA	2.6
3	28	26	ALA	2.6
3	28	119	ALA	2.6
3	28	131	GLY	2.6
3	Q9	172	TYR	2.6
3	X9	72	TYR	2.6
3	X9	179	TYR	2.6
3	D9	20	THR	2.6
3	Y9	122	THR	2.6
2	H6	69	GLU	2.6
3	G8	76	GLU	2.6
3	G9	184	GLU	2.6
3	L9	138	GLU	2.6
3	N9	184	GLU	2.6
3	Y9	41	GLU	2.6
3	Z8	157	GLU	2.6
3	18	133	MET	2.6
3	D9	21	PHE	2.6
3	M9	80	PHE	2.6
3	T9	29	PHE	2.6
3	Z9	166	LEU	2.6
3	J8	129	SER	2.6
3	L9	183	SER	2.6
3	B8	67	VAL	2.6
3	J9	117	VAL	2.6
3	O9	67	VAL	2.6
3	P8	32	VAL	2.6
3	S9	152	VAL	2.6
3	T8	65	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
3	U8	152	VAL	2.6
3	19	204	VAL	2.6
3	H9	124	ILE	2.6
3	L8	111	HIS	2.6
3	R9	92	ILE	2.6
3	R9	113	ILE	2.6
3	T8	165	HIS	2.6
3	T9	6	ARG	2.6
3	U8	70	ARG	2.6
3	B9	147	PRO	2.6
3	D9	31	PRO	2.6
3	X8	136	PRO	2.6
2	N5	2	ALA	2.6
3	E8	71	ALA	2.6
3	J8	28	GLY	2.6
3	K9	88	ALA	2.6
3	N9	82	GLN	2.6
3	O9	43	ALA	2.6
3	W9	107	GLN	2.6
3	Q9	28	GLY	2.6
3	Z9	34	GLY	2.6
3	19	36	ALA	2.6
3	29	71	ALA	2.6
3	39	193	ALA	2.6
1	41	90	ASP	2.6
2	B7	49	ASP	2.6
3	A8	179	TYR	2.6
3	P9	59	THR	2.6
3	R9	25	THR	2.6
3	28	94	ASP	2.6
3	29	150	TYR	2.6
2	G5	69	GLU	2.6
2	H3	69	GLU	2.6
3	F8	76	GLU	2.6
3	O9	144	GLU	2.6
3	S9	97	GLU	2.6
3	U9	76	GLU	2.6
3	W9	101	GLU	2.6
3	49	76	GLU	2.6
3	J8	175	PHE	2.6
3	M9	10	PHE	2.6
3	18	74	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
3	V9	126	ASN	2.6
3	V9	128	ASN	2.6
3	J9	202	SER	2.6
3	Q9	90	SER	2.6
3	S9	200	SER	2.6
3	V8	129	SER	2.6
3	E8	204	VAL	2.6
3	O9	40	VAL	2.6
3	P9	85	VAL	2.6
3	29	65	VAL	2.6
3	38	40	VAL	2.6
3	A9	6	ARG	2.6
3	K9	92	ILE	2.6
3	K9	124	ILE	2.6
3	O9	3	ILE	2.6
3	T9	198	ILE	2.6
3	W9	6	ARG	2.6
3	38	70	ARG	2.6
3	39	48	ILE	2.6
3	A9	106	PRO	2.6
3	G8	171	PRO	2.6
3	N8	33	PRO	2.6
3	P8	62	GLN	2.6
3	R8	62	GLN	2.6
3	S9	63	PRO	2.6
3	C8	174	ALA	2.6
3	F8	34	GLY	2.6
3	F9	47	ALA	2.6
3	G9	87	ALA	2.6
3	I9	205	ALA	2.6
3	J8	54	ALA	2.6
3	Y9	62	GLN	2.6
3	L8	45	GLY	2.6
3	M8	34	GLY	2.6
3	N9	28	GLY	2.6
3	O8	45	GLY	2.6
3	X8	149	GLY	2.6
3	X9	55	ALA	2.6
3	Z9	190	ALA	2.6
3	39	181	ALA	2.6
3	49	88	ALA	2.6
3	G9	94	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
3	I8	74	LEU	2.6
3	L9	110	THR	2.6
3	X8	132	MET	2.6
2	G3	49	ASP	2.6
2	M6	49	ASP	2.6
2	I7	69	GLU	2.6
2	K3	58	GLU	2.6
3	D9	10	PHE	2.6
3	I9	101	GLU	2.6
3	L9	144	GLU	2.6
3	T8	184	GLU	2.6
3	V9	21	PHE	2.6
3	W9	141	PHE	2.6
3	28	159	GLU	2.6
3	A9	163	ASN	2.6
3	F9	128	ASN	2.6
3	G9	139	SER	2.6
3	R9	49	ASN	2.6
3	T9	126	ASN	2.6
1	Y1	68	VAL	2.6
3	M9	51	VAL	2.6
3	A9	70	ARG	2.6
3	E8	177	ARG	2.6
3	E9	6	ARG	2.6
3	I8	177	ARG	2.6
3	T8	42	ILE	2.6
3	Z9	46	ILE	2.6
3	Q8	24	LYS	2.6
2	I7	2	ALA	2.6
2	25	74	HIS	2.6
3	B9	62	GLN	2.6
3	B9	106	PRO	2.6
3	C9	43	ALA	2.6
3	E9	79	HIS	2.6
3	I8	33	PRO	2.6
3	J9	147	PRO	2.6
3	K8	205	ALA	2.6
3	L8	165	HIS	2.6
3	P9	158	ALA	2.6
3	Q9	58	ALA	2.6
3	R9	161	ALA	2.6
3	T9	146	GLN	2.6

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Mol	Chain	Res	Type	RSRZ
3	Y9	146	GLN	2.6
3	39	33	PRO	2.6
3	H8	34	GLY	2.6
3	I9	56	LEU	2.6
3	R9	96	LEU	2.6
3	S8	30	LEU	2.6
3	38	74	LEU	2.6
3	F8	7	THR	2.6
3	N8	179	TYR	2.6
3	P9	172	TYR	2.6
3	V9	170	THR	2.6
3	Y9	7	THR	2.6
3	28	179	TYR	2.6
2	X7	49	ASP	2.6
3	H9	138	GLU	2.6
3	J8	69	GLU	2.6
3	L8	94	ASP	2.6
3	L8	192	GLU	2.6
3	M9	53	ASP	2.6
3	R8	41	GLU	2.6
3	S8	76	GLU	2.6
3	T8	69	GLU	2.6
3	V8	184	GLU	2.6
3	39	76	GLU	2.6
3	C9	90	SER	2.6
3	F8	134	ILE	2.6
3	N9	156	ASN	2.6
3	P9	48	ILE	2.6
3	S9	128	ASN	2.6
3	Y9	49	ASN	2.6
3	39	129	SER	2.6
3	G9	85	VAL	2.6
3	I9	51	VAL	2.6
3	T8	27	ARG	2.6
3	Z8	40	VAL	2.6
2	23	2	ALA	2.6
3	C8	54	ALA	2.6
3	E8	17	GLN	2.6
3	H9	43	ALA	2.6
3	Q9	62	GLN	2.6
3	R9	62	GLN	2.6
3	R9	71	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
3	R9	132	MET	2.6
3	T9	193	ALA	2.6
3	W9	96	LEU	2.6
3	W9	119	ALA	2.6
3	X9	13	ALA	2.6
3	Z9	171	PRO	2.6
3	38	135	LEU	2.6
3	39	31	PRO	2.6
3	48	171	PRO	2.6
3	C8	137	GLY	2.6
3	D9	45	GLY	2.6
3	G8	28	GLY	2.6
3	I9	137	GLY	2.6
3	O8	28	GLY	2.6
3	P9	89	GLY	2.6
3	B9	7	THR	2.6
3	F9	145	THR	2.6
3	N8	8	TYR	2.6
3	N9	4	THR	2.6
3	O9	110	THR	2.6
3	X8	20	THR	2.6
3	Y9	72	TYR	2.6
3	Z9	25	THR	2.6
3	U8	39	TRP	2.6
2	Y4	35	GLU	2.6
2	Y7	69	GLU	2.6
2	32	9	GLU	2.6
3	E8	76	GLU	2.6
3	G9	159	GLU	2.6
3	I9	157	GLU	2.6
3	L9	90	SER	2.6
3	M9	48	ILE	2.6
3	N9	101	GLU	2.6
3	O9	118	GLU	2.6
3	W9	186	GLU	2.6
3	38	69	GLU	2.6
1	V1	75	ASP	2.6
3	B9	81	ASP	2.6
3	U9	202	SER	2.6
3	V9	65	VAL	2.6
3	W9	27	ARG	2.6
3	39	50	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
3	49	94	ASP	2.6
3	A8	68	VAL	2.6
3	J8	163	ASN	2.6
3	M8	108	VAL	2.6
3	R9	57	LYS	2.6
3	48	95	LYS	2.6
3	A8	132	MET	2.6
3	B9	5	LEU	2.6
3	E9	109	MET	2.6
3	R9	153	LEU	2.6
3	Z9	56	LEU	2.6
2	A5	93	PRO	2.6
3	C9	47	ALA	2.6
3	D8	35	GLN	2.6
3	J8	136	PRO	2.6
3	K9	119	ALA	2.6
3	K9	146	GLN	2.6
3	K9	155	ALA	2.6
3	L9	35	GLN	2.6
3	O9	63	PRO	2.6
3	T8	13	ALA	2.6
3	X9	26	ALA	2.6
3	39	54	ALA	2.6
3	B9	89	GLY	2.6
3	I9	102	GLY	2.6
3	48	34	GLY	2.6
3	C8	79	HIS	2.5
3	V9	7	THR	2.5
3	F9	187	ILE	2.5
3	H9	113	ILE	2.5
3	Z9	124	ILE	2.5
2	E5	69	GLU	2.5
3	A8	76	GLU	2.5
3	F9	69	GLU	2.5
3	F9	84	GLU	2.5
3	H8	200	SER	2.5
3	L8	60	LYS	2.5
3	M9	27	ARG	2.5
3	M9	184	GLU	2.5
3	P8	159	GLU	2.5
3	Q9	37	SER	2.5
3	V9	183	SER	2.5

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Mol	Chain	Res	Type	RSRZ
3	X9	184	GLU	2.5
3	Y8	76	GLU	2.5
1	V1	68	VAL	2.5
3	A9	201	VAL	2.5
3	B9	108	VAL	2.5
3	E9	164	VAL	2.5
3	H9	169	VAL	2.5
3	N9	77	VAL	2.5
3	S8	108	VAL	2.5
1	E1	90	ASP	2.5
3	N9	126	ASN	2.5
3	R9	156	ASN	2.5
3	Y9	53	ASP	2.5
3	E8	96	LEU	2.5
3	Q9	166	LEU	2.5
3	U8	135	LEU	2.5
2	T6	2	ALA	2.5
2	Y7	2	ALA	2.5
3	E8	35	GLN	2.5
3	E9	130	GLN	2.5
3	H9	29	PHE	2.5
3	K8	54	ALA	2.5
3	K9	194	ALA	2.5
3	O9	181	ALA	2.5
3	S9	185	ALA	2.5
3	T9	154	ALA	2.5
3	V8	171	PRO	2.5
3	X8	33	PRO	2.5
3	Z9	197	ALA	2.5
3	19	19	ALA	2.5
3	19	121	GLN	2.5
2	Q7	68	GLY	2.5
2	X5	40	GLY	2.5
3	G9	131	GLY	2.5
3	I8	34	GLY	2.5
3	T8	137	GLY	2.5
3	V8	45	GLY	2.5
3	X8	28	GLY	2.5
3	E8	134	ILE	2.5
3	O9	122	THR	2.5
3	S8	25	THR	2.5
3	18	134	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
3	29	46	ILE	2.5
3	39	92	ILE	2.5
3	G8	179	TYR	2.5
3	J9	179	TYR	2.5
3	P9	179	TYR	2.5
3	Z8	120	TYR	2.5
1	D1	61	SER	2.5
3	G8	27	ARG	2.5
3	G9	37	SER	2.5
3	J8	177	ARG	2.5
3	X8	27	ARG	2.5
3	X8	70	ARG	2.5
3	Y8	27	ARG	2.5
3	28	177	ARG	2.5
2	L6	9	GLU	2.5
2	U3	69	GLU	2.5
2	17	69	GLU	2.5
3	A8	204	VAL	2.5
3	B9	41	GLU	2.5
3	B9	101	GLU	2.5
3	G8	159	GLU	2.5
3	G9	169	VAL	2.5
3	J8	67	VAL	2.5
3	J9	118	GLU	2.5
3	K9	167	VAL	2.5
3	N9	201	VAL	2.5
3	Q8	41	GLU	2.5
3	Q9	192	GLU	2.5
3	S9	101	GLU	2.5
3	U9	184	GLU	2.5
3	X8	68	VAL	2.5
3	Y9	167	VAL	2.5
3	29	76	GLU	2.5
2	F3	49	ASP	2.5
3	F9	156	ASN	2.5
3	G8	132	MET	2.5
3	O8	12	ASP	2.5
3	S8	128	ASN	2.5
3	T9	128	ASN	2.5
3	V9	81	ASP	2.5
3	29	168	ASN	2.5
3	39	132	MET	2.5

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Mol	Chain	Res	Type	RSRZ
3	48	12	ASP	2.5
2	G7	2	ALA	2.5
3	A9	197	ALA	2.5
3	B9	82	GLN	2.5
3	B9	87	ALA	2.5
3	G9	181	ALA	2.5
3	I9	55	ALA	2.5
3	K9	205	ALA	2.5
3	N9	47	ALA	2.5
3	P9	62	GLN	2.5
3	U9	31	PRO	2.5
3	U9	161	ALA	2.5
3	W9	15	GLN	2.5
3	X9	112	GLN	2.5
3	29	15	GLN	2.5
3	39	141	PHE	2.5
2	G4	39	GLY	2.5
3	H8	28	GLY	2.5
3	Q8	34	GLY	2.5
3	R8	137	GLY	2.5
3	R8	149	GLY	2.5
3	X9	45	GLY	2.5
3	J9	198	ILE	2.5
3	O8	3	ILE	2.5
3	G9	59	THR	2.5
3	N9	170	THR	2.5
3	N9	177	ARG	2.5
3	V9	165	HIS	2.5
3	D9	183	SER	2.5
3	I9	183	SER	2.5
3	J9	183	SER	2.5
3	K9	172	TYR	2.5
3	R9	37	SER	2.5
1	41	68	VAL	2.5
2	F6	18	GLU	2.5
2	X6	69	GLU	2.5
3	A9	11	LEU	2.5
3	C8	152	VAL	2.5
3	D9	104	LEU	2.5
3	E9	186	GLU	2.5
3	F9	138	GLU	2.5
3	H9	104	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
3	M9	144	GLU	2.5
3	N8	69	GLU	2.5
3	Q8	74	LEU	2.5
3	T8	108	VAL	2.5
3	U9	144	GLU	2.5
3	W9	201	VAL	2.5
3	Y8	67	VAL	2.5
3	39	96	LEU	2.5
3	39	100	GLU	2.5
3	B8	133	MET	2.5
3	C8	132	MET	2.5
3	18	132	MET	2.5
3	Q9	126	ASN	2.5
3	19	128	ASN	2.5
2	E2	84	ASP	2.5
2	U4	49	ASP	2.5
3	C8	12	ASP	2.5
3	H9	94	ASP	2.5
3	N8	29	PHE	2.5
3	X9	53	ASP	2.5
3	18	10	PHE	2.5
2	M3	2	ALA	2.5
2	O7	2	ALA	2.5
3	C8	33	PRO	2.5
3	D9	15	GLN	2.5
3	G9	148	ALA	2.5
3	K9	151	ALA	2.5
3	O9	205	ALA	2.5
3	O8	33	PRO	2.5
3	O9	33	PRO	2.5
3	P8	35	GLN	2.5
3	S8	33	PRO	2.5
3	U9	130	GLN	2.5
3	V9	43	ALA	2.5
3	Z8	43	ALA	2.5
3	F8	33	PRO	2.5
3	I9	44	PRO	2.5
3	C9	34	GLY	2.5
3	C9	60	LYS	2.5
3	D8	46	ILE	2.5
3	I8	45	GLY	2.5
3	L8	42	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
3	L9	73	GLY	2.5
3	M8	95	LYS	2.5
3	S9	131	GLY	2.5
3	U9	9	ILE	2.5
3	W9	48	ILE	2.5
3	18	149	GLY	2.5
3	38	73	GLY	2.5
3	A9	7	THR	2.5
3	B9	6	ARG	2.5
3	D8	177	ARG	2.5
3	F9	25	THR	2.5
3	G8	177	ARG	2.5
3	M9	52	THR	2.5
3	Q9	91	THR	2.5
3	W9	59	THR	2.5
3	B8	72	TYR	2.5
3	H8	111	HIS	2.5
3	I9	172	TYR	2.5
3	M8	179	TYR	2.5
3	P9	79	HIS	2.5
3	R9	56	LEU	2.5
3	38	150	TYR	2.5
3	38	179	TYR	2.5
3	E8	68	VAL	2.5
3	F8	204	VAL	2.5
3	Q9	67	VAL	2.5
3	V8	65	VAL	2.5
2	I3	9	GLU	2.5
2	I5	30	GLU	2.5
2	34	58	GLU	2.5
3	A9	69	GLU	2.5
3	J9	184	GLU	2.5
3	P8	192	GLU	2.5
3	R9	76	GLU	2.5
3	R9	101	GLU	2.5
3	S8	144	GLU	2.5
3	Y8	192	GLU	2.5
3	J9	175	PHE	2.5
3	R9	175	PHE	2.5
2	Q3	2	ALA	2.5
2	16	49	ASP	2.5
3	B9	66	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
3	E8	95	LYS	2.5
3	E9	53	ASP	2.5
3	F9	162	ALA	2.5
3	G9	82	GLN	2.5
3	F8	31	PRO	2.5
3	F8	171	PRO	2.5
3	I8	198	ILE	2.5
3	K9	82	GLN	2.5
3	M9	162	ALA	2.5
3	N9	94	ASP	2.5
3	S9	62	GLN	2.5
3	O9	31	PRO	2.5
3	Q9	46	ILE	2.5
3	V9	58	ALA	2.5
3	Y9	26	ALA	2.5
3	18	3	ILE	2.5
3	19	62	GLN	2.5
3	M9	136	PRO	2.5
3	28	81	ASP	2.5
2	G4	68	GLY	2.5
3	J9	149	GLY	2.5
3	L8	131	GLY	2.5
3	X9	149	GLY	2.5
3	A9	127	ARG	2.5
3	B9	115	ARG	2.5
3	G8	25	THR	2.5
3	J9	110	THR	2.5
3	K9	59	THR	2.5
3	S9	4	THR	2.5
3	T9	30	LEU	2.5
3	19	135	LEU	2.5
3	N9	120	TYR	2.5
3	P9	133	MET	2.5
3	W9	78	HIS	2.5
2	M2	58	GLU	2.5
2	14	69	GLU	2.5
2	43	69	GLU	2.5
3	C9	118	GLU	2.5
3	D8	97	GLU	2.5
3	Z9	118	GLU	2.5
3	49	175	PHE	2.5
3	C8	24	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
3	C9	168	ASN	2.5
3	E9	168	ASN	2.5
3	I9	49	ASN	2.5
3	P9	114	ILE	2.5
3	S9	168	ASN	2.5
3	Y8	24	LYS	2.5
3	F9	196	ALA	2.5
3	G8	35	GLN	2.5
3	I9	43	ALA	2.5
3	M9	55	ALA	2.5
3	Q8	35	GLN	2.5
3	Q9	54	ALA	2.5
3	S9	71	ALA	2.5
3	Y8	205	ALA	2.5
3	Z8	146	GLN	2.5
3	39	13	ALA	2.5
3	49	119	ALA	2.5
3	F9	44	PRO	2.5
3	H9	33	PRO	2.5
3	U9	44	PRO	2.5
3	X9	106	PRO	2.5
2	G6	49	ASP	2.5
2	35	84	ASP	2.5
3	B9	28	GLY	2.5
3	C9	99	ARG	2.5
3	D9	18	LEU	2.5
3	D9	53	ASP	2.5
3	G9	53	ASP	2.5
3	H8	70	ARG	2.5
3	N9	6	ARG	2.5
3	O8	137	GLY	2.5
3	O9	102	GLY	2.5
3	P8	177	ARG	2.5
3	R9	45	GLY	2.5
3	Z8	30	LEU	2.5
3	D9	145	THR	2.5
3	E8	4	THR	2.5
3	S8	20	THR	2.5
3	U9	59	THR	2.5
3	H9	37	SER	2.5
3	V9	109	MET	2.5
3	Z8	202	SER	2.5

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Mol	Chain	Res	Type	RSRZ
3	E9	169	VAL	2.5
3	L9	68	VAL	2.5
3	T8	67	VAL	2.5
3	W9	68	VAL	2.5
3	D9	72	TYR	2.5
3	O9	8	TYR	2.5
2	A5	58	GLU	2.4
2	D5	58	GLU	2.4
2	N3	58	GLU	2.4
3	C9	21	PHE	2.4
3	D8	175	PHE	2.4
3	O8	165	HIS	2.4
3	V8	100	GLU	2.4
3	B8	134	ILE	2.4
3	B9	9	ILE	2.4
3	D9	3	ILE	2.4
3	S9	187	ILE	2.4
2	J7	2	ALA	2.4
3	A9	174	ALA	2.4
3	D9	126	ASN	2.4
3	B9	135	LEU	2.4
3	E8	82	GLN	2.4
3	E9	66	GLN	2.4
3	E9	189	ALA	2.4
3	E9	194	ALA	2.4
3	F9	19	ALA	2.4
3	F9	56	LEU	2.4
3	F9	74	LEU	2.4
3	H8	62	GLN	2.4
3	I8	26	ALA	2.4
3	O9	87	ALA	2.4
3	P9	87	ALA	2.4
3	W9	71	ALA	2.4
3	Y9	119	ALA	2.4
3	Z9	146	GLN	2.4
3	19	35	GLN	2.4
3	39	43	ALA	2.4
3	39	158	ALA	2.4
3	48	43	ALA	2.4
3	F9	50	ARG	2.4
3	L8	70	ARG	2.4
3	L9	16	PRO	2.4

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Mol	Chain	Res	Type	RSRZ
3	N9	14	LEU	2.4
3	N9	135	LEU	2.4
3	29	70	ARG	2.4
2	S5	90	GLY	2.4
3	F8	23	GLY	2.4
3	K9	102	GLY	2.4
3	48	131	GLY	2.4
2	M7	49	ASP	2.4
2	Z6	49	ASP	2.4
3	K9	12	ASP	2.4
3	I9	202	SER	2.4
3	X9	20	THR	2.4
3	R9	117	VAL	2.4
3	19	67	VAL	2.4
3	B9	29	PHE	2.4
3	D8	141	PHE	2.4
3	H9	172	TYR	2.4
3	J9	8	TYR	2.4
3	S9	21	PHE	2.4
2	W7	69	GLU	2.4
3	B9	159	GLU	2.4
3	C9	192	GLU	2.4
3	H9	184	GLU	2.4
3	K8	192	GLU	2.4
3	N9	157	GLU	2.4
3	S9	3	ILE	2.4
3	W9	100	GLU	2.4
3	X9	134	ILE	2.4
3	B8	74	LEU	2.4
3	G9	58	ALA	2.4
3	H8	26	ALA	2.4
3	J8	96	LEU	2.4
3	C8	130	GLN	2.4
3	J9	197	ALA	2.4
3	K9	190	ALA	2.4
3	P9	174	ALA	2.4
3	S9	181	ALA	2.4
3	X8	74	LEU	2.4
3	V9	62	GLN	2.4
3	V9	99	ARG	2.4
3	V9	163	ASN	2.4
3	W8	126	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
3	19	71	ALA	2.4
3	48	13	ALA	2.4
3	R9	50	ARG	2.4
3	W9	127	ARG	2.4
3	D9	106	PRO	2.4
3	N9	44	PRO	2.4
2	P7	88	GLY	2.4
2	Q4	39	GLY	2.4
3	Q8	45	GLY	2.4
3	Q9	131	GLY	2.4
3	S8	131	GLY	2.4
3	X9	109	MET	2.4
1	F1	61	SER	2.4
2	L4	49	ASP	2.4
2	T7	49	ASP	2.4
2	U7	21	ASP	2.4
2	V6	49	ASP	2.4
2	Z3	49	ASP	2.4
3	A9	90	SER	2.4
3	K9	20	THR	2.4
3	48	129	SER	2.4
3	G9	167	VAL	2.4
3	J9	32	VAL	2.4
3	Q9	117	VAL	2.4
3	H9	141	PHE	2.4
3	I9	175	PHE	2.4
3	V9	141	PHE	2.4
3	28	95	LYS	2.4
3	H8	134	ILE	2.4
3	S8	134	ILE	2.4
3	T8	179	TYR	2.4
3	Z9	134	ILE	2.4
3	Z9	187	ILE	2.4
2	B7	58	GLU	2.4
2	C7	69	GLU	2.4
2	N2	9	GLU	2.4
2	45	58	GLU	2.4
3	B9	74	LEU	2.4
3	C9	41	GLU	2.4
3	D9	76	GLU	2.4
3	G9	41	GLU	2.4
3	K8	111	HIS	2.4

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Mol	Chain	Res	Type	RSRZ
3	K9	195	GLU	2.4
3	M9	138	GLU	2.4
3	O9	153	LEU	2.4
3	P8	79	HIS	2.4
3	V9	135	LEU	2.4
3	Z9	69	GLU	2.4
3	Z9	184	GLU	2.4
3	18	192	GLU	2.4
3	B9	196	ALA	2.4
3	C9	174	ALA	2.4
3	G9	196	ALA	2.4
3	J9	130	GLN	2.4
3	N9	88	ALA	2.4
3	O9	62	GLN	2.4
3	U8	27	ARG	2.4
3	V8	35	GLN	2.4
3	V9	82	GLN	2.4
3	W9	82	GLN	2.4
3	Y8	39	TRP	2.4
3	A9	128	ASN	2.4
3	B9	168	ASN	2.4
3	N9	168	ASN	2.4
3	R9	126	ASN	2.4
3	U8	163	ASN	2.4
3	G9	132	MET	2.4
1	O1	34	GLY	2.4
1	Y1	48	GLY	2.4
2	A7	68	GLY	2.4
3	A8	182	GLY	2.4
3	49	173	GLY	2.4
1	J1	61	SER	2.4
2	Y4	54	LYS	2.4
3	G9	145	THR	2.4
3	O9	59	THR	2.4
3	S8	90	SER	2.4
3	T9	105	LYS	2.4
3	U9	24	LYS	2.4
3	38	20	THR	2.4
3	F8	169	VAL	2.4
3	H9	152	VAL	2.4
3	R9	61	VAL	2.4
3	R9	80	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
3	Y8	10	PHE	2.4
3	Z9	204	VAL	2.4
2	G7	49	ASP	2.4
2	L7	49	ASP	2.4
2	O3	49	ASP	2.4
2	P6	49	ASP	2.4
2	S5	3	ASP	2.4
2	Z7	49	ASP	2.4
3	U8	12	ASP	2.4
3	L9	46	ILE	2.4
3	A8	135	LEU	2.4
3	R9	75	LEU	2.4
3	W9	86	LEU	2.4
1	Q1	67	GLU	2.4
2	M5	58	GLU	2.4
2	P3	69	GLU	2.4
2	U7	69	GLU	2.4
2	Z3	69	GLU	2.4
3	A9	101	GLU	2.4
3	F9	192	GLU	2.4
3	J9	159	GLU	2.4
3	O8	144	GLU	2.4
3	X8	192	GLU	2.4
3	Z8	138	GLU	2.4
3	49	138	GLU	2.4
2	Q6	2	ALA	2.4
3	D9	88	ALA	2.4
3	E9	71	ALA	2.4
3	H9	103	ARG	2.4
3	I8	27	ARG	2.4
3	K9	50	ARG	2.4
3	G9	121	GLN	2.4
3	I9	146	GLN	2.4
3	N9	146	GLN	2.4
3	W9	181	ALA	2.4
3	X9	47	ALA	2.4
3	19	151	ALA	2.4
3	19	155	ALA	2.4
1	W1	48	GLY	2.4
2	E3	93	PRO	2.4
3	I8	106	PRO	2.4
3	K8	16	PRO	2.4

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Mol	Chain	Res	Type	RSRZ
3	K9	149	GLY	2.4
3	P8	45	GLY	2.4
3	Q9	45	GLY	2.4
3	R8	95	LYS	2.4
3	S8	137	GLY	2.4
3	W9	33	PRO	2.4
3	Y8	149	GLY	2.4
3	Y9	171	PRO	2.4
3	Z8	149	GLY	2.4
1	N1	61	SER	2.4
1	21	37	THR	2.4
3	A8	29	PHE	2.4
3	C9	51	VAL	2.4
3	F9	164	VAL	2.4
3	J8	25	THR	2.4
3	J9	65	VAL	2.4
3	Q8	67	VAL	2.4
3	T9	51	VAL	2.4
3	T9	110	THR	2.4
3	W8	20	THR	2.4
3	W9	152	VAL	2.4
3	Y8	4	THR	2.4
3	E9	42	ILE	2.4
3	D9	5	LEU	2.4
3	P9	96	LEU	2.4
3	V9	74	LEU	2.4
3	B8	81	ASP	2.4
3	D8	94	ASP	2.4
3	E8	94	ASP	2.4
3	F9	94	ASP	2.4
3	R8	81	ASP	2.4
3	Q8	179	TYR	2.4
3	X8	172	TYR	2.4
2	I5	11	ARG	2.4
2	N5	69	GLU	2.4
2	W3	58	GLU	2.4
3	D8	101	GLU	2.4
3	G9	177	ARG	2.4
3	H8	184	GLU	2.4
3	M9	115	ARG	2.4
3	O9	6	ARG	2.4
3	S9	199	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
3	T8	41	GLU	2.4
3	V8	41	GLU	2.4
3	Y9	186	GLU	2.4
3	28	27	ARG	2.4
3	38	159	GLU	2.4
3	39	6	ARG	2.4
3	C8	26	ALA	2.4
3	C9	13	ALA	2.4
3	E9	161	ALA	2.4
3	G9	133	MET	2.4
3	I8	13	ALA	2.4
3	S9	154	ALA	2.4
3	T9	189	ALA	2.4
3	U9	82	GLN	2.4
3	Z9	189	ALA	2.4
3	Z9	191	ALA	2.4
3	18	15	GLN	2.4
3	18	35	GLN	2.4
3	38	26	ALA	2.4
3	39	82	GLN	2.4
3	39	107	GLN	2.4
3	39	174	ALA	2.4
3	B9	34	GLY	2.4
3	L9	156	ASN	2.4
3	P8	33	PRO	2.4
3	Q8	149	GLY	2.4
3	T8	28	GLY	2.4
3	T8	149	GLY	2.4
3	X8	131	GLY	2.4
3	X9	126	ASN	2.4
3	Y8	73	GLY	2.4
3	Z9	156	ASN	2.4
3	38	137	GLY	2.4
1	K1	61	SER	2.4
3	L9	37	SER	2.4
3	N9	80	PHE	2.4
3	U8	175	PHE	2.4
3	A9	113	ILE	2.4
3	B9	104	LEU	2.4
3	E8	40	VAL	2.4
3	I8	30	LEU	2.4
3	J9	67	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
3	K8	68	VAL	2.4
3	K9	30	LEU	2.4
3	K9	117	VAL	2.4
3	N9	18	LEU	2.4
3	R9	65	VAL	2.4
3	S8	142	ILE	2.4
3	Y9	59	THR	2.4
3	V9	56	LEU	2.4
3	Y9	56	LEU	2.4
3	Z8	108	VAL	2.4
3	19	170	THR	2.4
3	K9	166	LEU	2.4
3	Z9	135	LEU	2.4
3	19	187	ILE	2.4
3	38	198	ILE	2.4
1	Z1	45	ASP	2.4
2	A7	84	ASP	2.4
3	F9	199	ARG	2.4
3	I9	179	TYR	2.4
3	M9	70	ARG	2.4
3	M9	179	TYR	2.4
3	N9	172	TYR	2.4
3	P8	70	ARG	2.4
3	X8	188	ASP	2.4
3	B9	132	MET	2.4
2	J3	18	GLU	2.4
2	K4	2	ALA	2.4
2	O7	69	GLU	2.4
2	X4	58	GLU	2.4
2	Z7	9	GLU	2.4
2	47	69	GLU	2.4
3	B8	26	ALA	2.4
3	B8	184	GLU	2.4
3	B9	47	ALA	2.4
3	B9	154	ALA	2.4
3	B9	189	ALA	2.4
3	E9	64	ALA	2.4
3	F9	26	ALA	2.4
3	F9	181	ALA	2.4
3	I8	157	GLU	2.4
3	J9	151	ALA	2.4
3	J9	185	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
3	L8	184	GLU	2.4
3	O9	97	GLU	2.4
3	P9	161	ALA	2.4
3	Q9	47	ALA	2.4
3	R9	174	ALA	2.4
3	S9	84	GLU	2.4
3	T8	138	GLU	2.4
3	T9	13	ALA	2.4
3	U9	36	ALA	2.4
3	V9	88	ALA	2.4
3	Z8	174	ALA	2.4
3	19	186	GLU	2.4
3	29	88	ALA	2.4
3	39	26	ALA	2.4
3	39	154	ALA	2.4
3	49	26	ALA	2.4
3	49	190	ALA	2.4
2	44	54	LYS	2.4
3	A8	24	LYS	2.4
3	G8	95	LYS	2.4
3	O9	78	HIS	2.3
3	R8	79	HIS	2.3
3	V8	165	HIS	2.3
2	O7	68	GLY	2.3
2	S2	39	GLY	2.3
3	A9	173	GLY	2.3
3	F9	29	PHE	2.3
3	F9	129	SER	2.3
3	G9	182	GLY	2.3
3	I9	83	GLY	2.3
3	N9	163	ASN	2.3
3	S8	175	PHE	2.3
3	V9	80	PHE	2.3
3	W9	29	PHE	2.3
3	Z9	168	ASN	2.3
3	19	141	PHE	2.3
3	48	175	PHE	2.3
3	49	128	ASN	2.3
3	B8	30	LEU	2.3
3	I9	135	LEU	2.3
3	J8	134	ILE	2.3
3	F8	40	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
3	I9	167	VAL	2.3
3	L9	122	THR	2.3
3	M8	20	THR	2.3
3	O8	40	VAL	2.3
3	T8	169	VAL	2.3
3	W8	32	VAL	2.3
3	X9	117	VAL	2.3
3	39	65	VAL	2.3
3	B8	70	ARG	2.3
3	Y8	177	ARG	2.3
3	Z8	177	ARG	2.3
3	49	177	ARG	2.3
2	Q2	95	MET	2.3
1	Z1	90	ASP	2.3
2	B6	49	ASP	2.3
2	P7	47	ASP	2.3
3	E9	94	ASP	2.3
3	I8	94	ASP	2.3
3	I9	24	LYS	2.3
2	J3	69	GLU	2.3
2	M5	69	GLU	2.3
2	R7	58	GLU	2.3
2	T3	69	GLU	2.3
2	X4	69	GLU	2.3
2	X5	18	GLU	2.3
3	B9	97	GLU	2.3
3	C9	189	ALA	2.3
3	G9	26	ALA	2.3
3	H8	97	GLU	2.3
3	I9	162	ALA	2.3
3	S9	197	ALA	2.3
3	T8	47	ALA	2.3
3	O9	107	GLN	2.3
3	P8	76	GLU	2.3
3	P8	184	GLU	2.3
3	W9	26	ALA	2.3
3	Y8	26	ALA	2.3
3	38	41	GLU	2.3
3	39	47	ALA	2.3
3	39	15	GLN	2.3
1	A1	34	GLY	2.3
3	B8	3	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
3	D8	33	PRO	2.3
3	E8	129	SER	2.3
3	E9	75	LEU	2.3
3	F9	18	LEU	2.3
3	H8	80	PHE	2.3
3	G8	173	GLY	2.3
3	N9	56	LEU	2.3
3	O8	149	GLY	2.3
3	S9	198	ILE	2.3
3	Q9	168	ASN	2.3
3	T9	131	GLY	2.3
3	Y8	45	GLY	2.3
3	Z8	173	GLY	2.3
3	Z9	106	PRO	2.3
3	G9	128	ASN	2.3
3	R8	61	VAL	2.3
3	T8	39	TRP	2.3
3	V8	168	ASN	2.3
1	N1	37	THR	2.3
3	D9	110	THR	2.3
3	I9	59	THR	2.3
3	J9	20	THR	2.3
3	M9	98	VAL	2.3
3	X8	108	VAL	2.3
3	49	110	THR	2.3
3	F9	103	ARG	2.3
3	L9	99	ARG	2.3
3	Q8	70	ARG	2.3
3	S9	50	ARG	2.3
3	T8	6	ARG	2.3
3	W8	95	LYS	2.3
3	29	72	TYR	2.3
2	K6	2	ALA	2.3
3	A9	55	ALA	2.3
3	M9	194	ALA	2.3
3	O9	161	ALA	2.3
3	T9	55	ALA	2.3
3	Y9	155	ALA	2.3
3	19	26	ALA	2.3
2	A2	49	ASP	2.3
2	A2	84	ASP	2.3
2	P5	3	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
2	T4	69	GLU	2.3
2	Y6	49	ASP	2.3
3	G9	12	ASP	2.3
3	O9	94	ASP	2.3
3	Q8	97	GLU	2.3
3	V8	81	ASP	2.3
3	W8	35	GLN	2.3
3	W9	146	GLN	2.3
3	Z9	101	GLU	2.3
3	29	66	GLN	2.3
3	C9	141	PHE	2.3
3	D9	80	PHE	2.3
3	E8	86	LEU	2.3
3	R9	141	PHE	2.3
3	Z8	134	ILE	2.3
2	V4	68	GLY	2.3
3	E8	149	GLY	2.3
3	E9	202	SER	2.3
3	G9	137	GLY	2.3
3	H8	45	GLY	2.3
3	H8	73	GLY	2.3
3	Q8	23	GLY	2.3
3	Q9	44	PRO	2.3
3	U8	137	GLY	2.3
3	W9	147	PRO	2.3
3	Y8	16	PRO	2.3
3	Y9	33	PRO	2.3
3	E9	85	VAL	2.3
3	I9	168	ASN	2.3
3	J9	201	VAL	2.3
3	L8	68	VAL	2.3
3	P9	168	ASN	2.3
3	R8	65	VAL	2.3
3	28	204	VAL	2.3
3	48	168	ASN	2.3
3	E9	110	THR	2.3
3	G9	91	THR	2.3
3	L8	39	TRP	2.3
3	N9	110	THR	2.3
3	K9	115	ARG	2.3
3	L9	50	ARG	2.3
3	P8	115	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
3	R9	60	LYS	2.3
3	S9	109	MET	2.3
3	Y9	177	ARG	2.3
3	Z9	115	ARG	2.3
1	B1	12	ALA	2.3
1	R1	12	ALA	2.3
2	A5	2	ALA	2.3
2	E3	2	ALA	2.3
3	A8	8	TYR	2.3
3	G8	205	ALA	2.3
3	G9	179	TYR	2.3
3	G9	190	ALA	2.3
3	H8	174	ALA	2.3
3	I9	71	ALA	2.3
3	J8	150	TYR	2.3
3	J9	58	ALA	2.3
3	M8	43	ALA	2.3
3	M9	196	ALA	2.3
3	O9	185	ALA	2.3
3	P8	71	ALA	2.3
3	Q9	26	ALA	2.3
3	R9	43	ALA	2.3
3	X9	43	ALA	2.3
3	19	47	ALA	2.3
3	19	205	ALA	2.3
3	39	155	ALA	2.3
3	D9	29	PHE	2.3
1	A1	45	ASP	2.3
1	X1	75	ASP	2.3
2	H5	65	GLU	2.3
2	K2	9	GLU	2.3
2	K6	18	GLU	2.3
2	M6	69	GLU	2.3
2	Y6	21	ASP	2.3
2	37	35	GLU	2.3
3	J8	62	GLN	2.3
3	N8	130	GLN	2.3
3	R9	15	GLN	2.3
3	49	135	LEU	2.3
3	O8	188	ASP	2.3
3	S8	41	GLU	2.3
3	Z8	46	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
3	I8	81	ASP	2.3
3	Y9	81	ASP	2.3
3	Y9	94	ASP	2.3
3	18	157	GLU	2.3
3	19	195	GLU	2.3
3	48	144	GLU	2.3
3	39	202	SER	2.3
1	S1	88	GLY	2.3
3	A8	28	GLY	2.3
3	C9	106	PRO	2.3
3	E9	31	PRO	2.3
3	I9	63	PRO	2.3
3	L8	149	GLY	2.3
3	R9	31	PRO	2.3
3	S9	171	PRO	2.3
3	T8	45	GLY	2.3
3	V9	31	PRO	2.3
3	19	23	GLY	2.3
3	39	44	PRO	2.3
3	A9	165	HIS	2.3
3	C9	169	VAL	2.3
3	D9	85	VAL	2.3
3	H9	79	HIS	2.3
3	I9	78	HIS	2.3
3	Q9	68	VAL	2.3
3	U9	51	VAL	2.3
3	W9	108	VAL	2.3
3	19	165	HIS	2.3
3	E9	91	THR	2.3
3	H9	20	THR	2.3
3	O9	168	ASN	2.3
3	R9	128	ASN	2.3
3	S9	110	THR	2.3
3	39	25	THR	2.3
3	J8	27	ARG	2.3
3	Q8	27	ARG	2.3
3	X9	39	TRP	2.3
3	X9	133	MET	2.3
3	P8	74	LEU	2.3
3	P9	14	LEU	2.3
3	S9	11	LEU	2.3
3	29	96	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
3	E9	179	TYR	2.3
3	F8	42	ILE	2.3
3	F9	194	ALA	2.3
3	H8	42	ILE	2.3
3	I8	43	ALA	2.3
3	L9	42	ILE	2.3
3	N9	46	ILE	2.3
3	O9	54	ALA	2.3
3	O9	162	ALA	2.3
3	Q8	10	PHE	2.3
3	V9	10	PHE	2.3
3	V9	48	ILE	2.3
3	X8	10	PHE	2.3
3	X8	13	ALA	2.3
3	39	72	TYR	2.3
3	A8	146	GLN	2.3
3	I9	121	GLN	2.3
3	K9	17	GLN	2.3
3	29	121	GLN	2.3
2	B2	69	GLU	2.3
2	I3	58	GLU	2.3
2	T5	69	GLU	2.3
2	U3	58	GLU	2.3
3	C8	159	GLU	2.3
3	F9	144	GLU	2.3
3	H8	144	GLU	2.3
3	I9	192	GLU	2.3
3	J8	192	GLU	2.3
3	K9	97	GLU	2.3
3	K9	192	GLU	2.3
3	L8	41	GLU	2.3
3	T9	159	GLU	2.3
3	U9	41	GLU	2.3
3	Z9	192	GLU	2.3
3	39	192	GLU	2.3
3	A8	129	SER	2.3
3	O9	139	SER	2.3
1	E1	88	GLY	2.3
1	P1	45	ASP	2.3
1	P1	88	GLY	2.3
2	E3	84	ASP	2.3
2	G7	68	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
2	Q2	3	ASP	2.3
2	R2	12	GLY	2.3
3	B8	188	ASP	2.3
3	B9	149	GLY	2.3
3	D9	171	PRO	2.3
3	J9	44	PRO	2.3
3	R8	117	VAL	2.3
3	U8	182	GLY	2.3
3	V9	176	GLY	2.3
3	Z8	32	VAL	2.3
3	Z9	44	PRO	2.3
3	38	81	ASP	2.3
3	K9	68	VAL	2.3
3	M8	169	VAL	2.3
2	R2	95	MET	2.3
3	E8	70	ARG	2.3
3	E8	111	HIS	2.3
3	E9	50	ARG	2.3
3	G8	4	THR	2.3
3	G9	99	ARG	2.3
3	G9	109	MET	2.3
3	H9	70	ARG	2.3
3	N9	79	HIS	2.3
3	Q9	49	ASN	2.3
3	R9	91	THR	2.3
3	S9	99	ARG	2.3
3	U8	99	ARG	2.3
3	X9	110	THR	2.3
3	Z9	52	THR	2.3
3	28	168	ASN	2.3
3	I9	39	TRP	2.3
3	G8	96	LEU	2.3
3	H9	14	LEU	2.3
3	I9	75	LEU	2.3
3	K8	74	LEU	2.3
3	D9	9	ILE	2.3
3	R8	80	PHE	2.3
3	Z9	92	ILE	2.3
2	46	2	ALA	2.3
3	B9	58	ALA	2.3
3	G8	15	GLN	2.3
3	H8	150	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
3	H9	8	TYR	2.3
3	H9	47	ALA	2.3
3	L9	155	ALA	2.3
3	Q8	174	ALA	2.3
3	X9	205	ALA	2.3
3	Z9	13	ALA	2.3
3	29	172	TYR	2.3
3	49	197	ALA	2.3
1	W1	43	CYS	2.3
3	T9	107	GLN	2.3
3	X9	82	GLN	2.3
1	21	20	GLU	2.3
2	F3	69	GLU	2.3
2	L3	69	GLU	2.3
2	R2	69	GLU	2.3
2	V6	69	GLU	2.3
2	45	69	GLU	2.3
3	A9	192	GLU	2.3
3	B8	41	GLU	2.3
3	C9	97	GLU	2.3
3	G8	41	GLU	2.3
3	G8	100	GLU	2.3
3	H9	144	GLU	2.3
3	N8	97	GLU	2.3
3	N9	202	SER	2.3
3	T9	76	GLU	2.3
3	V9	118	GLU	2.3
3	29	138	GLU	2.3
3	38	184	GLU	2.3
1	D1	88	GLY	2.3
1	G1	47	VAL	2.3
1	H1	34	GLY	2.3
1	I1	95	LYS	2.3
2	B2	81	VAL	2.3
2	H5	39	GLY	2.3
2	U7	68	GLY	2.3
3	C9	67	VAL	2.3
3	E9	149	GLY	2.3
3	F8	45	GLY	2.3
3	G9	204	VAL	2.3
3	J9	60	LYS	2.3
3	K8	67	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
3	Z9	68	VAL	2.3
1	I1	90	ASP	2.3
1	M1	75	ASP	2.3
1	S1	45	ASP	2.3
2	J2	11	ARG	2.3
2	K4	49	ASP	2.3
2	N3	21	ASP	2.3
2	V2	78	ARG	2.3
3	F8	12	ASP	2.3
3	L9	53	ASP	2.3
3	P9	53	ASP	2.3
3	U8	109	MET	2.3
3	W9	103	ARG	2.3
3	A9	145	THR	2.2
3	B9	49	ASN	2.2
3	E9	49	ASN	2.2
3	G8	168	ASN	2.2
3	J9	49	ASN	2.2
3	R9	168	ASN	2.2
3	S8	4	THR	2.2
3	S9	165	HIS	2.2
3	T8	163	ASN	2.2
3	H9	11	LEU	2.2
3	Y8	104	LEU	2.2
3	A8	175	PHE	2.2
3	D8	134	ILE	2.2
3	E8	42	ILE	2.2
3	G9	92	ILE	2.2
3	K9	46	ILE	2.2
3	Q9	21	PHE	2.2
3	R9	29	PHE	2.2
3	R9	48	ILE	2.2
3	18	175	PHE	2.2
2	G4	2	ALA	2.2
2	I4	2	ALA	2.2
2	14	2	ALA	2.2
3	A9	181	ALA	2.2
3	D9	158	ALA	2.2
3	G8	71	ALA	2.2
3	G9	161	ALA	2.2
3	I8	64	ALA	2.2
3	J9	189	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
3	K9	36	ALA	2.2
3	K9	47	ALA	2.2
3	R8	13	ALA	2.2
3	T8	205	ALA	2.2
3	W9	43	ALA	2.2
3	B9	146	GLN	2.2
3	E9	172	TYR	2.2
3	J8	130	GLN	2.2
3	K8	35	GLN	2.2
3	K8	172	TYR	2.2
3	L9	146	GLN	2.2
3	U9	8	TYR	2.2
3	Y9	24	LYS	2.2
1	B1	86	GLU	2.2
2	R5	58	GLU	2.2
2	T4	58	GLU	2.2
3	N9	100	GLU	2.2
3	O8	192	GLU	2.2
3	P8	100	GLU	2.2
3	U8	192	GLU	2.2
3	Z8	184	GLU	2.2
3	18	100	GLU	2.2
1	H1	68	VAL	2.2
1	N1	48	GLY	2.2
2	F7	68	GLY	2.2
2	P6	16	MET	2.2
2	Q3	39	GLY	2.2
3	D9	177	ARG	2.2
3	G9	89	GLY	2.2
3	I9	6	ARG	2.2
3	J8	201	VAL	2.2
3	J9	50	ARG	2.2
3	P9	171	PRO	2.2
3	R9	131	GLY	2.2
3	T8	182	GLY	2.2
3	V9	45	GLY	2.2
3	W8	204	VAL	2.2
3	X9	89	GLY	2.2
3	Y9	65	VAL	2.2
3	Y9	127	ARG	2.2
3	Y9	164	VAL	2.2
3	39	98	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
3	49	31	PRO	2.2
1	C1	90	ASP	2.2
1	F1	37	THR	2.2
1	O1	90	ASP	2.2
2	C5	49	ASP	2.2
2	Y2	84	ASP	2.2
2	Y7	3	ASP	2.2
3	A9	81	ASP	2.2
3	L9	7	THR	2.2
3	M8	4	THR	2.2
3	O9	75	LEU	2.2
3	R9	53	ASP	2.2
3	R9	94	ASP	2.2
3	S9	166	LEU	2.2
3	U9	91	THR	2.2
3	V8	94	ASP	2.2
3	X8	53	ASP	2.2
3	29	94	ASP	2.2
3	Z9	126	ASN	2.2
3	48	165	HIS	2.2
3	B9	46	ILE	2.2
3	D9	46	ILE	2.2
3	J8	46	ILE	2.2
3	K8	42	ILE	2.2
3	L9	175	PHE	2.2
3	P9	141	PHE	2.2
3	S9	113	ILE	2.2
3	W9	187	ILE	2.2
3	O9	39	TRP	2.2
2	F3	2	ALA	2.2
2	X6	2	ALA	2.2
3	B9	54	ALA	2.2
3	E8	197	ALA	2.2
3	I9	151	ALA	2.2
3	K8	13	ALA	2.2
3	K9	185	ALA	2.2
3	L9	58	ALA	2.2
3	R8	71	ALA	2.2
3	Z9	87	ALA	2.2
3	19	197	ALA	2.2
3	E9	8	TYR	2.2
3	R9	172	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
3	Y8	82	GLN	2.2
3	39	130	GLN	2.2
1	U1	20	GLU	2.2
2	N4	58	GLU	2.2
3	A8	159	GLU	2.2
3	A9	167	VAL	2.2
3	A9	186	GLU	2.2
3	F8	100	GLU	2.2
3	G8	192	GLU	2.2
3	O9	32	VAL	2.2
3	O9	159	GLU	2.2
3	Q8	118	GLU	2.2
3	T9	69	GLU	2.2
3	W9	65	VAL	2.2
3	W9	138	GLU	2.2
3	29	67	VAL	2.2
3	29	97	GLU	2.2
1	31	36	PRO	2.2
2	17	68	GLY	2.2
3	D9	56	LEU	2.2
3	E8	28	GLY	2.2
3	F9	34	GLY	2.2
3	G9	45	GLY	2.2
3	I8	96	LEU	2.2
3	J9	176	GLY	2.2
3	N9	74	LEU	2.2
3	Q8	28	GLY	2.2
3	18	173	GLY	2.2
3	38	51	VAL	2.2
3	48	27	ARG	2.2
3	T9	93	LEU	2.2
3	V9	44	PRO	2.2
3	V9	86	LEU	2.2
3	W8	96	LEU	2.2
3	X9	33	PRO	2.2
3	C9	4	THR	2.2
3	F9	52	THR	2.2
3	T9	170	THR	2.2
3	39	91	THR	2.2
2	B6	21	ASP	2.2
2	O5	84	ASP	2.2
2	17	21	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
3	B8	53	ASP	2.2
3	D9	48	ILE	2.2
3	L8	128	ASN	2.2
3	Y8	168	ASN	2.2
3	Z8	168	ASN	2.2
3	49	29	PHE	2.2
2	H5	74	HIS	2.2
2	U4	2	ALA	2.2
2	Y4	2	ALA	2.2
3	C9	194	ALA	2.2
3	D8	205	ALA	2.2
3	E9	158	ALA	2.2
3	F8	24	LYS	2.2
3	G9	13	ALA	2.2
3	I8	116	ALA	2.2
3	I9	174	ALA	2.2
3	N8	54	ALA	2.2
3	P9	26	ALA	2.2
3	Y9	47	ALA	2.2
3	38	43	ALA	2.2
3	U9	146	GLN	2.2
3	Y9	66	GLN	2.2
3	19	66	GLN	2.2
3	J9	120	TYR	2.2
3	K9	120	TYR	2.2
3	U8	129	SER	2.2
3	U9	179	TYR	2.2
3	Y8	129	SER	2.2
3	Y9	202	SER	2.2
3	39	133	MET	2.2
2	G2	11	ARG	2.2
3	K9	177	ARG	2.2
3	R9	74	LEU	2.2
3	S8	32	VAL	2.2
3	T9	40	VAL	2.2
3	U8	204	VAL	2.2
3	V8	70	ARG	2.2
3	O8	102	GLY	2.2
3	O9	76	GLU	2.2
3	P9	77	VAL	2.2
3	Y9	5	LEU	2.2
1	T1	86	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
2	P3	18	GLU	2.2
2	S5	18	GLU	2.2
2	Z7	69	GLU	2.2
2	22	58	GLU	2.2
2	46	9	GLU	2.2
2	C3	93	PRO	2.2
2	H7	68	GLY	2.2
3	B9	184	GLU	2.2
3	D9	118	GLU	2.2
3	H8	69	GLU	2.2
3	L9	101	GLU	2.2
3	P9	186	GLU	2.2
3	W8	97	GLU	2.2
3	Z8	101	GLU	2.2
3	19	184	GLU	2.2
3	29	41	GLU	2.2
3	Q8	16	PRO	2.2
3	C9	110	THR	2.2
3	F9	110	THR	2.2
3	J9	92	ILE	2.2
3	Y8	110	THR	2.2
3	19	59	THR	2.2
3	49	4	THR	2.2
1	Q1	43	CYS	2.2
3	K9	80	PHE	2.2
1	W1	90	ASP	2.2
2	E2	49	ASP	2.2
2	J5	84	ASP	2.2
2	J6	49	ASP	2.2
3	A8	12	ASP	2.2
3	B9	24	LYS	2.2
3	M8	81	ASP	2.2
3	O8	95	LYS	2.2
3	Q9	188	ASP	2.2
3	19	126	ASN	2.2
3	D8	165	HIS	2.2
3	H8	79	HIS	2.2
3	29	78	HIS	2.2
1	H1	49	ALA	2.2
2	F2	2	ALA	2.2
2	S2	63	ALA	2.2
2	S4	22	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
2	U6	2	ALA	2.2
3	A9	19	ALA	2.2
3	F9	71	ALA	2.2
3	F9	158	ALA	2.2
3	I9	47	ALA	2.2
3	Q9	181	ALA	2.2
3	Q9	189	ALA	2.2
3	U9	185	ALA	2.2
3	V9	54	ALA	2.2
3	X8	43	ALA	2.2
3	38	205	ALA	2.2
3	B8	35	GLN	2.2
3	C8	62	GLN	2.2
3	D9	82	GLN	2.2
3	I8	146	GLN	2.2
3	I9	133	MET	2.2
3	Q8	133	MET	2.2
2	O2	66	ARG	2.2
3	D8	166	LEU	2.2
3	J9	75	LEU	2.2
3	K9	139	SER	2.2
3	R9	130	GLN	2.2
3	W9	62	GLN	2.2
3	38	15	GLN	2.2
3	F9	120	TYR	2.2
3	L8	177	ARG	2.2
3	M9	120	TYR	2.2
3	P9	135	LEU	2.2
3	P9	153	LEU	2.2
3	P9	166	LEU	2.2
3	R9	8	TYR	2.2
3	V9	11	LEU	2.2
3	W8	70	ARG	2.2
3	Z9	11	LEU	2.2
3	28	96	LEU	2.2
1	O1	68	VAL	2.2
3	H8	40	VAL	2.2
3	O9	152	VAL	2.2
3	S8	68	VAL	2.2
3	49	167	VAL	2.2
1	H1	20	GLU	2.2
2	A4	58	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
2	C4	58	GLU	2.2
2	G2	69	GLU	2.2
2	K6	69	GLU	2.2
2	S3	69	GLU	2.2
2	T6	65	GLU	2.2
2	W6	58	GLU	2.2
2	W7	68	GLY	2.2
2	Z3	18	GLU	2.2
2	23	69	GLU	2.2
2	37	58	GLU	2.2
3	A9	63	PRO	2.2
3	H9	159	GLU	2.2
3	J8	138	GLU	2.2
3	K8	45	GLY	2.2
3	K9	184	GLU	2.2
3	O9	44	PRO	2.2
3	O9	83	GLY	2.2
3	O9	106	PRO	2.2
3	P9	34	GLY	2.2
3	R8	118	GLU	2.2
3	U8	76	GLU	2.2
3	U8	138	GLU	2.2
3	U9	118	GLU	2.2
3	Z8	33	PRO	2.2
3	Z8	144	GLU	2.2
3	19	157	GLU	2.2
3	I9	48	ILE	2.2
3	28	33	PRO	2.2
3	29	31	PRO	2.2
3	E8	175	PHE	2.2
3	E9	25	THR	2.2
3	M9	20	THR	2.2
3	N8	4	THR	2.2
3	O9	80	PHE	2.2
3	Q9	29	PHE	2.2
3	X9	21	PHE	2.2
2	U7	2	ALA	2.2
2	X5	84	ASP	2.2
2	Z4	49	ASP	2.2
2	43	2	ALA	2.2
3	B8	12	ASP	2.2
3	C9	162	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
3	D9	161	ALA	2.2
3	E9	132	MET	2.2
3	E9	162	ALA	2.2
3	E9	205	ALA	2.2
3	H9	189	ALA	2.2
3	K8	188	ASP	2.2
3	K9	26	ALA	2.2
3	L8	13	ALA	2.2
3	N9	12	ASP	2.2
3	N9	174	ALA	2.2
3	R9	111	HIS	2.2
3	S9	151	ALA	2.2
3	T8	81	ASP	2.2
3	T9	54	ALA	2.2
3	T9	165	HIS	2.2
3	U9	79	HIS	2.2
3	Y9	190	ALA	2.2
3	Z9	94	ASP	2.2
3	48	174	ALA	2.2
3	A9	96	LEU	2.2
3	B9	14	LEU	2.2
3	B9	183	SER	2.2
3	D8	70	ARG	2.2
3	D9	39	TRP	2.2
3	E8	146	GLN	2.2
3	G8	112	GLN	2.2
3	N9	30	LEU	2.2
3	Q9	11	LEU	2.2
3	S8	62	GLN	2.2
3	U8	15	GLN	2.2
3	Y9	96	LEU	2.2
3	Y9	178	LEU	2.2
3	H9	177	ARG	2.2
3	V9	27	ARG	2.2
3	X9	115	ARG	2.2
3	Z9	15	GLN	2.2
3	18	70	ARG	2.2
3	G8	204	VAL	2.2
3	G9	72	TYR	2.2
3	I9	85	VAL	2.2
3	L8	67	VAL	2.2
3	L9	85	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
3	P9	67	VAL	2.2
3	W9	51	VAL	2.2
3	39	8	TYR	2.2
3	39	164	VAL	2.2
1	V1	34	GLY	2.2
2	E2	9	GLU	2.2
2	E6	58	GLU	2.2
2	O4	58	GLU	2.2
2	Q6	39	GLY	2.2
2	33	69	GLU	2.2
3	B8	137	GLY	2.2
3	F9	142	ILE	2.2
3	C9	157	GLU	2.2
3	D9	157	GLU	2.2
3	E9	101	GLU	2.2
3	M8	137	GLY	2.2
3	N9	76	GLU	2.2
3	T9	89	GLY	2.2
3	W8	137	GLY	2.2
3	W9	46	ILE	2.2
3	O8	175	PHE	2.2
3	P9	21	PHE	2.2
3	T9	192	GLU	2.2
3	U8	157	GLU	2.2
3	Y9	138	GLU	2.2
3	Z9	138	GLU	2.2
3	Z9	173	GLY	2.2
3	18	101	GLU	2.2
3	19	144	GLU	2.2
3	48	100	GLU	2.2
3	D8	60	LYS	2.2
3	D8	110	THR	2.2
3	D9	91	THR	2.2
3	S8	95	LYS	2.2
3	U8	160	LYS	2.2
3	28	20	THR	2.2
3	29	91	THR	2.2
3	D8	163	ASN	2.2
3	M9	168	ASN	2.2
2	O4	2	ALA	2.1
3	F8	205	ALA	2.1
3	G9	19	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
3	H9	153	LEU	2.2
3	J9	47	ALA	2.1
3	K8	14	LEU	2.2
3	M8	135	LEU	2.2
3	Q8	104	LEU	2.2
3	R9	166	LEU	2.2
3	S9	26	ALA	2.1
3	V9	155	ALA	2.1
3	X9	158	ALA	2.1
3	Y9	174	ALA	2.1
3	Z8	93	LEU	2.2
3	Z9	155	ALA	2.1
3	29	196	ALA	2.1
3	49	155	ALA	2.1
1	U1	90	ASP	2.1
2	Q3	49	ASP	2.1
2	26	49	ASP	2.1
1	P1	65	GLN	2.1
2	L7	78	ARG	2.1
2	N5	84	ASP	2.1
2	N6	49	ASP	2.1
2	O6	49	ASP	2.1
3	A9	202	SER	2.1
3	B8	130	GLN	2.1
3	D8	183	SER	2.1
3	E8	27	ARG	2.1
3	G9	90	SER	2.1
3	N8	27	ARG	2.1
3	O9	90	SER	2.1
3	Q9	183	SER	2.1
3	S8	165	HIS	2.1
3	39	37	SER	2.1
3	B8	108	VAL	2.1
3	C9	167	VAL	2.1
3	F8	46	ILE	2.1
3	I9	152	VAL	2.1
3	L9	172	TYR	2.1
3	N8	134	ILE	2.1
3	R9	46	ILE	2.1
3	R9	164	VAL	2.1
3	S9	51	VAL	2.1
1	Q1	89	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	T1	34	GLY	2.1
1	11	34	GLY	2.1
1	11	95	LYS	2.1
2	E2	39	GLY	2.1
3	B8	45	GLY	2.1
3	I8	175	PHE	2.1
3	J9	102	GLY	2.1
3	N9	171	PRO	2.1
3	Z8	175	PHE	2.1
2	B6	65	GLU	2.1
2	U4	58	GLU	2.1
2	Y2	9	GLU	2.1
3	C9	69	GLU	2.1
3	E9	159	GLU	2.1
3	I9	76	GLU	2.1
3	K9	60	LYS	2.1
3	K9	157	GLU	2.1
3	L9	69	GLU	2.1
3	N8	76	GLU	2.1
3	P9	192	GLU	2.1
3	X9	76	GLU	2.1
3	18	33	PRO	2.1
1	A1	37	THR	2.1
3	K9	91	THR	2.1
2	W4	95	MET	2.1
3	K9	38	LEU	2.1
3	Q9	132	MET	2.1
3	V9	14	LEU	2.1
3	Y8	38	LEU	2.1
3	Z9	5	LEU	2.1
2	O6	2	ALA	2.1
2	Z2	2	ALA	2.1
2	36	2	ALA	2.1
3	A8	71	ALA	2.1
3	C9	49	ASN	2.1
3	F9	193	ALA	2.1
3	H9	88	ALA	2.1
3	I9	87	ALA	2.1
3	I9	185	ALA	2.1
3	J9	13	ALA	2.1
3	J9	190	ALA	2.1
3	M9	174	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
3	P9	47	ALA	2.1
3	T9	191	ALA	2.1
3	V9	116	ALA	2.1
3	W9	87	ALA	2.1
3	18	174	ALA	2.1
3	G9	50	ARG	2.1
3	L8	27	ARG	2.1
3	Z9	99	ARG	2.1
3	29	177	ARG	2.1
3	48	115	ARG	2.1
3	49	70	ARG	2.1
1	X1	61	SER	2.1
3	D9	107	GLN	2.1
3	H9	35	GLN	2.1
3	H9	121	GLN	2.1
3	Q9	82	GLN	2.1
3	R9	146	GLN	2.1
3	X8	62	GLN	2.1
3	X8	112	GLN	2.1
3	X9	121	GLN	2.1
3	18	130	GLN	2.1
3	39	35	GLN	2.1
1	A1	75	ASP	2.1
1	T1	75	ASP	2.1
2	W5	21	ASP	2.1
2	44	21	ASP	2.1
3	N9	167	VAL	2.1
3	O8	108	VAL	2.1
3	Q9	92	ILE	2.1
3	Q9	169	VAL	2.1
3	U9	3	ILE	2.1
3	W9	12	ASP	2.1
3	X8	81	ASP	2.1
3	Y9	12	ASP	2.1
1	L1	68	VAL	2.1
3	A9	39	TRP	2.1
3	F9	167	VAL	2.1
3	L9	164	VAL	2.1
3	M8	61	VAL	2.1
2	R3	28	LYS	2.1
3	B8	95	LYS	2.1
3	C9	10	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
3	G9	172	TYR	2.1
3	J9	172	TYR	2.1
3	O8	72	TYR	2.1
3	Q9	10	PHE	2.1
2	G3	39	GLY	2.1
3	C8	45	GLY	2.1
3	C9	131	GLY	2.1
3	E8	137	GLY	2.1
3	G9	102	GLY	2.1
3	J8	34	GLY	2.1
3	N8	149	GLY	2.1
2	27	69	GLU	2.1
3	B9	195	GLU	2.1
3	M9	41	GLU	2.1
3	U9	101	GLU	2.1
3	U9	159	GLU	2.1
3	W8	157	GLU	2.1
3	Y8	159	GLU	2.1
3	28	69	GLU	2.1
3	Q9	110	THR	2.1
3	V9	4	THR	2.1
2	T2	95	MET	2.1
3	F9	5	LEU	2.1
3	V8	109	MET	2.1
1	S1	71	ASN	2.1
2	Y3	66	ARG	2.1
3	B9	155	ALA	2.1
3	G9	154	ALA	2.1
3	H8	177	ARG	2.1
3	I9	26	ALA	2.1
3	I9	193	ALA	2.1
3	K9	197	ALA	2.1
3	M9	26	ALA	2.1
3	M9	126	ASN	2.1
3	N9	154	ALA	2.1
3	P8	26	ALA	2.1
3	P9	205	ALA	2.1
3	R9	47	ALA	2.1
3	R9	87	ALA	2.1
3	S9	70	ARG	2.1
3	T8	168	ASN	2.1
3	W8	43	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
3	Y9	158	ALA	2.1
3	19	6	ARG	2.1
3	19	43	ALA	2.1
3	29	26	ALA	2.1
3	39	168	ASN	2.1
3	49	49	ASN	2.1
3	49	151	ALA	2.1
3	S9	129	SER	2.1
3	T9	183	SER	2.1
3	F8	35	GLN	2.1
3	G9	9	ILE	2.1
3	I8	42	ILE	2.1
3	N9	121	GLN	2.1
3	P8	130	GLN	2.1
3	P9	121	GLN	2.1
3	Q8	146	GLN	2.1
3	Q9	130	GLN	2.1
3	T9	35	GLN	2.1
3	T9	48	ILE	2.1
3	Z8	42	ILE	2.1
1	R1	68	VAL	2.1
1	L1	90	ASP	2.1
2	K6	84	ASP	2.1
3	B9	10	PHE	2.1
3	F9	60	LYS	2.1
3	H9	201	VAL	2.1
3	I9	108	VAL	2.1
3	K9	61	VAL	2.1
3	K9	164	VAL	2.1
3	J8	94	ASP	2.1
3	L9	80	PHE	2.1
3	O8	169	VAL	2.1
3	V8	79	HIS	2.1
3	V8	204	VAL	2.1
3	X8	80	PHE	2.1
3	X9	78	HIS	2.1
3	Y8	108	VAL	2.1
3	F9	8	TYR	2.1
3	28	39	TRP	2.1
1	U1	88	GLY	2.1
2	V3	39	GLY	2.1
3	P9	149	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
3	Q9	182	GLY	2.1
3	U8	102	GLY	2.1
3	W8	173	GLY	2.1
3	F9	31	PRO	2.1
3	M9	31	PRO	2.1
3	Q8	136	PRO	2.1
2	B3	69	GLU	2.1
2	B5	69	GLU	2.1
2	K5	35	GLU	2.1
2	P2	9	GLU	2.1
2	T6	69	GLU	2.1
2	Z5	58	GLU	2.1
2	14	9	GLU	2.1
3	B8	97	GLU	2.1
3	F9	93	LEU	2.1
3	G9	157	GLU	2.1
3	H8	41	GLU	2.1
3	J9	144	GLU	2.1
3	N8	157	GLU	2.1
3	P9	195	GLU	2.1
3	Q9	159	GLU	2.1
3	T8	86	LEU	2.1
3	V9	18	LEU	2.1
3	Z9	14	LEU	2.1
3	29	192	GLU	2.1
3	49	96	LEU	2.1
1	C1	37	THR	2.1
3	D8	170	THR	2.1
3	Q8	7	THR	2.1
3	R9	170	THR	2.1
3	Y9	110	THR	2.1
3	J9	99	ARG	2.1
3	O8	199	ARG	2.1
3	P9	99	ARG	2.1
3	V9	177	ARG	2.1
3	W9	70	ARG	2.1
3	X9	70	ARG	2.1
3	X9	177	ARG	2.1
3	49	127	ARG	2.1
2	B4	2	ALA	2.1
2	E6	2	ALA	2.1
3	B9	197	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
3	D9	87	ALA	2.1
3	F9	13	ALA	2.1
3	G9	189	ALA	2.1
3	G9	205	ALA	2.1
3	H9	174	ALA	2.1
3	K9	87	ALA	2.1
3	L9	197	ALA	2.1
3	N8	116	ALA	2.1
3	P9	196	ALA	2.1
3	Q9	155	ALA	2.1
3	T9	194	ALA	2.1
3	U8	119	ALA	2.1
3	U9	88	ALA	2.1
3	X9	151	ALA	2.1
3	Y9	54	ALA	2.1
1	V1	61	SER	2.1
3	M9	128	ASN	2.1
3	T9	42	ILE	2.1
3	Y9	48	ILE	2.1
3	E9	146	GLN	2.1
3	F9	146	GLN	2.1
3	G8	62	GLN	2.1
3	N9	112	GLN	2.1
3	P9	15	GLN	2.1
3	W8	62	GLN	2.1
3	X9	57	LYS	2.1
3	F8	175	PHE	2.1
3	F9	40	VAL	2.1
3	G8	80	PHE	2.1
3	H8	169	VAL	2.1
3	J9	169	VAL	2.1
3	L8	65	VAL	2.1
3	U9	68	VAL	2.1
3	U9	204	VAL	2.1
3	W9	117	VAL	2.1
3	29	204	VAL	2.1
3	39	80	PHE	2.1
3	49	40	VAL	2.1
3	X8	78	HIS	2.1
1	D1	75	ASP	2.1
2	23	49	ASP	2.1
3	A9	149	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
3	E9	45	GLY	2.1
3	F9	172	TYR	2.1
3	I8	179	TYR	2.1
3	J9	28	GLY	2.1
3	K9	18	LEU	2.1
3	P8	34	GLY	2.1
3	U9	96	LEU	2.1
3	28	45	GLY	2.1
3	38	8	TYR	2.1
3	49	81	ASP	2.1
3	X8	137	GLY	2.1
3	Z9	73	GLY	2.1
3	E9	106	PRO	2.1
3	J8	33	PRO	2.1
3	29	63	PRO	2.1
2	A5	18	GLU	2.1
2	H5	58	GLU	2.1
2	K4	69	GLU	2.1
2	Q3	58	GLU	2.1
2	T5	58	GLU	2.1
2	W4	58	GLU	2.1
3	F8	25	THR	2.1
3	I8	76	GLU	2.1
3	I9	159	GLU	2.1
3	K8	184	GLU	2.1
3	W9	110	THR	2.1
3	X8	100	GLU	2.1
3	18	76	GLU	2.1
3	19	192	GLU	2.1
2	I2	66	ARG	2.1
2	I3	11	ARG	2.1
3	A8	70	ARG	2.1
3	J9	127	ARG	2.1
2	T2	44	ALA	2.1
2	W3	20	ALA	2.1
3	A9	46	ILE	2.1
3	D8	47	ALA	2.1
3	D9	190	ALA	2.1
3	E9	24	LYS	2.1
3	G9	158	ALA	2.1
3	L9	26	ALA	2.1
3	M8	13	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
3	N9	189	ALA	2.1
3	Q9	185	ALA	2.1
3	S9	19	ALA	2.1
3	T9	158	ALA	2.1
3	U8	47	ALA	2.1
3	Y8	13	ALA	2.1
3	Z9	154	ALA	2.1
3	19	46	ILE	2.1
3	19	134	ILE	2.1
3	39	189	ALA	2.1
3	49	47	ALA	2.1
3	H8	202	SER	2.1
3	A9	29	PHE	2.1
3	N9	49	ASN	2.1
3	T8	15	GLN	2.1
3	U9	62	GLN	2.1
1	T1	68	VAL	2.1
3	A9	51	VAL	2.1
3	A9	164	VAL	2.1
3	E9	108	VAL	2.1
3	K8	98	VAL	2.1
3	Q9	152	VAL	2.1
3	X9	167	VAL	2.1
3	39	77	VAL	2.1
3	D8	14	LEU	2.1
3	D8	93	LEU	2.1
3	H9	30	LEU	2.1
3	O8	135	LEU	2.1
3	Y9	79	HIS	2.1
1	D1	57	TYR	2.1
1	J1	45	ASP	2.1
1	T1	89	GLY	2.1
1	W1	34	GLY	2.1
2	F3	3	ASP	2.1
2	F5	84	ASP	2.1
2	L5	3	ASP	2.1
2	V3	84	ASP	2.1
2	W5	84	ASP	2.1
2	X7	68	GLY	2.1
3	A9	8	TYR	2.1
3	B9	102	GLY	2.1
3	E8	150	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
3	F8	102	GLY	2.1
3	V9	172	TYR	2.1
3	C9	63	PRO	2.1
3	I8	171	PRO	2.1
3	N9	81	ASP	2.1
3	T9	44	PRO	2.1
3	V8	188	ASP	2.1
3	W9	39	TRP	2.1
3	38	106	PRO	2.1
2	N2	69	GLU	2.1
2	Q2	30	GLU	2.1
2	U4	69	GLU	2.1
2	V3	69	GLU	2.1
2	Y5	57	GLU	2.1
3	A9	110	THR	2.1
3	I8	159	GLU	2.1
3	J9	97	GLU	2.1
3	K9	101	GLU	2.1
3	K9	118	GLU	2.1
3	M9	7	THR	2.1
3	Q9	157	GLU	2.1
3	Z8	20	THR	2.1
3	Z9	159	GLU	2.1
3	49	144	GLU	2.1
3	D9	127	ARG	2.1
3	H8	27	ARG	2.1
3	Q8	199	ARG	2.1
3	Q9	99	ARG	2.1
3	B8	46	ILE	2.1
3	G9	124	ILE	2.1
1	G1	49	ALA	2.1
3	A9	189	ALA	2.1
3	B9	181	ALA	2.1
3	C8	47	ALA	2.1
3	D9	13	ALA	2.1
3	E9	47	ALA	2.1
3	E9	197	ALA	2.1
3	F8	119	ALA	2.1
3	F9	90	SER	2.1
3	M8	205	ALA	2.1
3	N9	162	ALA	2.1
3	Q9	55	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
3	R9	190	ALA	2.1
3	W9	183	SER	2.1
3	X8	64	ALA	2.1
3	Y9	183	SER	2.1
3	29	202	SER	2.1
3	C9	130	GLN	2.1
1	N1	68	VAL	2.1
3	D9	49	ASN	2.1
3	F8	130	GLN	2.1
3	F8	135	LEU	2.1
3	G9	108	VAL	2.1
3	I8	40	VAL	2.1
3	J8	108	VAL	2.1
3	K8	49	ASN	2.1
3	V9	49	ASN	2.1
3	X9	66	GLN	2.1
3	Y8	146	GLN	2.1
3	Y9	121	GLN	2.1
3	49	112	GLN	2.1
3	N9	117	VAL	2.1
3	O8	38	LEU	2.1
3	W8	65	VAL	2.1
3	19	164	VAL	2.1
3	28	30	LEU	2.1
3	I9	109	MET	2.1
2	A6	39	GLY	2.0
3	28	34	GLY	2.0
3	K9	63	PRO	2.0
3	W9	106	PRO	2.0
3	W9	171	PRO	2.0
1	G1	45	ASP	2.0
2	I5	3	ASP	2.0
2	W5	3	ASP	2.0
2	H7	9	GLU	2.0
2	H7	58	GLU	2.0
2	W5	11	ARG	2.0
2	Y2	49	ASP	2.0
2	12	3	ASP	2.0
2	37	21	ASP	2.0
3	B8	27	ARG	2.0
3	D8	81	ASP	2.0
2	X3	58	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
3	D9	50	ARG	2.0
3	F8	138	GLU	2.0
3	F9	170	THR	2.0
3	F9	46	ILE	2.0
3	G9	95	LYS	2.0
3	I8	41	GLU	2.0
3	J9	4	THR	2.0
3	J9	157	GLU	2.0
3	K8	4	THR	2.0
3	C9	48	ILE	2.0
3	C9	134	ILE	2.0
3	D9	22	ILE	2.0
3	I8	46	ILE	2.0
3	K9	134	ILE	2.0
3	K9	159	GLU	2.0
3	P8	42	ILE	2.0
3	P9	184	GLU	2.0
3	R9	124	ILE	2.0
3	T8	157	GLU	2.0
3	T8	177	ARG	2.0
3	U8	118	GLU	2.0
3	U9	50	ARG	2.0
3	W9	177	ARG	2.0
3	W9	184	GLU	2.0
3	X8	4	THR	2.0
3	X9	41	GLU	2.0
3	38	7	THR	2.0
1	X1	23	SER	2.0
2	N4	2	ALA	2.0
2	P3	2	ALA	2.0
3	B9	37	SER	2.0
3	D8	64	ALA	2.0
3	J8	26	ALA	2.0
3	K9	193	ALA	2.0
3	M9	193	ALA	2.0
3	O9	36	ALA	2.0
3	O9	129	SER	2.0
3	V9	161	ALA	2.0
3	W9	154	ALA	2.0
3	Y9	189	ALA	2.0
3	Z9	36	ALA	2.0
3	19	37	SER	2.0

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Mol	Chain	Res	Type	RSRZ
3	29	36	ALA	2.0
3	A9	80	PHE	2.0
3	29	21	PHE	2.0
3	B8	201	VAL	2.0
3	L9	62	GLN	2.0
3	N8	108	VAL	2.0
3	N8	204	VAL	2.0
3	P9	65	VAL	2.0
3	R8	35	GLN	2.0
3	R9	68	VAL	2.0
3	T9	68	VAL	2.0
3	U9	117	VAL	2.0
3	19	77	VAL	2.0
3	39	66	GLN	2.0
3	L8	163	ASN	2.0
3	W8	49	ASN	2.0
3	R9	133	MET	2.0
1	P1	34	GLY	2.0
2	N7	68	GLY	2.0
2	U7	12	GLY	2.0
2	27	12	GLY	2.0
3	B8	28	GLY	2.0
3	I9	45	GLY	2.0
3	J9	182	GLY	2.0
3	X9	131	GLY	2.0
3	28	149	GLY	2.0
2	U7	62	ARG	2.0
3	E9	95	LYS	2.0
3	G8	115	ARG	2.0
3	I8	115	ARG	2.0
3	M9	50	ARG	2.0
3	N8	171	PRO	2.0
3	S8	16	PRO	2.0
3	S8	111	HIS	2.0
3	S9	103	ARG	2.0
3	V8	199	ARG	2.0
3	W8	6	ARG	2.0
3	W8	147	PRO	2.0
3	W9	124	ILE	2.0
3	X9	24	LYS	2.0
3	38	142	ILE	2.0
3	39	99	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
3	48	16	PRO	2.0
3	49	44	PRO	2.0
1	B1	37	THR	2.0
3	A9	91	THR	2.0
3	B9	59	THR	2.0
3	H8	4	THR	2.0
3	R9	122	THR	2.0
3	Z9	125	ILE	2.0
3	49	170	THR	2.0
1	K1	90	ASP	2.0
2	E6	9	GLU	2.0
2	F3	58	GLU	2.0
2	O5	69	GLU	2.0
2	Q7	9	GLU	2.0
2	37	9	GLU	2.0
3	C9	144	GLU	2.0
3	E9	84	GLU	2.0
3	F9	195	GLU	2.0
3	J9	192	GLU	2.0
3	N8	138	GLU	2.0
3	O8	76	GLU	2.0
3	P8	94	ASP	2.0
3	P9	159	GLU	2.0
3	S9	94	ASP	2.0
3	V8	76	GLU	2.0
3	Y9	76	GLU	2.0
3	Y9	97	GLU	2.0
3	48	41	GLU	2.0
2	F7	2	ALA	2.0
2	K2	2	ALA	2.0
2	W4	2	ALA	2.0
3	A9	139	SER	2.0
3	B8	175	PHE	2.0
3	D9	90	SER	2.0
3	D9	162	ALA	2.0
3	G8	54	ALA	2.0
3	H9	56	LEU	2.0
3	K8	135	LEU	2.0
3	M9	90	SER	2.0
3	O9	200	SER	2.0
3	Q9	80	PHE	2.0
3	U8	26	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
3	V9	196	ALA	2.0
3	X9	71	ALA	2.0
3	Z8	197	ALA	2.0
3	19	161	ALA	2.0
3	29	29	PHE	2.0
3	38	86	LEU	2.0
3	39	56	LEU	2.0
1	I1	68	VAL	2.0
2	R6	67	VAL	2.0
3	A8	15	GLN	2.0
3	D9	204	VAL	2.0
3	G8	152	VAL	2.0
3	M8	35	GLN	2.0
3	T9	82	GLN	2.0
3	T9	108	VAL	2.0
3	V9	107	GLN	2.0
3	X9	15	GLN	2.0
3	28	62	GLN	2.0
3	39	68	VAL	2.0
3	39	201	VAL	2.0
3	49	35	GLN	2.0
3	C9	133	MET	2.0
3	Y9	133	MET	2.0
3	B8	128	ASN	2.0
3	J9	126	ASN	2.0
1	J1	52	GLY	2.0
2	S5	94	GLY	2.0
3	C9	70	ARG	2.0
3	D8	8	TYR	2.0
3	F8	177	ARG	2.0
3	F9	124	ILE	2.0
3	I9	120	TYR	2.0
3	J9	46	ILE	2.0
3	L9	8	TYR	2.0
3	L9	127	ARG	2.0
3	N8	99	ARG	2.0
3	T8	24	LYS	2.0
3	U8	60	LYS	2.0
3	V9	131	GLY	2.0
3	R8	147	PRO	2.0
3	S9	22	ILE	2.0
3	Y9	125	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
3	19	3	ILE	2.0
3	48	42	ILE	2.0
3	I9	79	HIS	2.0
3	T9	59	THR	2.0
3	V8	110	THR	2.0
3	X8	111	HIS	2.0
3	49	7	THR	2.0
1	M1	86	GLU	2.0
2	K3	69	GLU	2.0
2	Q2	58	GLU	2.0
2	R6	58	GLU	2.0
2	V2	9	GLU	2.0
2	Z4	58	GLU	2.0
2	36	58	GLU	2.0
1	I1	83	ASP	2.0
3	D8	104	LEU	2.0
3	D8	135	LEU	2.0
3	H8	104	LEU	2.0
3	I9	21	PHE	2.0
3	M9	29	PHE	2.0
3	M9	195	GLU	2.0
3	O9	41	GLU	2.0
3	O9	101	GLU	2.0
3	O9	157	GLU	2.0
3	O9	175	PHE	2.0
3	P8	104	LEU	2.0
3	V8	101	GLU	2.0
3	V9	184	GLU	2.0
3	Y9	195	GLU	2.0
3	E9	81	ASP	2.0
3	F8	129	SER	2.0
3	F9	191	ALA	2.0
3	G8	129	SER	2.0
3	H9	87	ALA	2.0
3	N9	158	ALA	2.0
3	P9	139	SER	2.0
3	P9	202	SER	2.0
3	W9	37	SER	2.0
3	18	12	ASP	2.0
3	18	94	ASP	2.0
3	18	183	SER	2.0
3	19	90	SER	2.0

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Mol	Chain	Res	Type	RSRZ
3	19	191	ALA	2.0
3	38	129	SER	2.0
3	39	196	ALA	2.0
3	I8	108	VAL	2.0
3	K9	152	VAL	2.0
3	L9	167	VAL	2.0
3	V9	67	VAL	2.0
3	X8	61	VAL	2.0
3	29	164	VAL	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.